



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number 156807**

**TO: Elizabeth McElwain**  
**Location: REM/2A11/2C18**  
**Art Unit: 1638**  
**Friday, June 10, 2005**

**Case Serial Number: 10/029756**

**From: Toby Port**

**Location: Biotech-Chem Library**  
**REM1-A59**

**Phone: 272-2523**

**[toby.port@uspto.gov](mailto:toby.port@uspto.gov)**

### **Search Notes**

Dear Examiner McElwain,

Here are the results of your search. Please note in the sequence files, we don't limit by date. If you'd like this run as an STN search, please let me know.

Please feel free to contact me if you have any questions.

Toby Port

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STIC-Biotech/ChemLib

155007

From: McElwain, Elizabeth  
Sent: Tuesday, May 31, 2005 4:26 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Please search 10/029,756 - for DNA encoding any of SEQ ID NO: 6, 12 or 20  
Good dates would be prior to 1/28/1997.

Thank you,  
Beth

Elizabeth F. McElwain, Ph.D.  
U.S. Patent and Trademark Office  
Tech Center 1600, Art Unit 1638  
room Remsen 2A11  
mailbox Remsen 2C18  
571-272-0802  
elizabeth.mcelwain@uspto.gov

STIC  
MAY 31 2005  
(610)

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Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
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Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 11:36:25 ; Search time 122.105 Seconds

(without alignments)  
107.204 Million cell updates/sec

Title: US-10-029-756-6

Perfect score: 53

Sequence: 1 WIGHDAGH 8

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool\_p/US10029756/runat\_07062005\_122751\_28805/app.query.fasta\_1.597  
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCUI=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=1000 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10029756@cgn 1 1 177 @runat 07062005\_122751\_28805 -NCPUI=6 -ICPU=3  
-NO WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*

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5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	1684	2	US-08-831-570-1
2	53	100.0	1684	2	US-08-831-575-1
3	53	100.0	1685	1	US-08-366-779-4
4	53	100.0	1685	1	US-08-789-936-4
5	53	100.0	1685	3	US-08-934-254-4
6	53	100.0	1685	4	US-09-685-775-4
7	44	83.0	162	4	US-09-270-767-29759
8	44	83.0	833	4	US-09-270-767-13737
9	42.5	80.2	1152	4	US-09-252-991A-5494
10	42	79.2	601	4	US-09-949-016-21341
11	42	79.2	601	4	US-09-949-016-36968
12	42	79.2	601	4	US-09-949-016-46094

13	42	79.2	601	4	US-09-949-016-74333	Sequence 74333, A
C 14	42	79.2	601	4	US-09-949-016-183604	Sequence 183604, A
C 15	42	79.2	650	4	US-09-669-751-180	Sequence 183604, App
C 16	42	79.2	760	4	US-09-949-016-1322	Sequence 1322, Ap
C 17	42	79.2	816	4	US-09-270-767-13129	Sequence 13129, A
C 18	42	79.2	2238	4	US-09-673-395A-136	Sequence 136, App
C 19	42	79.2	2307	2	US-08-967-101-28	Sequence 28, Appl
C 20	42	79.2	2307	2	US-08-592-541-28	Sequence 28, Appl
C 21	42	79.2	2307	3	US-09-124-698-28	Sequence 28, Appl
C 22	42	79.2	2307	3	US-09-127-480-28	Sequence 28, Appl
C 23	42	79.2	2307	3	US-08-496-841C-28	Sequence 28, Appl
C 24	42	79.2	2307	3	US-09-124-523-28	Sequence 28, Appl
C 25	42	79.2	2307	4	US-08-636-796A-28	Sequence 28, Appl
C 26	42	79.2	2307	4	US-08-431-048F-28	Sequence 28, Appl
C 27	42	79.2	3050	4	US-09-949-016-973	Sequence 973, App
C 28	42	79.2	3144	4	US-09-620-312D-1097	Sequence 1097, Ap
C 29	42	79.2	28556	4	US-09-949-016-13064	Sequence 13064, A
C 30	42	79.2	40037	4	US-09-949-016-12715	Sequence 12715, A
C 31	42	79.2	84761	4	US-09-949-016-11919	Sequence 11919, A
C 32	42	79.2	84763	4	US-09-949-016-13914	Sequence 13914, A
C 33	42	79.2	205163	4	US-09-949-016-17009	Sequence 17009, A
C 34	42	77.4	2463	4	US-09-583-110-1558	Sequence 1558, Ap
C 35	41	77.4	2466	1	US-09-377-465A-1	Sequence 1, Appli
C 36	41	77.4	2466	1	US-09-377-465A-3	Sequence 3, Appli
C 37	41	77.4	2505	4	US-09-107-433-2157	Sequence 2157, Ap
C 38	41	77.4	4965	3	US-08-961-527-143	Sequence 143, App
C 39	41	77.4	5095	1	US-08-092-817-3	Sequence 3, Appli
C 40	41	77.4	5095	3	US-08-485-128-3	Sequence 3, Appli
C 41	41	77.4	5095	4	US-09-824-637-3	Sequence 3, Appli
C 42	41	77.4	46499	4	US-09-949-016-14032	Sequence 14032, A
C 43	41	77.4	119930	4	US-09-949-016-12677	Sequence 12677, A
C 44	41	77.4	119931	4	US-09-949-016-16319	Sequence 16319, A
C 45	41	77.4	125536	4	US-09-949-016-14186	Sequence 14186, A
C 46	40	75.5	828	4	US-09-107-433-2018	Sequence 2018, Ap
C 47	40	75.5	945	4	US-09-583-110-2134	Sequence 2134, Ap
C 48	40	75.5	1460	4	US-09-569-771B-20	Sequence 20, Appl
C 49	40	75.5	1702	3	US-08-934-254-26	Sequence 26, Appl
C 50	40	75.5	1702	4	US-09-685-775-26	Sequence 26, Appl
C 51	40	75.5	1702	4	US-09-902-540-67	Sequence 67, App
C 52	40	75.5	6827	3	US-08-961-527-60	Sequence 60, Appl
C 53	40	75.5	11382	4	US-09-902-540-904	Sequence 904, App
C 54	40	75.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 55	40	75.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 56	39.5	74.5	8521	4	US-09-949-016-12800	Sequence 12800, A
C 57	39.5	74.5	13117	4	US-09-949-016-15804	Sequence 15804, A
C 58	39	73.6	415	4	US-09-513-999C-8520	Sequence 8520, Ap
C 59	39	73.6	600	4	US-09-902-540-6391	Sequence 6391, Ap
C 60	39	73.6	1644	4	US-09-949-016-1172	Sequence 1172, Ap
C 61	39	73.6	1788	4	US-09-902-540-8493	Sequence 8493, Ap
C 62	39	73.6	1950	4	US-09-614-891-2	Sequence 2, Appli
C 63	39	73.6	2380	4	US-08-635-130A-3	Sequence 3, Appli
C 64	39	73.6	2501	4	US-09-614-891-3	Sequence 3, Appli
C 65	39	73.6	2993	4	US-09-949-016-5096	Sequence 5096, Ap
C 66	39	73.6	3394	4	US-09-949-016-205	Sequence 205, App
C 67	39	73.6	3394	4	US-09-902-540-894	Sequence 894, App
C 68	39	73.6	7538	4	US-09-949-016-16838	Sequence 16838, A
C 69	39	73.6	9948	4	US-09-949-016-12914	Sequence 12914, A
C 70	39	73.6	10367	4	US-09-949-016-1048	Sequence 1048, Ap
C 71	39	73.6	12865	4	US-09-902-540-13343	Sequence 13343, A
C 72	39	73.6	18955	4	US-09-949-016-16788	Sequence 16788, A
C 73	39	73.6	29905	4	US-09-949-016-13610	Sequence 13610, A
C 74	39	73.6	30678	4	US-09-949-016-12818	Sequence 12818, A
C 75	39	73.6	83428	4	US-09-949-016-13610	Sequence 13610, A
C 76	39	73.6	121049	4	US-09-949-016-17513	Sequence 17513, A
C 77	39	73.6	536165	4	US-09-214-808-1	Sequence 1, Appli
C 78	38	71.7	187	4	US-09-513-999C-2339	Sequence 2339, Ap
C 79	38	71.7	348	4	US-09-252-991A-4689	Sequence 4689, Ap
C 80	38	71.7	371	4	US-09-621-976-15096	Sequence 15096, A
C 81	38	71.7	379	4	US-09-854-133-354	Sequence 354, App
C 82	38	71.7	405	2	US-08-125-462-4	Sequence 4, Appli
C 83	38	71.7	405	2	US-08-891-848-4	Sequence 4, Appli
C 84	38	71.7	436	4	US-09-621-976-19010	Sequence 19010, A
C 85	38	71.7	459	4	US-09-513-999C-12630	Sequence 12630, A

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87	38	71.7	601	4	US-09-949-016-143643	Sequence 143643, A	c 160	38	71.7	51621	4	US-09-949-016-16503	Sequence 16503, A
88	38	71.7	601	4	US-09-949-016-143644	Sequence 143644, A	c 161	38	71.7	60304	4	US-09-949-016-12218	Sequence 12218, A
c 89	38	71.7	601	4	US-09-949-016-171125	Sequence 171125, A	c 162	38	71.7	60305	4	US-09-949-016-15791	Sequence 15791, A
c 90	38	71.7	601	4	US-09-949-016-171126	Sequence 171126, A	c 163	38	71.7	97989	4	US-09-949-016-13268	Sequence 13268, A
c 91	38	71.7	601	4	US-09-949-016-171255	Sequence 171255, A	c 164	38	71.7	110243	4	US-09-949-016-13698	Sequence 13698, A
c 92	38	71.7	601	4	US-09-949-016-171256	Sequence 171256, A	c 165	38	71.7	112507	4	US-09-949-016-12420	Sequence 12420, A
c 93	38	71.7	601	4	US-09-949-016-179881	Sequence 179881, A	c 166	38	71.7	112507	4	US-09-949-016-12794	Sequence 12794, A
c 94	38	71.7	601	4	US-09-949-016-200124	Sequence 200124, A	c 167	38	71.7	112508	4	US-09-949-016-16589	Sequence 16589, A
c 95	38	71.7	601	4	US-09-949-016-205533	Sequence 205533, A	c 168	38	71.7	112508	4	US-09-949-016-16590	Sequence 16590, A
c 96	38	71.7	603	4	US-09-543-681A-1128	Sequence 1128, Ap	c 169	38	71.7	128723	4	US-09-949-016-17533	Sequence 17533, A
c 97	38	71.7	624	4	US-09-252-991A-4810	Sequence 4810, Ap	c 170	38	71.7	156942	4	US-09-949-016-12227	Sequence 12227, A
c 98	38	71.7	699	4	US-09-252-991A-7908	Sequence 7908, Ap	c 171	38	71.7	156950	4	US-09-949-016-15946	Sequence 15946, A
c 99	38	71.7	737	4	US-09-270-767-11527	Sequence 11527, A	c 172	38	71.7	177293	4	US-09-949-016-16513	Sequence 16513, A
c 100	38	71.7	753	4	US-09-902-540-5908	Sequence 5908, Ap	c 173	38	71.7	271134	4	US-09-949-016-12705	Sequence 12705, A
c 101	38	71.7	771	4	US-09-902-540-7200	Sequence 7200, Ap	c 174	38	71.7	275110	4	US-09-949-016-12706	Sequence 12706, A
c 102	38	71.7	834	4	US-09-252-991A-7643	Sequence 7643, Ap	c 175	38	71.7	275110	4	US-09-949-016-16070	Sequence 16070, A
c 103	38	71.7	894	4	US-09-252-991A-7841	Sequence 7841, Ap	c 176	38	71.7	305491	4	US-09-949-016-17550	Sequence 17550, A
c 104	38	71.7	1050	4	US-09-949-016-3035	Sequence 3035, Ap	c 177	38	71.7	330416	4	US-09-949-016-16923	Sequence 16923, A
c 105	38	71.7	1176	4	US-09-252-991A-7571	Sequence 7571, Ap	c 178	38	71.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 106	38	71.7	1197	3	US-08-494-921-1	Sequence 1, Appli	c 179	38	71.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 107	38	71.7	1197	3	US-09-494-921-28	Sequence 28, Appl	c 180	37.5	70.8	3581	4	US-09-949-016-4965	Sequence 4965, Ap
c 108	38	71.7	1197	3	US-09-494-921-29	Sequence 29, Appl	c 181	37.5	70.8	25559	4	US-09-949-016-16707	Sequence 16707, A
c 109	38	71.7	1197	4	US-09-734-237B-1	Sequence 1, Appli	c 182	37.5	70.8	177797	4	US-09-949-016-14125	Sequence 14125, A
c 110	38	71.7	1197	4	US-09-734-237B-28	Sequence 28, Appl	c 183	37.5	70.8	227979	4	US-09-949-016-11842	Sequence 11842, A
c 111	38	71.7	1197	4	US-09-734-237B-29	Sequence 29, Appl	c 184	37.5	70.8	312957	4	US-09-949-001-31	Sequence 31, Appl
c 112	38	71.7	1299	2	US-08-125-462-6	Sequence 6, Appli	c 185	37.5	70.8	312972	4	US-09-949-001-34	Sequence 34, Appl
c 113	38	71.7	1299	2	US-08-891-848-6	Sequence 6, Appli	c 186	37	69.8	55	5	FCT-US92-1002A-20	Sequence 20, Appl
c 114	38	71.7	1320	2	US-08-641-038A-1	Sequence 1, Appli	c 187	37	69.8	259	3	US-09-172-108-35	Sequence 35, Appl
c 115	38	71.7	1320	2	US-09-059-178-1	Sequence 1, Appli	c 188	37	69.8	259	3	US-09-172-711-33	Sequence 33, Appl
c 116	38	71.7	1356	4	US-09-902-540-171	Sequence 171, App	c 189	37	69.8	280	4	US-09-313-294A-5391	Sequence 5391, Ap
c 117	38	71.7	1369	2	US-08-642-541-1	Sequence 1, Appli	c 190	37	69.8	304	3	US-09-439-261-4	Sequence 4, Appli
c 118	38	71.7	1369	2	US-08-642-541-3	Sequence 3, Appli	c 191	37	69.8	304	3	US-09-227-613-4	Sequence 4, Appli
c 119	38	71.7	1369	3	US-09-260-889-1	Sequence 1, Appli	c 192	37	69.8	350	1	US-08-263-413-12	Sequence 12, Appl
c 120	38	71.7	1369	3	US-09-260-889-3	Sequence 3, Appli	c 193	37	69.8	392	4	US-09-402-532-23	Sequence 23, Appl
c 121	38	71.7	1369	3	US-09-347-878-11	Sequence 11, Appli	c 194	37	69.8	411	1	US-07-650-795A-3	Sequence 3, Appli
c 122	38	71.7	1369	3	US-09-479-275-6	Sequence 6, Appli	c 195	37	69.8	455	4	US-09-513-999C-11089	Sequence 11089, A
c 123	38	71.7	1417	4	US-09-904-615-31	Sequence 31, Appl	c 196	37	69.8	601	4	US-09-949-016-28975	Sequence 28975, A
c 124	38	71.7	2316	4	US-08-252-991A-6950	Sequence 6950, Ap	c 197	37	69.8	601	4	US-09-949-016-28976	Sequence 28976, A
c 125	38	71.7	3016	3	US-08-971-188-2	Sequence 2, Appli	c 198	37	69.8	601	4	US-09-949-016-49966	Sequence 49966, A
c 126	38	71.7	3171	4	US-09-016-434-1348	Sequence 1348, Ap	c 199	37	69.8	601	4	US-09-949-016-49967	Sequence 49967, A
c 127	38	71.7	3219	4	US-09-895-652A-17	Sequence 17, Appl	c 200	37	69.8	601	4	US-09-949-016-69688	Sequence 69688, A
c 128	38	71.7	3282	3	US-08-971-188-3	Sequence 3, Appli	c 201	37	69.8	601	4	US-09-949-016-76312	Sequence 76312, A
c 129	38	71.7	4112	4	US-09-799-451-706	Sequence 706, App	c 202	37	69.8	601	4	US-09-949-016-89845	Sequence 89845, A
c 130	38	71.7	4494	4	US-08-620-312D-861	Sequence 861, App	c 203	37	69.8	601	4	US-09-949-016-117017	Sequence 117017, A
c 131	38	71.7	4498	4	US-09-949-016-17059	Sequence 17059, A	c 204	37	69.8	601	4	US-09-949-016-119238	Sequence 119238, A
c 132	38	71.7	4615	1	US-08-180-582-1	Sequence 1, Appli	c 205	37	69.8	601	4	US-09-949-016-119239	Sequence 119239, A
c 133	38	71.7	5140	3	US-08-646-715-1	Sequence 1, Appli	c 206	37	69.8	601	4	US-09-949-016-119240	Sequence 119240, A
c 134	38	71.7	6230	3	US-08-971-188-1	Sequence 1, Appli	c 207	37	69.8	601	4	US-09-949-016-172552	Sequence 172552, A
c 135	38	71.7	6230	3	US-08-902-540-569	Sequence 569, App	c 208	37	69.8	601	4	US-09-949-016-176854	Sequence 176854, A
c 136	38	71.7	6756	1	US-08-151-574-31	Sequence 31, Appl	c 209	37	69.8	601	4	US-09-949-016-179801	Sequence 179801, A
c 137	38	71.7	6756	1	US-08-419-448-31	Sequence 31, Appl	c 210	37	69.8	604	4	US-09-774-528-233	Sequence 233, App
c 138	38	71.7	6756	2	US-09-233-510-31	Sequence 31, Appl	c 211	37	69.8	699	4	US-09-252-991A-10959	Sequence 10959, A
c 139	38	71.7	6756	3	US-09-419-448-31	Sequence 31, Appl	c 212	37	69.8	816	4	US-09-461-912A-12	Sequence 12, Appl
c 140	38	71.7	6799	2	US-08-125-462-5	Sequence 5, Appli	c 213	37	69.8	816	4	US-09-461-912A-30	Sequence 30, Appl
c 141	38	71.7	6799	2	US-08-891-848-5	Sequence 5, Appli	c 214	37	69.8	828	3	US-09-149-476-303	Sequence 303, App
c 142	38	71.7	7080	3	US-09-380-190A-21	Sequence 21, Appl	c 215	37	69.8	831	4	US-09-252-991A-11166	Sequence 11166, A
c 143	38	71.7	9932	4	US-09-949-016-16727	Sequence 16727, A	c 216	37	69.8	864	3	US-09-439-261-12	Sequence 12, Appl
c 144	38	71.7	15027	4	US-09-949-016-12660	Sequence 12660, A	c 217	37	69.8	864	3	US-09-227-613-13	Sequence 13, Appl
c 145	38	71.7	15036	4	US-09-949-016-13351	Sequence 13351, A	c 218	37	69.8	918	3	US-09-439-261-5	Sequence 5, Appli
c 146	38	71.7	16438	4	US-09-949-016-16165	Sequence 16165, A	c 219	37	69.8	918	3	US-09-227-613-5	Sequence 5, Appli
c 147	38	71.7	18037	4	US-09-949-016-13678	Sequence 13678, A	c 220	37	69.8	960	3	US-09-439-261-36	Sequence 36, Appl
c 148	38	71.7	22339	4	US-09-949-016-14777	Sequence 14777, A	c 221	37	69.8	960	3	US-09-227-613-35	Sequence 35, Appl
c 149	38	71.7	23193	4	US-09-949-016-17215	Sequence 17215, A	c 222	37	69.8	960	4	US-09-270-767-7794	Sequence 7794, Ap
c 150	38	71.7	23496	4	US-09-902-540-5645	Sequence 5645, Ap	c 223	37	69.8	960	4	US-09-270-767-23076	Sequence 23076, A
c 151	38	71.7	30001	1	US-08-125-468-1	Sequence 1, Appli	c 224	37	69.8	966	4	US-09-894-844-72	Sequence 72, Appl
c 152	38	71.7	30068	4	US-08-474-933-1	Sequence 1, Appli	c 225	37	69.8	972	4	US-09-949-016-2218	Sequence 2218, Ap
c 153	38	71.7	37068	4	US-09-949-016-12543	Sequence 12543, A	c 226	37	69.8	990	3	US-09-439-261-35	Sequence 35, Appl
c 154	38	71.7	44353	4	US-09-949-016-17376	Sequence 17376, A	c 227	37	69.8	990	3	US-09-227-613-34	Sequence 34, Appl
c 155	38	71.7	45427	4	US-09-949-016-15302	Sequence 15302, A	c 228	37	69.8	995	3	US-08-484-841A-5	Sequence 5, Appli
c 156	38	71.7	47698	4	US-09-949-016-16243	Sequence 16243, A	c 229	37	69.8	1137	4	US-09-402-532-12	Sequence 12, Appl
c 157	38	71.7	51354	4	US-09-949-016-13514	Sequence 13514, A	c 230	37	69.8	1146	4	US-09-402-532-15	Sequence 15, Appl
c 158	38	71.7	51354	4	US-09-902-540-1270	Sequence 1270, Ap	c 231	37	69.8	1233	4	US-09-402-532-13	Sequence 13, Appl

232	37	69.8	1236	4	US-09-402-532-17	Sequence 17, Appl	C 305	36	67.9	325	4	US-09-614-124B-1202	Sequence 1202, Ap
233	37	69.8	1242	4	US-09-402-532-16	Sequence 16, Appl	C 306	36	67.9	325	4	US-09-671-325-1202	Sequence 1202, Ap
234	37	69.8	1332	4	US-09-402-532-18	Sequence 18, Appl	C 307	36	67.9	325	4	US-09-658-824-1202	Sequence 1202, Ap
235	37	69.8	1335	3	US-09-439-261-1	Sequence 1, Appl	C 308	36	67.9	426	3	US-09-072-596-241	Sequence 241, App
236	37	69.8	1335	3	US-09-227-613-1	Sequence 1, Appl	C 309	36	67.9	426	3	US-09-072-967-246	Sequence 246, App
237	37	69.8	1383	1	US-07-874-848B-3	Sequence 3, Appl	C 310	36	67.9	472	2	US-08-244-205-16	Sequence 16, Appl
238	37	69.8	1448	4	US-09-903-840A-16	Sequence 416, App	C 311	36	67.9	472	5	PCT-US92-10284-16	Sequence 16, Appl
239	37	69.8	1550	4	US-09-023-655-101	Sequence 101, App	C 312	36	67.9	474	4	US-09-902-540-1884	Sequence 1884, Ap
240	37	69.8	1580	4	US-09-573-080A-147	Sequence 147, App	C 313	36	67.9	478	4	US-09-270-767-3656	Sequence 3656, Ap
241	37	69.8	1843	3	US-09-439-261-7	Sequence 7, Appl	C 314	36	67.9	478	4	US-09-270-767-18938	Sequence 18938, A
242	37	69.8	1843	3	US-09-227-613-7	Sequence 7, Appl	C 315	36	67.9	537	4	US-09-252-991A-1106	Sequence 1106, Ap
243	37	69.8	1843	4	US-09-048-888-4	Sequence 4, Appl	C 316	36	67.9	540	4	US-09-023-655-1384	Sequence 1384, Ap
244	37	69.8	1940	4	US-09-620-312D-980	Sequence 980, App	C 317	36	67.9	601	4	US-09-949-016-28733	Sequence 28733, A
245	37	69.8	1975	3	US-09-130-616-175	Sequence 175, App	C 318	36	67.9	601	4	US-09-949-016-28734	Sequence 28734, A
246	37	69.8	2257	3	US-09-439-261-8	Sequence 8, Appl	C 319	36	67.9	601	4	US-09-949-016-70718	Sequence 70718, A
247	37	69.8	2257	3	US-09-227-613-8	Sequence 8, Appl	C 320	36	67.9	601	4	US-09-949-016-77727	Sequence 77727, A
248	37	69.8	2620	4	US-09-270-767-14652	Sequence 14652, A	C 321	36	67.9	601	4	US-09-949-016-77728	Sequence 77728, A
249	37	69.8	2687	4	US-09-489-847-57	Sequence 57, Appl	C 322	36	67.9	601	4	US-09-949-016-103458	Sequence 103458, A
250	37	69.8	3158	4	US-09-949-016-1613	Sequence 4613, App	C 323	36	67.9	601	4	US-09-949-016-120619	Sequence 120619, A
251	37	69.8	3173	3	US-09-149-416-174	Sequence 174, App	C 324	36	67.9	601	4	US-09-949-016-130375	Sequence 130375, A
252	37	69.8	3296	4	US-09-949-016-1456	Sequence 1456, App	C 325	36	67.9	601	4	US-09-949-016-167941	Sequence 167941, A
253	37	69.8	3299	4	US-09-949-016-557	Sequence 557, App	C 326	36	67.9	729	4	US-09-489-039A-4962	Sequence 4962, Ap
254	37	69.8	5483	4	US-09-949-016-61	Sequence 61, Appl	C 327	36	67.9	750	4	US-09-902-540-5834	Sequence 5834, Ap
255	37	69.8	5487	4	US-09-949-016-4997	Sequence 4997, App	C 328	36	67.9	771	4	US-09-583-110-2399	Sequence 2399, Ap
256	37	69.8	5599	2	US-08-477-451-9	Sequence 9, Appl	C 329	36	67.9	801	4	US-09-252-991A-1075	Sequence 1075, Ap
257	37	69.8	5599	2	US-08-477-451-13	Sequence 13, Appl	C 330	36	67.9	866	4	US-09-620-312D-682	Sequence 682, App
258	37	69.8	6608	4	US-09-949-016-13960	Sequence 13960, A	C 331	36	67.9	930	4	US-09-107-433-464	Sequence 464, App
259	37	69.8	7710	4	US-09-949-016-738	Sequence 738, App	C 332	36	67.9	946	4	US-09-904-615-24	Sequence 24, Appl
260	37	69.8	8242	4	US-09-949-016-4620	Sequence 4620, App	C 333	36	67.9	963	4	US-09-248-796A-3965	Sequence 3965, Ap
261	37	69.8	8252	1	US-08-046-585-15	Sequence 15, Appl	C 334	36	67.9	984	4	US-09-489-039A-890	Sequence 890, App
262	37	69.8	8252	1	US-08-393-703-15	Sequence 15, Appl	C 335	36	67.9	1143	4	US-09-252-991A-1032	Sequence 1032, Ap
263	37	69.8	8252	5	PCT-US93-11721-15	Sequence 15, Appl	C 336	36	67.9	1257	4	US-09-489-039A-1557	Sequence 1557, Ap
264	37	69.8	12061	4	US-08-477-451-25	Sequence 25, Appl	C 337	36	67.9	1341	4	US-09-372-425A-7	Sequence 7, Appl
265	37	69.8	19332	2	US-09-949-016-16134	Sequence 16134, A	C 338	36	67.9	1350	2	US-08-244-205-1	Sequence 1, Appl
266	37	69.8	21170	4	US-09-949-016-12480	Sequence 12480, A	C 339	36	67.9	1350	5	PCT-US92-10284-1	Sequence 1, Appl
267	37	69.8	2166	4	US-09-949-016-16072	Sequence 16072, A	C 340	36	67.9	1353	3	US-09-330-235-7	Sequence 7, Appl
268	37	69.8	2630	4	US-09-949-016-16362	Sequence 16362, A	C 341	36	67.9	1353	5	PCT-US94-01321-1	Sequence 1, Appl
269	37	69.8	37475	4	US-09-949-016-12299	Sequence 12299, A	C 342	36	67.9	1369	4	US-09-205-258-174	Sequence 174, App
270	37	69.8	37492	4	US-09-949-016-13198	Sequence 13198, A	C 343	36	67.9	1410	4	US-09-489-039A-1920	Sequence 1920, Ap
271	37	69.8	40512	4	US-09-949-016-16612	Sequence 16612, A	C 344	36	67.9	1410	4	US-09-489-039A-1936	Sequence 1936, Ap
272	37	69.8	43102	4	US-09-949-016-16615	Sequence 16615, A	C 345	36	67.9	1429	2	US-08-244-205-6	Sequence 6, Appl
273	37	69.8	4727	4	US-09-949-016-12904	Sequence 12904, A	C 346	36	67.9	1429	2	US-08-244-205-8	Sequence 8, Appl
274	37	69.8	49301	4	US-09-949-016-16296	Sequence 16296, A	C 347	36	67.9	1429	5	PCT-US92-10284-6	Sequence 6, Appl
275	37	69.8	53789	4	US-09-949-016-12130	Sequence 12130, A	C 348	36	67.9	1429	5	PCT-US92-10284-8	Sequence 8, Appl
276	37	69.8	53790	4	US-09-949-016-16641	Sequence 16641, A	C 349	36	67.9	1525	2	US-08-244-205-4	Sequence 4, Appl
277	37	69.8	53260	4	US-09-949-016-14298	Sequence 14298, A	C 350	36	67.9	1525	5	PCT-US92-10284-4	Sequence 4, Appl
278	37	69.8	57559	4	US-09-949-016-13077	Sequence 13077, A	C 351	36	67.9	1525	5	PCT-US94-01321-11	Sequence 11, Appl
279	37	69.8	57560	4	US-09-949-016-12536	Sequence 12536, A	C 352	36	67.9	1540	1	US-07-932-915-1	Sequence 1, Appl
280	37	69.8	60788	4	US-09-949-016-16789	Sequence 16789, A	C 353	36	67.9	1540	5	PCT-US91-05826-1	Sequence 1, Appl
281	37	69.8	61462	4	US-09-949-016-17522	Sequence 17522, A	C 354	36	67.9	1599	4	US-09-489-039A-1971	Sequence 1971, Ap
282	37	69.8	62728	4	US-09-949-016-12539	Sequence 12539, A	C 355	36	67.9	1645	5	PCT-US94-01321-9	Sequence 9, Appl
283	37	69.8	63129	4	US-09-949-016-16579	Sequence 16579, A	C 356	36	67.9	1675	2	US-08-244-205-12	Sequence 12, Appl
284	37	69.8	63213	4	US-09-949-016-11803	Sequence 11803, A	C 357	36	67.9	1675	5	PCT-US92-10284-12	Sequence 12, Appl
285	37	69.8	66213	4	US-09-949-016-16739	Sequence 16739, A	C 358	36	67.9	1776	4	US-09-495-050A-229	Sequence 229, App
286	37	69.8	68213	4	US-09-949-016-16739	Sequence 16739, A	C 359	36	67.9	1836	4	US-09-252-991A-1026	Sequence 1026, Ap
287	37	69.8	79595	4	US-09-949-016-15601	Sequence 15601, A	C 360	36	67.9	2001	3	US-09-341-587-2	Sequence 2, Appl
288	37	69.8	79634	4	US-09-949-016-15318	Sequence 15318, A	C 361	36	67.9	2169	4	US-09-489-039A-1771	Sequence 1771, Ap
289	37	69.8	84156	4	US-09-949-016-12388	Sequence 12388, A	C 362	36	67.9	2181	2	US-08-244-205-10	Sequence 10, Appl
290	37	69.8	98037	4	US-09-949-016-16623	Sequence 16623, A	C 363	36	67.9	2181	5	PCT-US92-10284-10	Sequence 10, Appl
291	37	69.8	102406	4	US-09-949-016-14673	Sequence 14673, A	C 364	36	67.9	2523	2	US-08-410-784A-3	Sequence 3, Appl
292	37	69.8	112623	4	US-09-949-016-14374	Sequence 14374, A	C 365	36	67.9	2674	4	US-09-372-425A-1	Sequence 1, Appl
293	37	69.8	123863	4	US-09-949-016-14374	Sequence 14374, A	C 366	36	67.9	2700	2	US-09-731-166-15	Sequence 15, Appl
294	37	69.8	135667	4	US-09-949-016-14202	Sequence 14202, A	C 367	36	67.9	2712	2	US-08-410-784A-1	Sequence 1, Appl
295	37	69.8	148794	4	US-09-949-016-15051	Sequence 15051, A	C 368	36	67.9	2905	4	US-09-976-594-1031	Sequence 1031, Ap
296	37	69.8	325034	4	US-09-949-016-14957	Sequence 14957, A	C 369	36	67.9	2905	4	US-09-919-039-381	Sequence 381, App
297	37	69.8	389504	4	US-09-949-016-11774	Sequence 11774, A	C 370	36	67.9	3195	4	US-09-252-991A-937	Sequence 937, App
298	37	69.8	767677	4	US-09-949-016-12147	Sequence 12147, A	C 371	36	67.9	3778	4	US-09-799-451-160	Sequence 160, App
299	37	69.8	767677	4	US-09-949-016-12147	Sequence 12147, A	C 372	36	67.9	4140	4	US-09-248-796A-6403	Sequence 6403, Ap
300	37	69.8	786431	4	US-09-751-389-3	Sequence 3, Appl	C 373	36	67.9	4360	1	US-08-470-350B-1	Sequence 1, Appl
301	36.5	68.9	107458	4	US-09-949-016-15687	Sequence 15687, A	C 374	36	67.9	5943	4	US-09-341-587-4	Sequence 4, Appl
302	36	67.9	266	4	US-09-016-434-424	Sequence 424, App	C 375	36	67.9	5943	4	US-09-976-594-272	Sequence 272, App
303	36	67.9	325	4	US-09-702-705-1202	Sequence 1202, Ap	C 376	36	67.9	5973	4	US-09-902-540-3951	Sequence 3951, Ap
304	36	67.9	325	4	US-09-736-457-1202	Sequence 1202, Ap	C 377	36	67.9	5992	4	US-09-949-016-546	Sequence 546, App

C 378	36	67.9	5992	4	US-09-949-016-2263	Sequence 2263, Ap	C 451	601	4	US-09-949-016-28118	Sequence 28118, A
C 379	36	67.9	6776	4	US-09-902-540-884	Sequence 884, App	C 452	601	4	US-09-949-016-69208	Sequence 69208, A
C 380	36	67.9	12078	4	US-09-799-451-835	Sequence 835, App	C 453	601	4	US-09-949-016-69209	Sequence 69209, A
C 381	36	67.9	12308	4	US-09-854-133-422	Sequence 422, App	C 454	601	4	US-09-949-016-69210	Sequence 69210, A
C 382	36	67.9	18627	3	US-08-961-527-113	Sequence 113, App	C 455	601	4	US-09-949-016-69210	Sequence 69210, A
C 383	36	67.9	19566	4	US-09-949-016-12096	Sequence 12096, A	C 456	601	4	US-09-949-016-74405	Sequence 74405, A
C 384	36	67.9	19567	4	US-09-949-016-14114	Sequence 14114, A	C 457	601	4	US-09-949-016-83529	Sequence 83529, A
C 385	36	67.9	20870	4	US-09-949-016-16017	Sequence 16017, A	C 458	601	4	US-09-949-016-85332	Sequence 85332, A
C 386	36	67.9	21360	4	US-09-949-016-12857	Sequence 12857, A	C 459	601	4	US-09-949-016-92668	Sequence 92668, A
C 387	36	67.9	21361	4	US-09-949-016-16245	Sequence 16245, A	C 460	601	4	US-09-949-016-92669	Sequence 92669, A
C 388	36	67.9	21920	4	US-09-949-016-15609	Sequence 15609, A	C 461	601	4	US-09-949-016-115233	Sequence 115233, A
C 389	36	67.9	22156	4	US-09-902-540-1195	Sequence 1195, Ap	C 462	601	4	US-09-949-016-115234	Sequence 115234, A
C 390	36	67.9	22339	4	US-09-949-016-14777	Sequence 14777, A	C 463	601	4	US-09-949-016-116738	Sequence 116738, A
C 391	36	67.9	28720	3	US-09-341-587-7	Sequence 7, Appli	C 464	601	4	US-09-949-016-116928	Sequence 116928, A
C 392	36	67.9	29598	3	US-09-341-587-6	Sequence 6, Appli	C 465	601	4	US-09-949-016-122594	Sequence 122594, A
C 393	36	67.9	35524	3	US-08-923-137-1	Sequence 1, Appli	C 466	601	4	US-09-949-016-153630	Sequence 153630, A
C 394	36	67.9	54420	4	US-09-949-016-15422	Sequence 15422, A	C 467	601	4	US-09-949-016-156172	Sequence 156172, A
C 395	36	67.9	63183	4	US-09-949-016-13047	Sequence 13047, A	C 468	601	4	US-09-949-016-164640	Sequence 164640, A
C 396	36	67.9	63183	4	US-09-949-016-13048	Sequence 13048, A	C 469	601	4	US-09-949-016-179055	Sequence 179055, A
C 397	36	67.9	66986	4	US-09-596-002-29	Sequence 29, Appl	C 470	601	4	US-09-949-016-179611	Sequence 179611, A
C 398	36	67.9	72704	4	US-09-902-540-1273	Sequence 1273, Ap	C 471	601	4	US-09-949-016-179612	Sequence 179612, A
C 399	36	67.9	76164	4	US-09-949-016-12288	Sequence 12288, A	C 472	601	4	US-09-949-016-184717	Sequence 184717, A
C 400	36	67.9	76165	4	US-09-949-016-14005	Sequence 14005, A	C 473	601	4	US-09-949-016-194510	Sequence 194510, A
C 401	36	67.9	78157	4	US-09-949-016-16466	Sequence 16466, A	C 474	601	4	US-09-949-016-194510	Sequence 194510, A
C 402	36	67.9	78157	4	US-09-949-016-16467	Sequence 16467, A	C 475	601	4	US-09-949-016-194510	Sequence 194510, A
C 403	36	67.9	100990	4	US-09-409-800B-2	Sequence 2, Appli	C 476	601	4	US-09-949-016-194510	Sequence 194510, A
C 404	36	67.9	108924	4	US-09-949-016-13834	Sequence 13834, A	C 477	601	4	US-09-949-016-194510	Sequence 194510, A
C 405	36	67.9	137226	4	US-09-949-016-13763	Sequence 13763, A	C 478	601	4	US-09-949-016-194510	Sequence 194510, A
C 406	36	67.9	141560	4	US-09-949-016-16476	Sequence 16476, A	C 479	601	4	US-09-949-016-194510	Sequence 194510, A
C 407	36	67.9	190078	4	US-09-949-016-12707	Sequence 12707, A	C 480	601	4	US-09-949-016-194510	Sequence 194510, A
C 408	36	67.9	190078	4	US-09-949-016-17026	Sequence 17026, A	C 481	601	4	US-09-949-016-194510	Sequence 194510, A
C 409	36	67.9	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 482	601	4	US-09-949-016-194510	Sequence 194510, A
C 410	36	67.9	193303	4	US-09-497-855A-44	Sequence 44, Appl	C 483	601	4	US-09-949-016-194510	Sequence 194510, A
C 411	36	67.9	205163	4	US-09-949-016-17009	Sequence 17009, A	C 484	601	4	US-09-949-016-194510	Sequence 194510, A
C 412	36	67.9	209210	4	US-09-949-016-15094	Sequence 15094, A	C 485	601	4	US-09-949-016-194510	Sequence 194510, A
C 413	36	67.9	250715	4	US-09-949-016-13294	Sequence 13294, A	C 486	601	4	US-09-949-016-194510	Sequence 194510, A
C 414	36	67.9	254405	4	US-09-949-016-14381	Sequence 14381, A	C 487	601	4	US-09-949-016-194510	Sequence 194510, A
C 415	36	67.9	256287	4	US-09-949-016-14608	Sequence 14608, A	C 488	601	4	US-09-949-016-194510	Sequence 194510, A
C 416	35.5	67.0	156	4	US-09-513-999C-18557	Sequence 18557, A	C 489	601	4	US-09-949-016-194510	Sequence 194510, A
C 417	35.5	67.0	601	4	US-09-949-016-81525	Sequence 81525, A	C 490	601	4	US-09-949-016-194510	Sequence 194510, A
C 418	35.5	67.0	857	4	US-09-270-767-28776	Sequence 28776, A	C 491	601	4	US-09-949-016-194510	Sequence 194510, A
C 419	35.5	67.0	1326	4	US-09-543-681A-846	Sequence 846, App	C 492	601	4	US-09-949-016-194510	Sequence 194510, A
C 420	35.5	67.0	1740	4	US-09-949-016-2873	Sequence 2873, Ap	C 493	601	4	US-09-949-016-194510	Sequence 194510, A
C 421	35.5	67.0	1767	4	US-09-949-016-49	Sequence 49, Appl	C 494	601	4	US-09-949-016-194510	Sequence 194510, A
C 422	35.5	67.0	2862	4	US-09-270-767-12914	Sequence 12914, A	C 495	601	4	US-09-949-016-194510	Sequence 194510, A
C 423	35.5	67.0	8801	4	US-09-949-016-11791	Sequence 11791, A	C 496	601	4	US-09-949-016-194510	Sequence 194510, A
C 424	35.5	67.0	8801	4	US-09-949-016-14615	Sequence 14615, A	C 497	601	4	US-09-949-016-194510	Sequence 194510, A
C 425	35.5	67.0	12880	4	US-09-949-016-16733	Sequence 16733, A	C 498	601	4	US-09-949-016-194510	Sequence 194510, A
C 426	35.5	67.0	19319	4	US-09-949-016-14107	Sequence 14107, A	C 499	601	4	US-09-949-016-194510	Sequence 194510, A
C 427	35.5	67.0	93778	4	US-09-949-016-15096	Sequence 15096, A	C 500	601	4	US-09-949-016-194510	Sequence 194510, A
C 428	35	66.0	28	4	US-08-559-306-27	Sequence 27, Appl	C 501	601	4	US-09-949-016-194510	Sequence 194510, A
C 429	35	66.0	47	3	US-09-338-907-261	Sequence 261, App	C 502	601	4	US-09-949-016-194510	Sequence 194510, A
C 430	35	66.0	47	3	US-09-218-207-261	Sequence 261, App	C 503	601	4	US-09-949-016-194510	Sequence 194510, A
C 431	35	66.0	183	4	US-09-248-796A-13029	Sequence 13029, A	C 504	601	4	US-09-949-016-194510	Sequence 194510, A
C 432	35	66.0	249	4	US-09-328-352-845	Sequence 845, App	C 505	601	4	US-09-949-016-194510	Sequence 194510, A
C 433	35	66.0	268	3	US-08-928-881-20	Sequence 20, Appl	C 506	601	4	US-09-949-016-194510	Sequence 194510, A
C 434	35	66.0	268	3	US-09-543-921-20	Sequence 20, Appl	C 507	601	4	US-09-949-016-194510	Sequence 194510, A
C 435	35	66.0	268	3	US-09-266-014-2	Sequence 2, Appli	C 508	601	4	US-09-949-016-194510	Sequence 194510, A
C 436	35	66.0	268	4	US-09-491-759-20	Sequence 20, Appl	C 509	601	4	US-09-949-016-194510	Sequence 194510, A
C 437	35	66.0	285	4	US-09-621-976-462	Sequence 462, App	C 510	601	4	US-09-949-016-194510	Sequence 194510, A
C 438	35	66.0	415	4	US-09-621-976-17129	Sequence 17129, A	C 511	601	4	US-09-949-016-194510	Sequence 194510, A
C 439	35	66.0	422	4	US-09-270-767-7856	Sequence 7856, Ap	C 512	601	4	US-09-949-016-194510	Sequence 194510, A
C 440	35	66.0	422	4	US-09-270-767-23138	Sequence 23138, A	C 513	601	4	US-09-949-016-194510	Sequence 194510, A
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C 443	35	66.0	465	4	US-09-229-583A-20	Sequence 20, Appl	C 516	601	4	US-09-949-016-194510	Sequence 194510, A
C 444	35	66.0	465	4	US-10-187-904-20	Sequence 20, Appl	C 517	601	4	US-09-949-016-194510	Sequence 194510, A
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C 446	35	66.0	492	4	US-09-603-208A-299	Sequence 299, App	C 519	601	4	US-09-949-016-194510	Sequence 194510, A
C 447	35	66.0	525	4	US-09-252-991A-5225	Sequence 5225, Ap	C 520	601	4	US-09-949-016-194510	Sequence 194510, A
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529	35	66.0	1814	4	US-09-702-705-319	Sequence 319, App	c 602	35	66.0	9267	4	US-09-949-016-17441	Sequence 17441, A
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531	35	66.0	1814	4	US-09-614-124B-319	Sequence 319, App	604	35	66.0	10711	3	US-08-961-527-145	Sequence 145, App
532	35	66.0	1814	4	US-09-671-325-319	Sequence 319, App	c 605	35	66.0	11490	4	US-09-949-016-14149	Sequence 14149, A
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544	35	66.0	2086	3	US-09-221-017B-188	Sequence 188, App	617	35	66.0	20520	4	US-09-949-016-14394	Sequence 14394, A
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553	35	66.0	2459	4	US-09-799-451-853	Sequence 853, App	626	35	66.0	36651	3	US-09-738-894A-3	Sequence 3, Appli
554	35	66.0	2460	4	US-09-328-352-1216	Sequence 1216, Ap	627	35	66.0	36651	4	US-09-964-469-3	Sequence 3, Appli
555	35	66.0	2478	4	US-09-949-016-3640	Sequence 3640, Ap	628	35	66.0	44608	4	US-09-949-016-15604	Sequence 15604, A
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c 671	35	66.0	199945	4	US-09-949-016-15436	Sequence 15436, A	744	34	64.2	344	4	US-09-644-460-16	Sequence 16, Appl
c 672	35	66.0	212449	4	US-09-949-016-15419	Sequence 15419, A	745	34	64.2	366	4	US-09-902-540-2718	Sequence 2718, Ap
c 673	35	66.0	234288	4	US-09-949-016-17272	Sequence 17272, A	746	34	64.2	368	4	US-09-513-999C-2349	Sequence 2349, Ap
c 674	35	66.0	247781	4	US-09-949-016-14193	Sequence 14193, A	747	34	64.2	382	4	US-09-513-999C-34543	Sequence 34543, A
c 675	35	66.0	251672	4	US-09-949-016-17296	Sequence 17296, A	748	34	64.2	408	4	US-09-134-000C-2905	Sequence 2905, Ap
c 676	35	66.0	251682	4	US-09-949-016-11793	Sequence 11793, A	749	34	64.2	411	3	US-09-071-035-433	Sequence 433, App
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c 679	35	66.0	304533	4	US-09-949-016-15372	Sequence 15372, A	c 752	34	64.2	433	4	US-09-169-789-167	Sequence 167, App
c 680	35	66.0	312470	4	US-09-949-016-14043	Sequence 14043, A	753	34	64.2	439	4	US-09-270-767-835	Sequence 835, App
c 681	35	66.0	319608	4	US-09-539-333D-1	Sequence 1, Appli	754	34	64.2	439	4	US-09-270-767-16117	Sequence 16117, A
c 682	35	66.0	319608	4	US-09-679-409-1	Sequence 1, Appli	755	34	64.2	441	4	US-09-252-991A-9359	Sequence 9359, Ap
c 683	35	66.0	325034	4	US-09-949-016-14957	Sequence 14957, A	c 756	34	64.2	459	4	US-09-621-976-18643	Sequence 18643, Ap
c 684	35	66.0	336024	4	US-09-949-016-12373	Sequence 12373, A	757	34	64.2	461	4	US-09-513-999C-4024	Sequence 4024, Ap
c 685	35	66.0	389504	4	US-09-949-016-12373	Sequence 12373, A	758	34	64.2	479	4	US-09-495-050A-278	Sequence 278, App
c 686	35	66.0	421491	4	US-09-949-016-12805	Sequence 12805, A	759	34	64.2	492	4	US-09-252-991A-12040	Sequence 12040, A
c 687	35	66.0	421494	4	US-09-949-016-14060	Sequence 14060, A	c 760	34	64.2	517	4	US-09-621-976-2387	Sequence 2387, Ap
c 688	35	66.0	455726	4	US-09-949-016-14157	Sequence 14157, A	c 761	34	64.2	537	4	US-09-252-991A-15043	Sequence 15043, A
c 689	35	66.0	481115	4	US-09-949-016-11940	Sequence 11940, A	c 762	34	64.2	591	4	US-09-949-016-18456	Sequence 18456, A
c 690	35	66.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli	763	34	64.2	601	4	US-09-949-016-18456	Sequence 18456, A
c 691	35	66.0	1230230	4	US-09-438-185A-1	Sequence 1, Appli	764	34	64.2	601	4	US-09-949-016-19999	Sequence 19999, A
c 692	35	66.0	1830121	4	US-09-557-884-1	Sequence 1, Appli	c 765	34	64.2	601	4	US-09-949-016-24098	Sequence 24098, A
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c 695	34.5	65.1	1128	3	US-09-161-994A-1	Sequence 1, Appli	768	34	64.2	601	4	US-09-949-016-31754	Sequence 31754, A
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c 698	34.5	65.1	1222	3	US-08-819-037-43	Sequence 43, Appl	c 771	34	64.2	601	4	US-09-949-016-34020	Sequence 34020, A
c 699	34.5	65.1	1222	3	US-09-045-940-43	Sequence 43, Appl	c 772	34	64.2	601	4	US-09-949-016-34021	Sequence 34021, A
c 700	34.5	65.1	1311	4	US-09-638-937-3	Sequence 3, Appli	c 773	34	64.2	601	4	US-09-949-016-34032	Sequence 34032, A
c 701	34.5	65.1	1312	3	US-09-059-769-3	Sequence 3, Appli	c 774	34	64.2	601	4	US-09-949-016-34326	Sequence 34326, A
c 702	34.5	65.1	1337	3	US-09-638-937-12	Sequence 12, Appl	c 775	34	64.2	601	4	US-09-949-016-38964	Sequence 38964, A
c 703	34.5	65.1	1358	3	US-09-059-769-1	Sequence 1, Appli	c 776	34	64.2	601	4	US-09-949-016-46868	Sequence 46868, A
c 704	34.5	65.1	1361	4	US-09-638-937-10	Sequence 10, Appl	c 777	34	64.2	601	4	US-09-949-016-53273	Sequence 53273, A
c 705	34.5	65.1	1364	2	US-08-872-302-3	Sequence 3, Appli	c 778	34	64.2	601	4	US-09-949-016-53274	Sequence 53274, A
c 706	34.5	65.1	1369	3	US-09-133-962A-11	Sequence 11, Appl	c 779	34	64.2	601	4	US-09-949-016-53275	Sequence 53275, A
c 707	34.5	65.1	1448	1	US-08-314-596-39	Sequence 39, Appl	780	34	64.2	601	4	US-09-949-016-55181	Sequence 55181, A
c 708	34.5	65.1	1448	1	US-08-320-982-39	Sequence 39, Appl	781	34	64.2	601	4	US-09-949-016-59863	Sequence 59863, A
c 709	34.5	65.1	1448	3	US-08-819-037-39	Sequence 39, Appl	782	34	64.2	601	4	US-09-949-016-59904	Sequence 59904, A
c 710	34.5	65.1	1448	3	US-09-045-940-39	Sequence 39, Appl	c 783	34	64.2	601	4	US-09-949-016-60298	Sequence 60298, A
c 711	34.5	65.1	1457	4	US-09-638-937-1	Sequence 1, Appli	c 784	34	64.2	601	4	US-09-949-016-64344	Sequence 64344, A
c 712	34.5	65.1	1855	3	US-08-530-862B-3	Sequence 3, Appli	c 785	34	64.2	601	4	US-09-949-016-64375	Sequence 64375, A
c 713	34.5	65.1	1855	3	US-08-597-333D-3	Sequence 3, Appli	c 786	34	64.2	601	4	US-09-949-016-64406	Sequence 64406, A
c 714	34.5	65.1	3670	2	US-08-898-038-1	Sequence 1, Appli	c 787	34	64.2	601	4	US-09-949-016-64437	Sequence 64437, A
c 715	34.5	65.1	3670	3	US-09-352-125-1	Sequence 1, Appli	c 788	34	64.2	601	4	US-09-949-016-64468	Sequence 64468, A
c 716	34	64.2	18	2	US-08-244-205-22	Sequence 22, Appl	c 789	34	64.2	601	4	US-09-949-016-64499	Sequence 64499, A
c 717	34	64.2	18	2	US-08-244-205-23	Sequence 23, Appl	c 790	34	64.2	601	4	US-09-949-016-64530	Sequence 64530, A
c 718	34	64.2	18	5	PCT-US92-10284-22	Sequence 22, Appl	c 791	34	64.2	601	4	US-09-949-016-64561	Sequence 64561, A
c 719	34	64.2	18	5	PCT-US92-10284-23	Sequence 23, Appl	792	34	64.2	601	4	US-09-949-016-70469	Sequence 70469, A
c 720	34	64.2	36	2	US-08-244-205-21	Sequence 21, Appl	793	34	64.2	601	4	US-09-949-016-70470	Sequence 70470, A
c 721	34	64.2	36	2	US-08-244-205-28	Sequence 28, Appl	794	34	64.2	601	4	US-09-949-016-73554	Sequence 73554, A
c 722	34	64.2	36	2	US-08-244-205-29	Sequence 29, Appl	795	34	64.2	601	4	US-09-949-016-73555	Sequence 73555, A
c 723	34	64.2	36	5	PCT-US92-10284-21	Sequence 21, Appl	c 796	34	64.2	601	4	US-09-949-016-73556	Sequence 73556, A
c 724	34	64.2	36	5	PCT-US92-10284-28	Sequence 28, Appl	797	34	64.2	601	4	US-09-949-016-81450	Sequence 81450, A
c 725	34	64.2	36	5	PCT-US92-10284-29	Sequence 29, Appl	798	34	64.2	601	4	US-09-949-016-84790	Sequence 84790, A
c 726	34	64.2	42	2	US-08-244-205-20	Sequence 20, Appl	c 799	34	64.2	601	4	US-09-949-016-87022	Sequence 87022, A
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c 728	34	64.2	52	4	US-10-256-221-4	Sequence 4, Appli	c 801	34	64.2	601	4	US-09-949-016-92523	Sequence 92523, A
c 729	34	64.2	93	4	US-09-902-540-3263	Sequence 3262, Ap	c 802	34	64.2	601	4	US-09-949-016-93861	Sequence 93861, A
c 730	34	64.2	122	4	US-09-508-930D-43	Sequence 43, Appl	803	34	64.2	601	4	US-09-949-016-109768	Sequence 109768, A
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c 732	34	64.2	220	4	US-09-621-976-12040	Sequence 33184, A	c 805	34	64.2	601	4	US-09-949-016-117004	Sequence 117004, A
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c 736	34	64.2	269	4	US-09-313-294A-3371	Sequence 3371, Ap	c 809	34	64.2	601	4	US-09-949-016-119529	Sequence 119529, A
c 737	34	64.2	295	4	US-09-313-294A-5348	Sequence 5348, Ap	c 810	34	64.2	601	4	US-09-949-016-119555	Sequence 119555, A
c 738	34	64.2	297	4	US-09-313-294A-1438	Sequence 1438, Ap	c 811	34	64.2	601	4	US-09-949-016-119581	Sequence 119581, A
c 739	34	64.2	309	3	US-09-071-035-435	Sequence 435, App	c 812	34	64.2	601	4	US-09-949-016-119607	Sequence 119607, A
c 740	34	64.2	312	4	US-09-248-796A-13669	Sequence 13669, A	c 813	34	64.2	601	4	US-09-949-016-119633	Sequence 119633, A
c 741	34	64.2	321	4	US-09-313-294A-4657	Sequence 4657, Ap	c 814	34	64.2	601	4	US-09-949-016-119659	Sequence 119659, A
c 742	34	64.2	338	3	US-08-905-223-259	Sequence 259, App	c 815	34	64.2	601	4	US-09-949-016-119685	Sequence 119685, A

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C 817	34	64.2	601	4	US-09-949-016-119735	Sequence 119735,	C 890	34	64.2	1083	4	US-09-902-540-8906	Sequence 8906, Ap
C 818	34	64.2	601	4	US-09-949-016-119759	Sequence 119759,	C 891	34	64.2	1098	4	US-09-902-540-7748	Sequence 7748, Ap
C 819	34	64.2	601	4	US-09-949-016-119783	Sequence 119783,	C 892	34	64.2	1110	4	US-09-252-991A-5978	Sequence 5978, Ap
C 820	34	64.2	601	4	US-09-949-016-119807	Sequence 119807,	C 893	34	64.2	1120	1	US-07-882-329-3	Sequence 3, Appl
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C 823	34	64.2	601	4	US-09-949-016-126327	Sequence 126327,	C 896	34	64.2	1134	4	US-09-252-991A-13901	Sequence 13901, A
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C 825	34	64.2	601	4	US-09-949-016-128283	Sequence 128283,	C 898	34	64.2	1154	4	US-09-949-016-4530	Sequence 4530, Ap
C 826	34	64.2	601	4	US-09-949-016-128843	Sequence 128843,	C 899	34	64.2	1156	4	US-09-252-991A-4834	Sequence 4834, Ap
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C 828	34	64.2	601	4	US-09-949-016-138766	Sequence 138766,	C 901	34	64.2	1182	4	US-09-252-991A-6534	Sequence 6534, Ap
C 829	34	64.2	601	4	US-09-949-016-138767	Sequence 138767,	C 902	34	64.2	1206	4	US-09-252-991A-1208	Sequence 1208, Ap
C 830	34	64.2	601	4	US-09-949-016-140134	Sequence 140134,	C 903	34	64.2	1208	3	US-09-461-474-11	Sequence 11, Appl
C 831	34	64.2	601	4	US-09-949-016-140135	Sequence 140135,	C 904	34	64.2	1212	4	US-09-252-991A-5892	Sequence 5892, Ap
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C 834	34	64.2	601	4	US-09-949-016-147831	Sequence 147831,	C 907	34	64.2	1221	4	US-09-902-540-4571	Sequence 4571, Ap
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C 837	34	64.2	601	4	US-09-949-016-162233	Sequence 162233,	C 910	34	64.2	1269	4	US-09-252-991A-5607	Sequence 5607, Ap
C 838	34	64.2	601	4	US-09-949-016-166234	Sequence 166234,	C 911	34	64.2	1287	4	US-09-489-039A-6809	Sequence 6809, Ap
C 839	34	64.2	601	4	US-09-949-016-168324	Sequence 168324,	C 912	34	64.2	1310	4	US-09-724-623-32	Sequence 32, Appl
C 840	34	64.2	601	4	US-09-949-016-168325	Sequence 168325,	C 913	34	64.2	1311	4	US-09-252-991A-1355	Sequence 1355, Ap
C 841	34	64.2	601	4	US-09-949-016-168326	Sequence 168326,	C 914	34	64.2	1320	4	US-09-763-863-28	Sequence 28, Appl
C 842	34	64.2	601	4	US-09-949-016-168327	Sequence 168327,	C 915	34	64.2	1326	4	US-09-902-540-3917	Sequence 3917, Ap
C 843	34	64.2	601	4	US-09-949-016-169075	Sequence 169075,	C 916	34	64.2	1329	1	US-07-882-329-4	Sequence 4, Appl
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C 851	34	64.2	601	4	US-09-949-016-191344	Sequence 191344,	C 924	34	64.2	1548	4	US-09-489-039A-5135	Sequence 5135, Ap
C 852	34	64.2	601	4	US-09-949-016-194221	Sequence 194221,	C 925	34	64.2	1551	3	US-09-461-474-7	Sequence 7, Appl
C 853	34	64.2	601	4	US-09-949-016-202771	Sequence 202771,	C 926	34	64.2	1554	4	US-09-252-991A-4893	Sequence 4893, Ap
C 854	34	64.2	601	4	US-09-949-016-203436	Sequence 203436,	C 927	34	64.2	1572	4	US-09-620-312D-664	Sequence 664, Ap
C 855	34	64.2	601	4	US-09-949-016-203636	Sequence 203636,	C 928	34	64.2	1620	3	US-09-360-197-3	Sequence 3, Appl
C 856	34	64.2	601	4	US-09-949-016-205267	Sequence 205267,	C 929	34	64.2	1631	4	US-09-799-451-527	Sequence 527, Ap
C 857	34	64.2	622	4	US-09-435-05A-15	Sequence 15, Appl	C 930	34	64.2	1653	4	US-09-252-991A-14765	Sequence 14765, A
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C 859	34	64.2	645	4	US-09-585-645A-4	Sequence 4, Appl	C 932	34	64.2	1685	1	US-08-362-512A-1	Sequence 1, Appl
C 860	34	64.2	729	4	US-09-252-991A-14854	Sequence 14854, A	C 933	34	64.2	1685	3	US-08-964-979-1	Sequence 1, Appl
C 861	34	64.2	742	3	US-09-085-848-2	Sequence 2, Appl	C 934	34	64.2	1685	4	US-09-854-734-1	Sequence 4368, Ap
C 862	34	64.2	742	4	US-09-562-616-2	Sequence 2, Appl	C 935	34	64.2	1698	4	US-09-902-540-4368	Sequence 4368, Ap
C 863	34	64.2	765	4	US-09-270-767-11774	Sequence 11774, A	C 936	34	64.2	1711	4	US-09-976-594-497	Sequence 497, Ap
C 864	34	64.2	786	4	US-09-902-540-8280	Sequence 8280, Ap	C 937	34	64.2	1752	4	US-09-902-540-8626	Sequence 8626, Ap
C 865	34	64.2	789	4	US-09-252-991A-12447	Sequence 12447, A	C 938	34	64.2	1784	1	US-08-554-612C-13	Sequence 13, Appl
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C 868	34	64.2	831	1	US-08-183-213-1	Sequence 1, Appl	C 941	34	64.2	1863	4	US-09-252-991A-730	Sequence 730, Ap
C 869	34	64.2	840	4	US-09-902-540-8432	Sequence 8432, Ap	C 942	34	64.2	1873	3	US-09-461-474-9	Sequence 9, Appl
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C 871	34	64.2	861	4	US-09-585-645A-24	Sequence 24, Appl	C 944	34	64.2	1929	3	US-09-040-229B-7	Sequence 7, Appl
C 872	34	64.2	867	4	US-09-252-991A-681	Sequence 681, Ap	C 945	34	64.2	1941	4	US-09-976-594-1047	Sequence 1047, Ap
C 873	34	64.2	870	4	US-09-252-991A-14598	Sequence 14598, A	C 946	34	64.2	1980	4	US-09-270-767-15138	Sequence 15138, A
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C 875	34	64.2	897	4	US-09-709-785-3	Sequence 3, Appl	C 948	34	64.2	1995	4	US-09-107-433-172	Sequence 172, Ap
C 876	34	64.2	903	4	US-09-252-991A-10886	Sequence 10886, A	C 949	34	64.2	2008	4	US-09-270-767-13658	Sequence 13658, A
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C 878	34	64.2	927	4	US-09-252-991A-229	Sequence 229, Ap	C 951	34	64.2	2067	4	US-09-252-991A-16177	Sequence 16177, A
C 879	34	64.2	936	4	US-09-328-352-1255	Sequence 1255, Ap	C 952	34	64.2	2107	4	US-09-949-016-2630	Sequence 2630, Ap
C 880	34	64.2	948	4	US-09-724-623-60	Sequence 60, Appl	C 953	34	64.2	2107	4	US-09-949-016-3025	Sequence 3025, Ap
C 881	34	64.2	972	4	US-09-534-229C-7	Sequence 7, Appl	C 954	34	64.2	2139	4	US-09-252-991A-4910	Sequence 4910, Ap
C 882	34	64.2	1014	4	US-09-252-991A-15183	Sequence 15183, A	C 955	34	64.2	2157	1	US-08-471-119A-7	Sequence 7, Appl
C 883	34	64.2	1017	4	US-09-252-991A-14584	Sequence 14584, A	C 956	34	64.2	2250	4	US-09-252-991A-760	Sequence 760, Ap
C 884	34	64.2	1020	4	US-09-252-991A-5960	Sequence 5960, Ap	C 957	34	64.2	2250	4	US-09-614-221A-365	Sequence 365, Ap
C 885	34	64.2	1024	4	US-09-328-475C-76	Sequence 76, Appl	C 958	34	64.2	2294	4	US-09-270-767-2111	Sequence 2111, Ap
C 886	34	64.2	1026	4	US-09-902-540-9683	Sequence 9683, Ap	C 959	34	64.2	2294	4	US-09-270-767-17393	Sequence 17393, A
C 887	34	64.2	1047	4	US-09-252-991A-13520	Sequence 13520, A	C 960	34	64.2	2339	4	US-09-495-050A-26	Sequence 26, Appl
C 888	34	64.2	1050	3	US-09-137-855-1	Sequence 1, Appl	C 961	34	64.2	2340	4	US-09-252-991A-14719	Sequence 14719, A



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C 993 34 64.2 4524 3 US-09-206-537-7  
C 994 34 64.2 4524 3 US-09-430-854-7  
C 995 34 64.2 4568 4 US-09-949-016-2498  
C 996 34 64.2 4643 3 US-09-453-702B-22  
C 997 34 64.2 4800 3 US-08-941-445A-4  
C 998 34 64.2 4837 3 US-09-629-616-1  
C 999 34 64.2 4854 4 US-09-902-540-768  
C1000 34 64.2 5288 2 US-08-540-406-18

## ALIGNMENTS

RESULT 1  
US-08-831-570-1  
; Sequence 1, Application US/08831570  
; Patent No. 5959175  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; APPLICANT: Nunberg, Andrew N.  
; APPLICANT: Berenbaum, Phillip D.  
; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION  
; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID  
; TITLE OF INVENTION: COMPOSITION  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/831,570  
; FILING DATE: 09-APR-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.

; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10545  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 743-4366  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1684 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 43..1387  
US-08-831-570-1  
Alignment Scores:  
Pred. No.: 2 Length: 1684  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
US-10-029-756-6 (1-8) x US-08-831-570-1 (1-1684)  
Qy 1 TrrileglyHisaspAlaGlyHis 8  
Db 508 TGGATTGGACATGATGCTGGCAT 531  
RESULT 2  
US-08-831-575-1  
; Sequence 1, Application US/08831575  
; Patent No. 5977436  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; APPLICANT: Li, Zhongnan  
; TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE  
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/831,575  
; FILING DATE: 09-APR-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1684 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS



LOCATION: 43...1387  
US-08-831-575-1  
Alignment Scores:  
Pred. No.: 2 Length: 1684  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
US-10-029-756-6 (1-8) x US-08-831-575-1 (1-1684)  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 508 TGGATTGGACATGATGCTGGGCAT 531  
RESULT 3  
US-08-366-779-4  
; Sequence 4, Application US/08366779  
; Patent No. 5614393  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; APPLICANT: Reddy, Avutu S.  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Freyesinet, Georges L.  
; APPLICANT: Nunberg, Andrew N.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; TITLE OF INVENTION: DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/366.779  
; FILING DATE: 30-DEC-1994  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 8383ZYXW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-366-779-4  
Alignment Scores:  
Pred. No.: 2 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-10-029-756-6 (1-8) x US-08-366-779-4 (1-1685)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
RESULT 4  
US-08-789-936-4  
; Sequence 4, Application US/08789936  
; Patent No. 5789220  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; APPLICANT: Reddy, Avutu S.  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Freyesinet, Georges L.  
; APPLICANT: Nunberg, Andrew N.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; TITLE OF INVENTION: DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789.936  
; FILING DATE: 28-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/366,779  
; FILING DATE: 30-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 8383ZYXW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-789-936-4  
Alignment Scores:  
Pred. No.: 2 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-10-029-756-6 (1-8) x US-08-789-936-4 (1-1685)  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
RESULT 5  
US-08-934-254-4  
; Sequence 4, Application US/08934254  
; Patent No. 6355861  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.

;; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
;; TITLE OF INVENTION: DELTA 6-DESATURASE  
;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Scully, Scott, Murphy & Presser  
;; STREET: 400 Garden City Plaza  
;; CITY: Garden City  
;; STATE: New York  
;; COUNTRY: United States  
;; ZIP: 11530  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/934,254  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Presser, Leopold  
;; REGISTRATION NUMBER: 19,827  
;; REFERENCE/DOCKET NUMBER: 8383ZYXWVU  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (516) 742-4343  
;; TELEFAX: (516) 742-4366  
;; TELEX: 230 901 SANS UR  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1685 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-934-254-4  
  
Alignment Scores:  
Pred. No.: 2 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
  
US-10-029-756-6 (1-8) x US-08-934-254-4 (1-1685)  
  
Qy 1 TtpileGlyHisaspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
  
RESULT 6  
US-09-685-775-4  
; Sequence 4, Application US/09685775  
; Patent No. 6683232  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/685,775

;; FILING DATE: 10-Oct-2000  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/934,254  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Presser, Leopold  
;; REGISTRATION NUMBER: 19,827  
;; REFERENCE/DOCKET NUMBER: 8383ZYXWVU  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (516) 742-4343  
;; TELEFAX: (516) 742-4366  
;; TELEX: 230 901 SANS UR  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1685 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-685-775-4  
  
Alignment Scores:  
Pred. No.: 2 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-029-756-6 (1-8) x US-09-685-775-4 (1-1685)  
  
Qy 1 TtpileGlyHisaspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
  
RESULT 7  
US-09-270-767-29759/C  
; Sequence 29759, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 29759  
; LENGTH: 162  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-29759  
  
Alignment Scores:  
Pred. No.: 656 Length: 162  
Score: 44.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 83.02% Indels: 0  
DB: 4 -Gaps: 0  
  
US-10-029-756-6 (1-8) x US-09-270-767-29759 (1-162)  
  
Qy 1 TtpileGlyHisaspAlaGlyHis 8  
Db 509 TGGATTGGGCATTCAGCTGGGCAT 27  
  
RESULT 8  
US-09-270-767-13737/C  
; Sequence 13737, Application US/09270767  
; Patent No. 6703491

; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13737  
; LENGTH: 833  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-13737

Alignment Scores:  
Pred. No.: 38.6 Length: 833  
Score: 44.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 83.02% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-270-767-13737 (1-833)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
||||:||||| |||||  
Db 721 TGGATGGGGCATTGCTGGGCAT 698

## RESULT 9

US-09-252-991A-5494  
; Sequence 5494, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; TITLE OF INVENTION: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5494  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5494

Alignment Scores:  
Pred. No.: 102 Length: 1152  
Score: 42.50 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 0  
Query Match: 80.19% Indels: 1  
DB: 4 Gaps: 1

US-10-029-756-6 (1-8) x US-09-252-991A-5494 (1-1152)

Qy 1 Trp----IleGlyHisAspAlaGlyHis 8  
||| ||||| ||||| |||||  
Db 1075 TGGAGCATTTGGCCATGACGCGGCAC 1101

## RESULT 10

US-09-949-016-21341  
; Sequence 21341, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21341  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-21341

Alignment Scores:  
Pred. No.: 62 Length: 601  
Score: 42.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-21341 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
||||:||||| |||||  
Db 578 TGGCTAGGTCATTGTGCTGGTCAC 601

## RESULT 11

US-09-949-016-36968  
; Sequence 36968, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36968  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-36968

Alignment Scores:  
Pred. No.: 62 Length: 601  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-36968 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
||||:||||| |||||  
Db 356 TGGATTGGGCACAGCATGGGCCAC 379

## RESULT 12

US-09-949-016-46094  
; Sequence 46094, Application US/09949016  
; Patent No. 6812339

```

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46094
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-46094

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-46094 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 356 TGGATTGGGCACAGCATGGCCAC 379

RESULT 13
US-09-949-016-74333
; Sequence 74333, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74333
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-74333

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-74333 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 578 TGGCTAGGTCATTGCTGCTGCAC 601

```

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RESULT 14
US-09-949-016-183604/c
; Sequence 183604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183604
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183604

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-183604 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 509 TGGTTAGGCCATGACTCTAATCAC 486

RESULT 15
US-09-669-751-180/c
; Sequence 180, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; Motion Sickness, Vertigo and Other Disorders Related to
; Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-180

Alignment Scores:
Pred. No.: 67.5 Length: 650
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-669-751-180 (1-650)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

```

Db 415 TGGTGTGGGCATAGCGCGGCAC 392

RESULT 16  
US-09-949-016-1322/c  
; Sequence 1322, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1322  
; LENGTH: 760  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1322

Alignment Scores:  
Pred. No.: 79.9 Length: 760  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-1322 (1-760)

Qy 1 TtpileGlyHisAspAlaGlyHis 8  
|||||  
Db 582 TGGATTGGGCACGACGATGGCCAC 559

RESULT 17  
US-09-270-767-13129/c  
; Sequence 13129, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13129  
; LENGTH: 816  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-13129

Alignment Scores:  
Pred. No.: 86.3 Length: 816  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-270-767-13129 (1-816)

Qy 1 TtpileGlyHisAspAlaGlyHis 8  
|||||  
Db 415 TGGTGTGGGCATAGCGCGGCAC 392

RESULT 18

US-09-673-395A-136/c  
; Sequence 136, Application US/09673395A  
; Patent No. 6620923  
; GENERAL INFORMATION:  
; APPLICANT: SPECHT, THOMAS  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHMITT, ARMIN  
; APPLICANT: PILARSKY, CHRISTIAN  
; APPLICANT: DAHL, EDGAR  
; APPLICANT: ROSENTHAL, ANDRE  
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE  
; FILE REFERENCE: ALBRE-12  
; CURRENT APPLICATION NUMBER: US/09/673.395A  
; CURRENT FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 637  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 136  
; LENGTH: 2238  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-673-395A-136

Alignment Scores:  
Pred. No.: 257 Length: 2238  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-673-395A-136 (1-2238)

Qy 1 TtpileGlyHisAspAlaGlyHis 8  
|||||  
Db 331 TGGATAGGGCATTCATTGGCCAC 308

RESULT 19

US-08-967-101-28/c  
; Sequence 28, Application US/08967101  
; Patent No. 5840540  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 183  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: High Street Tower - 125 High Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,101  
; FILING DATE: 10-NOV-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/592,541  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100

;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2307 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-967-101-28

Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x US-08-967-101-28 (1-2307)

Qy 1 TtpileGlyHisaspAlaGlyHis 8  
Db 550 TGGATAGGGCATTCCATTGGCCAC 527

RESULT 20  
US-08-592-541-28/c  
; Sequence 28, Application US/08592541  
; Patent No. 5986054  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 183  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: High Street Tower - 125 High Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,541  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 28:  
; LENGTH: 2307 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-592-541-28

Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x US-08-592-541-28 (1-2307)

Qy 1 TtpileGlyHisaspAlaGlyHis 8  
Db 550 TGGATAGGGCATTCCATTGGCCAC 527

RESULT 21  
US-09-124-698-28/c  
; Sequence 28, Application US/09124698  
; Patent No. 6117978  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 183  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: High Street Tower - 125 High Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/124,698  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/592,541  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2307 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-124-698-28

Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-124-698-28 (1-2307)

Qy 1 TtpileGlyHisaspAlaGlyHis 8  
Db 550 TGGATAGGGCATTCCATTGGCCAC 527

RESULT 22  
US-09-127-480-28/c  
; Sequence 28, Application US/09127480  
; Patent No. 6194153  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/127,480  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-127-480-28  
Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-6 (1-8) x US-09-127-480-28 (1-2307)  
Qy 1 TptlleglyHisAspAlaGlyHis 8  
Db 550 TGGATAGGCGCATTCATTGGCCAC 527  
RESULT 23  
US-08-496-841C-28/c  
Sequence 28, Application US/08496841C  
Patent No. 6210919  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
ROMMENS, JOHANNA M  
FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby, PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/496,841C

FILING DATE: 28-Jun-1995  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul F. Fehlner, Ph.D.  
REGISTRATION NUMBER: 35,135  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 527-7700  
TELEFAX: (212) 753-6237  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-08-496-841C-28  
Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-6 (1-8) x US-08-496-841C-28 (1-2307)  
Qy 1 TptlleglyHisAspAlaGlyHis 8  
Db 550 TGGATAGGCGCATTCATTGGCCAC 527  
RESULT 24  
US-09-124-523-28/c  
Sequence 28, Application US/09124523  
Patent No. 6395960  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
ROMMENS, JOHANNA M  
FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)  
US-09-124-523-28

Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-124-523-28 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 550 TGGATAGGCATTCATTGGCCAC 527

RESULT 25

US-09-636-796A-28/c  
; Sequence 28, Application US/09636796A  
; Patent No. 6485911  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; ROMMENS, JOHANNA M  
; FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 183  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: High Street Tower - 125 High Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 11-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-636-796A-28

Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-636-796A-28 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 550 TGGATAGGCATTCATTGGCCAC 527

RESULT 26

US-08-431-048F-28/c  
; Sequence 28, Application US/08431048F  
; Patent No. 6531586  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; ROMMENS, JOHANNA M  
; FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 155  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DARBY & DARBY P.C.  
; STREET: 805 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: N.Y.  
; COUNTRY: U.S.A.  
; ZIP: 10022-7513

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,048F  
FILING DATE: 28-Apr-1995  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: FEHLNER, PAUL F.  
REGISTRATION NUMBER: 35135  
REFERENCE/DOCKET NUMBER: 1034/0F808  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-527-6237

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-08-431-048F-28

Alignment Scores:  
Pred. No.: 266 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-08-431-048F-28 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 550 TGGATAGGCATTCATTGGCCAC 527

RESULT 27

US-09-949-016-973/c  
; Sequence 973, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755





; LENGTH: 40037  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) ..(40037)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12715

Alignment Scores:  
Pred. No.: 5.84e+03 Length: 40037  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12715 (1-40037)

Qy 1 TrrileGlyHisAspAlaGlyHis 8  
Db 34941 TGGATTGGGCACAGCATGGGCCAC 34918

## RESULT 31

US-09-949-016-11919  
; Sequence 11919, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11919

; LENGTH: 84761  
; TYPE: DNA

; ORGANISM: Human  
US-09-949-016-11919

Alignment Scores:  
Pred. No.: 1.32e+04 Length: 84761  
Score: 42.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-11919 (1-84761)

Qy 1 TrrileGlyHisAspAlaGlyHis 8  
Db 58464 TGGCTAGTCATTGTGCTGGTCAC 58487

## RESULT 32

US-09-949-016-13914  
; Sequence 13914, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13914  
; LENGTH: 84763  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13914

Alignment Scores:  
Pred. No.: 1.32e+04 Length: 84763  
Score: 42.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-13914 (1-84763)

Qy 1 TrrileGlyHisAspAlaGlyHis 8  
Db 58464 TGGCTAGTCATTGTGCTGGTCAC 58487

## RESULT 33

US-09-949-016-17009/c  
; Sequence 17009, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17009

; LENGTH: 205163  
; TYPE: DNA

; ORGANISM: Human  
US-09-949-016-17009

Alignment Scores:  
Pred. No.: 3.4e+04 Length: 205163  
Score: 42.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-17009 (1-205163)

Qy 1 TrrileGlyHisAspAlaGlyHis 8  
Db 179865 TGGTTAGCCATGACTCTAATCAC 179842

## RESULT 34

US-09-583-110-1558  
; Sequence 1558, Application US/09583110  
; Patent No. 6699703

; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.

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; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1558
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1558

Alignment Scores:
Pred. No.: 432 Length: 2463
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-583-110-1558 (1-2463)

Qy 1 TrrpleGlyHisAspAlaGlyHis 8
Db 2023 TGGATTGGCGATGATGATAATCAT 2046

RESULT 35
US-09-377-465A-1
; Sequence 1, Application US/09377465A
; Patent No. H002021
; GENERAL INFORMATION:
; APPLICANT: Hoskins, JoAnn
; APPLICANT: Jaskunas, Stanley R
; APPLICANT: Zhao, Genshi
; APPLICANT: Rockey, Pamela K
; TITLE OF INVENTION: NOVEL PENICILLIN BINDING PROTEIN FROM STREPTOCOCCUS
; FILE REFERENCE: X12498 Sequence List
; Patent No. H002021
; CURRENT APPLICATION NUMBER: US/09/377,465A
; CURRENT FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: CDS
; LOCATION: (1)...(2466)
US-09-377-465A-1

Alignment Scores:
Pred. No.: 432 Length: 2466
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-6 (1-8) x US-09-377-465A-1 (1-2466)

Qy 1 TrrpleGlyHisAspAlaGlyHis 8
Db 2023 TGGATTGGCGATGATGATAATCAT 2046

RESULT 36
US-09-377-465A-3
; Sequence 3, Application US/09377465A
; Patent No. H002021
; GENERAL INFORMATION:
; APPLICANT: Hoskins, JoAnn
; APPLICANT: Jaskunas, Stanley R
; APPLICANT: Zhao, Genshi
; APPLICANT: Rockey, Pamela K
; TITLE OF INVENTION: NOVEL PENICILLIN BINDING PROTEIN FROM STREPTOCOCCUS
; FILE REFERENCE: X12498 Sequence List
; Patent No. H002021
; CURRENT APPLICATION NUMBER: US/09/377,465A
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/100,887
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2466
; TYPE: RNA
; ORGANISM: Streptococcus pneumoniae
; US-09-377-465A-3

Alignment Scores:
Pred. No.: 432 Length: 2466
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-6 (1-8) x US-09-377-465A-3 (1-2466)

Qy 1 TrrpleGlyHisAspAlaGlyHis 8
Db 2023 UGGAUUGGCAUGAUGAUCAU 2046

RESULT 37
US-09-107-433-2157
; Sequence 2157, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
```

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; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...2505
; SEQUENCE DESCRIPTION: SEQ ID NO: 2157:
US-09-107-433-2157
Alignment Scores:
Pred. No.: 440 Length: 2505
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-107-433-2157 (1-2505)
Qy 1 TtpIlleGlyHisAspAlaGlyHis 8
Db 2065 TGGATTGGCGCATGATGATCAT 2088
RESULT 38
; Sequence 143, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/961,527
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14...2593
; NAME/KEY: mat peptide
; LOCATION: 77..2593
US-08-092-817-3
Alignment Scores:
Pred. No.: 922 Length: 4965
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-6 (1-8) x US-08-961-527-143 (1-4965)
Qy 1 TtpIlleGlyHisAspAlaGlyHis 8
Db 485 TGGATTGGCGCATGATGATCAT 462
RESULT 39
; Sequence 3, Application US/08092817
; Patent No. 5496926
; GENERAL INFORMATION:
; APPLICANT: RUBINSTEIN, Menachem
; APPLICANT: NOVICK, Daniela
; APPLICANT: TAL, Nathan
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/092,817
; FILING DATE: 19-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 100696
; FILING DATE: 19-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 102915
; FILING DATE: 23-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: TOWNSEND, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: RUBINSTEIN=5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14...2593
; NAME/KEY: mat peptide
; LOCATION: 77..2593
US-08-092-817-3
```

US-08-485-128-3

RESULT 42  
US-09-949-016-14032  
; Sequence 14032, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20

```
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14032
; LENGTH: 46499
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(46499)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14032

Alignment Scores:
Pred. No.: 1.04e+04 Length: 46499
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-14032 (1-46499)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 15201 TGGGCTGGACATCCAGCTGGCCAC 15224

RESULT 43
US-09-949-016-12677/c
; Sequence 12677, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12677
; LENGTH: 119930
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12677

Alignment Scores:
Pred. No.: 2.88e+04 Length: 119930
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12677 (1-119930)

Qy 1 TrpIleGlyHisAspAlaGly 7
Db 111718 TGGATAGTCATGAGGCTGGG 111698

RESULT 44
US-09-949-016-16319/c
; Sequence 16319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16319
; LENGTH: 119931
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16319

Alignment Scores:
Pred. No.: 2.88e+04 Length: 119931
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-16319 (1-119931)

Qy 1 TrpIleGlyHisAspAlaGly 7
Db 111718 TGGATAGTCATGAGGCTGGG 111698

RESULT 45
US-09-949-016-14186/c
; Sequence 14186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14186
; LENGTH: 125536
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14186

Alignment Scores:
Pred. No.: 3.02e+04 Length: 125536
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-14186 (1-125536)

Qy 1 TrpIleGlyHisAspAlaGly 7
Db 111718 TGGATAGTCATGAGGCTGGG 111698
```

RESULT 46  
US-09-107-433-2018/c  
; Sequence 2018, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneka  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 2018:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 828 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULAR TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8) LOCATION 1...828  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2018:  
US-09-107-433-2018  
Alignment Scores:  
Pred. No.: 201 Length: 828  
Score: 40.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 75.47% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x US-09-107-433-2018 (1-828)  
Qy 1 TrrlleGlyHisAspAlaGlyHis 8  
Db 678 TGGGATGGACATGACGATGGTCAC 655  
RESULT 47  
US-09-583-110-2134/c  
; Sequence 2134, Application US/09583110  
; Patent No. 6699703

; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 2134  
; LENGTH: 945  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-2134  
Alignment Scores:  
Pred. No.: 231 Length: 945  
Score: 40.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 75.47% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x US-09-583-110-2134 (1-945)  
Qy 1 TrrlleGlyHisAspAlaGlyHis 8  
Db 795 TGGGATGGACATGACGATGGTCAC 772  
RESULT 48  
US-09-569-771B-20  
; Sequence 20, Application US/09569771B  
; Patent No. 6815580  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Philip W  
; APPLICANT: Staub, Robin L  
; TITLE OF INVENTION: Expression of Sedoheptulose 1, 7 Bisphosphatase in Transgenic  
; Plants  
; FILE REFERENCE: 38-21(15408)B  
; CURRENT APPLICATION NUMBER: US/09/569,771B  
; CURRENT FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: 60/133,964  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 20  
; TYPE: DNA  
; ORGANISM: Chlorella sorokiniana  
US-09-569-771B-20  
Alignment Scores:  
Pred. No.: 371 Length: 1460  
Score: 40.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 85.71% Mismatches: 0  
Query Match: 75.47% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x US-09-569-771B-20 (1-1460)  
Qy 2 lleGlyHisAspAlaGlyHis 8  
Db 28 CTCGGCAGCATGACGAGCCAC 48  
RESULT 49  
US-09-569-771B-22  
; Sequence 22, Application US/09569771B







; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2 4403765  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Alignment Scores:  
Pred. No.: 1.43e+06 Length: 4403765  
Score: 40.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 75.47% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-103-840A-2 (1-4403765)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 1104932 TGGCAAGGCCATCAAGCGGCCAT 1104909

## RESULT 56

US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Alignment Scores:  
Pred. No.: 1.43e+06 Length: 4411529  
Score: 40.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 75.47% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-103-840A-1 (1-4411529)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 1104909 TGGCAAGGCCATCAAGCGGCCAT 1104886

## RESULT 57

US-09-949-016-12800/c  
; Sequence 12800, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12800  
; LENGTH: 8521  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12800

Alignment Scores:  
Pred. No.: 3.08e+03 Length: 8521  
Score: 39.50 Matches: 8  
Percent Similarity: 53.33% Conservative: 0  
Best Local Similarity: 53.33% Mismatches: 0  
Query Match: 74.53% Indels: 7  
DB: 4 Gaps: 1

US-10-029-756-6 (1-8) x US-09-949-016-12800 (1-8521)

Qy 1 TrpIle-----GlyHisAspAlaGlyHis 8

Db 7835 TGGATCCAGATGCCCTCTCTGCCCCAGGTCATGACGCTGGGCAC 7791

## RESULT 58

US-09-949-016-15804/c  
; Sequence 15804, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15804  
; LENGTH: 13117  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(13117)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15804

Alignment Scores:  
Pred. No.: 4.91e+03 Length: 13117  
Score: 39.50 Matches: 8  
Percent Similarity: 53.33% Conservative: 0

Best Local Similarity: 53.33% Mismatches: 0  
Query Match: 74.53% Indels: 7  
DB: 4 Gaps: 1  
US-10-029-756-6 (1-8) x US-09-949-016-15804 (1-13117)  
Qy 1 TptileGlyHisAspAlaGlyHis 8  
Db 13046 TGGATCCAGTCCCTCTCTGCCCCCAGGGTCTAGCTGCGGCAC 13002

RESULT 59  
US-09-513-999C-8520  
; Sequence 8520, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 8520  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 88  
; OTHER INFORMATION: m-a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 108  
; OTHER INFORMATION: r-a or g  
US-09-513-999C-8520

Alignment Scores:  
Pred. No.: 144 Length: 415  
Score: 39.00 Matches: 5  
Percent Similarity: 75.00% Conservatives: 1  
Best Local Similarity: 62.50% Mismatches: 2  
Query Match: 73.58% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-8520 (1-415)

Qy 1 TptileGlyHisAspAlaGlyHis 8  
Db 45 TGGCTTGACATGATGTTCCGCAT 68

RESULT 60  
US-09-513-999C-8520  
; Sequence 8520, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 8520  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 88  
; OTHER INFORMATION: m-a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 108  
; OTHER INFORMATION: r-a or g  
US-09-513-999C-8520

Alignment Scores:  
Pred. No.: 637 Length: 1644  
Score: 39.00 Matches: 6  
Percent Similarity: 75.00% Conservatives: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 73.58% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-1172 (1-1644)

Qy 1 TptileGlyHisAspAlaGlyHis 8  
Db 169 TGGCAGGGCCACCCGCGAGGCAC 146

RESULT 62  
US-09-902-540-8493  
; Sequence 8493, Application US/09902540  
; Patent No. 683447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 2001-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SOFTWARE: Patent.pm  
; SEQ ID NO 8493  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 2001-07-10  
; NUMBER OF SEQ ID NOS: 16825

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; SEQ ID NO 8493
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8493

Alignment Scores:
Pred. No.: 698 Length: 1788
Score: 39.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-8493 (1-1788)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1749 TGGCGGGACATGGCGTGGTGCAC 1772

RESULT 63
US-09-614-891-2/c
; Sequence 2, Application US/09614891
; Patent No. 6680379
; GENERAL INFORMATION:
; APPLICANT: SUN, WILLIAM
; TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS
; FILE REFERENCE: 030727.0022.CIP.1
; CURRENT APPLICATION NUMBER: US/09/614,891
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,771
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-891-2

Alignment Scores:
Pred. No.: 767 Length: 1950
Score: 39.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-614-891-2 (1-1950)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 200 TGGCAGGGGCACCCGGCAGGCAC 177

RESULT 64
US-08-635-130A-3
; Sequence 3, Application US/08635130A
; Patent No. 6696557
; GENERAL INFORMATION:
; APPLICANT: Caras, Ingrid W
; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

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; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,130A
; FILING DATE: 19-Mar-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2380 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-635-130A-3

Alignment Scores:
Pred. No.: 951 Length: 2380
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-08-635-130A-3 (1-2380)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1976 TGGTGGGTGATGACAGCTACCAT 1999

RESULT 65
US-09-614-891-3/c
; Sequence 3, Application US/09614891
; Patent No. 6680379
; GENERAL INFORMATION:
; APPLICANT: SUN, WILLIAM
; TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS
; FILE REFERENCE: 030727.0022.CIP.1
; CURRENT APPLICATION NUMBER: US/09/614,891
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,771
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-891-3

Alignment Scores:
Pred. No.: 1e+03 Length: 2501
Score: 39.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-614-891-3 (1-2501)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 200 TGGCAGGGGCACCCGGCAGGCAC 177

RESULT 66
US-09-949-016-5096
; Sequence 5096, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

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```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5096
; LENGTH: 2993
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5096

Alignment Scores:
Pred. No.: 1.22e+03 Length: 2993
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-5096 (1-2993)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1948 TGGTGGGTGTCAGACAGTACCATT 1971

RESULT 67
US-09-949-016-205
; Sequence 205, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 3394
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205

Alignment Scores:
Pred. No.: 1.4e+03 Length: 3394
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-205 (1-3394)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 2346 TGGTGGGTGTCAGACAGTACCATT 2369
```

```
RESULT 68
US-09-902-540-894
; Sequence 894, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 894
; LENGTH: 7538
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-894

Alignment Scores:
Pred. No.: 3.31e+03 Length: 7538
Score: 39.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-894 (1-7538)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 3597 TGGCGGACATGGCGCTGGTCC 3620

RESULT 69
US-09-949-016-16838
; Sequence 16838, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16838
; LENGTH: 9948
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16838

Alignment Scores:
Pred. No.: 4.47e+03 Length: 9948
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-16838 (1-9948)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1948 TGGTGGGTGTCAGACAGTACCATT 1971
```



Pred. No.: 1.47e+04 Length: 29905  
Score: 39.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 73.58% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-16788 (1-29905)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 17368 TGGAGTGGCCGGATGACGGGCAC 17391

## RESULT 74

US-09-949-016-12818/c  
; Sequence 12818, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12818  
; LENGTH: 30678  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(30678)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12818

Alignment Scores:  
Pred. No.: 1.51e+04 Length: 30678  
Score: 39.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 73.58% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7  
Db 21624 TGGATAGGCCACCTAGCTGGA 21604

## RESULT 75

US-09-949-016-13610  
; Sequence 13610, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13610  
; LENGTH: 83428  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13610

Alignment Scores:  
Pred. No.: 4.43e+04 Length: 83428  
Score: 39.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 82.50% Mismatches: 1  
Query Match: 73.58% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-13610 (1-83428)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 39116 TGGGTGGGCACTGATGTGGGCAC 39139

## RESULT 76

US-09-949-016-17513/c  
; Sequence 17513, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17513  
; LENGTH: 121049  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17513

Alignment Scores:  
Pred. No.: 6.6e+04 Length: 121049  
Score: 39.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 71.43% Mismatches: 0  
Query Match: 73.58% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-17513 (1-121049)

Qy 1 TrpIleGlyHisAspAlaGly 7  
Db 106843 TGGTAGTCTATGAGGCTGGA 106823

## RESULT 77

US-09-214-808-1  
; Sequence 1, Application US/09214808A  
; Patent No. 6475793  
; GENERAL INFORMATION:  
; APPLICANT: Rosenthal, Andre  
; APPLICANT: Freiberg, Christoph  
; APPLICANT: Perret, Xavier Philippe  
; APPLICANT: Broughton, William John  
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP., NGR 234 Symbiotic  
; Patent No. 6475793  
; TITLE OF INVENTION: Plasmid

```
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/214,808A
; CURRENT FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/IB97/00950
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1

Alignment Scores:
Pred. No.: 3.13e+05 Length: 536165
Score: 39.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-214-808-1 (1-536165)

Qy 1 TrrlleGlyHisAspAlaGlyHis 8
Db 416103 TGGTGTGACATGACTCTGCCCAT 416126

RESULT 78
US-09-513-999C-2339/c
; Sequence 2339, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2339
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..186
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 147
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 149
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 152
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 153
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 43
; OTHER INFORMATION: Xaa=Leu or Pro
; FEATURE:
; NAME/KEY: UNSURE
```

---

```
; LOCATION: 44
; OTHER INFORMATION: Xaa= * or Cys or Phe or Leu or Ser or Tyr
US-09-513-999C-2339

Alignment Scores:
Pred. No.: 91.6 Length: 187
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-2339 (1-187)

Qy 1 TrrlleGlyHisAspAlaGlyHis 8
Db 33 TGGCAAACCATGATGTGGTCAC 10

RESULT 79
US-09-252-991A-4689
; Sequence 4689, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4689
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4689

Alignment Scores:
Pred. No.: 179 Length: 348
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-252-991A-4689 (1-348)

Qy 3 GlyHisAspAlaGlyHis 8
Db 115 GGCCACGACGCTGCCCAT 132

RESULT 80
US-09-621-976-15096
; Sequence 15096, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15096
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```



```
; NAME/KEY: misc_feature
; LOCATION: 281
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15096

Alignment Scores:
Pred. No.: 192 Length: 371
Score: 38.00 Matches: 6
Percent Similarity: 75.00% Conservativeness: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-621-976-15096 (1-371)
Oy 1 TptlGlyHisAspAlaGlyHis 8
Db 49 TGGAGCTTTCATGACGCTGGTCAT 72

RESULT 81
US-09-854-133-354
; Sequence 354, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(379)
; OTHER INFORMATION: n = A,T,C or G
US-09-854-133-354

Alignment Scores:
Pred. No.: 197 Length: 379
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-854-133-354 (1-379)
Oy 3 GlyHisAspAlaGlyHis 8
Db 40 GGCCATGATGCTGGACAC 57

RESULT 82
US-08-125-462-4/c
; Sequence 4, Application US/08125462
; Patent No. 5840840
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```

```
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,462
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-110-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..405
; OTHER INFORMATION: /standard_name= "Synthetic EDN"
; OTHER INFORMATION: "Gene"
; OTHER INFORMATION: /note= "Expression of the synthetic gene generates
; OTHER INFORMATION: a protein identical to the natural product, with
; OTHER INFORMATION: the exception that an additional methionine
US-08-125-462-4

Alignment Scores:
Pred. No.: 211 Length: 405
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x US-08-125-462-4 (1-405)
Oy 3 GlyHisAspAlaGlyHis 8
Db 361 GGTCAAGAGCTGGTGCAC 344

RESULT 83
US-08-891-848-4/c
; Sequence 4, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,848  
FILING DATE: No. 5955073 yet assigned  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,462  
FILING DATE: 22-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,082  
FILING DATE: 04-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,195  
FILING DATE: 22-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/510,696  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-110310US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..405  
OTHER INFORMATION: /note= "synthetic eosinophil derived  
neurotoxin (EDN) gene sequence"  
US-08-891-848-4

Alignment Scores:  
Pred. No.: 211 Length: 405  
Score: 38.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.70% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x US-08-891-848-4 (1-405)

Qy 3 GlyHisaspAlaGlyHis 8  
Db 361 GGTCAAGCGTGGTGCAC 344

RESULT 84  
US-09-621-976-19010  
Sequence 19010, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621.976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 19010  
LENGTH: 436  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-621-976-19010

Alignment Scores:  
Pred. No.: 229 Length: 436  
Score: 38.00 Matches: 5  
Percent Similarity: 62.50% Conservative: 0  
Best Local Similarity: 62.50% Mismatches: 3  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-621-976-19010 (1-436)

Qy 1 TrpIleGlyHisaspAlaGlyHis 8  
Db 133 TGGGCTGGGCATGATGGCTCACAC 156

RESULT 85  
US-09-513-999C-12630  
Sequence 12630, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59 US2 REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 12630  
LENGTH: 459  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 18  
OTHER INFORMATION: r=a or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 52  
OTHER INFORMATION: n=a, g, c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 53  
OTHER INFORMATION: y=c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 97  
OTHER INFORMATION: y=c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 391  
OTHER INFORMATION: k=g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 393  
OTHER INFORMATION: n=a, g, c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 396  
OTHER INFORMATION: r=a or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 401  
OTHER INFORMATION: y=c or t  
US-09-513-999C-12630

Alignment Scores:  
Pred. No.: 242 Length: 459  
Score: 38.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-12630 (1-459)

Qy 3 GlyHisAspAlaGlyHis 8

Db 105 GGACACGATGCAGGCCAT 122

#### RESULT 86

US-09-513-999C-1880  
; Sequence 1880, Application US/09513999C  
; Patent No. 6783961

#### GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 1880

; LENGTH: 486

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 112...486

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 18

; OTHER INFORMATION: r=a or g

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 52

; OTHER INFORMATION: n=a, g, c or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 53

; OTHER INFORMATION: y=c or t

US-09-513-999C-1880

#### Alignment Scores:

Pred. No.: 258 Length: 486  
Score: 38.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-1880 (1-486)

Qy 3 GlyHisAspAlaGlyHis 8

Db 105 GGACACGATGCAGGCCAT 122

#### RESULT 87

US-09-949-016-143643

; Sequence 143643, Application US/09949016

; Patent No. 6812339

#### GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 143643

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-143643

#### Alignment Scores:

Pred. No.: 324 Length: 601  
Score: 38.00 Matches: 5  
Percent Similarity: 75.00% Conservative: 1  
Best Local Similarity: 62.50% Mismatches: 2  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-143643 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 505 TGGGTGGTCACAGTGCCTGGCAT 528

#### RESULT 88

US-09-949-016-143644

; Sequence 143644, Application US/09949016

; Patent No. 6812339

#### GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 143644

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-143644

#### Alignment Scores:

Pred. No.: 324 Length: 601  
Score: 38.00 Matches: 5  
Percent Similarity: 75.00% Conservative: 1  
Best Local Similarity: 62.50% Mismatches: 2  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-143644 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 231 TGGGTGGTCACAGTGCCTGGCAT 254

#### RESULT 89

US-09-949-016-171125/c

; Sequence 171125, Application US/09949016

; Patent No. 6812339

#### GENERAL INFORMATION:

```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171125
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171125

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171125 (1-601)
Qy 1 TrrpIcGlyHisAspAlaGlyHis 8
Db 44 TGGGCTGGGCATGATGGCTCACAC 21

RESULT 90
US-09-949-016-171126/c
; Sequence 171126, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171126
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171126

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171126 (1-601)
Qy 1 TrrpIcGlyHisAspAlaGlyHis 8
Db 210 TGGGCTGGGCATGATGGCTCACAC 187

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RESULT 91
US-09-949-016-171255/c
; Sequence 171255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171255
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171255

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171255 (1-601)
Qy 1 TrrpIcGlyHisAspAlaGlyHis 8
Db 44 TGGGCTGGGCATGATGGCTCACAC 21

RESULT 92
US-09-949-016-171256/c
; Sequence 171256, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171256
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171256

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171256 (1-601)

```

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
||| ||||| |||||  
Db 210 TGGGCTGGGCATGATGGCTCACAC 187

```

RESULT 93
US-09-949-016-179881/c
; Sequence 179881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179881
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-179881

```

Alignment Scores:			
Pred. No.:	324	Length:	601
Score:	38.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	83.33%	Mismatches:	0
Query Match:	71.70%	Indels:	0
DB:	4	Gaps:	0

US-10-029-756-6 (1-8) x US-09-949-016-179881 (1-601)

Qy 1 TrpIleGlyHisAspAla 6  
|||::|||  
Db 322 TGGGTTGGGCACGATGCC 305

```

RESULT 94
US-09-949-016-200124
; Sequence 200124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200124
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-200124

```

```
Alignment Scores:
Pred. No.:      324      Length:      601
Score:          38.00    Matches:      5
Percent Similarity: 62.50% Conservative: 0
```

```

Best Local Similarity: 62.50%
Query Match: 71.70%
DB: 4
Mismatches: 3
Indels: 0
Gaps: 0

```

US-10-029-756-6 (1-8) x US-09-949-016-200124 (1-601)

1 T p I l e G l y H i s A s p A l a G l y H i s 8  
Qy  
61 T G G G C G G G G C A C G A T G G C T C A C A C 84  
p b

RESULT 95  
US-09-949-016-205533  
; Sequence 205533, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 205533  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-205533

Alignment Scores:		
Pred. No.:	324	Length: 601
Score:	38.00	Matches: 6
Percent Similarity:	75.00%	Conservative: 0
Best Local Similarity:	75.00%	Mismatches: 2
Query Match:	71.70%	Indels: 0
DB:	4	Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-205533 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
pB 378 TGGGCTGGAGCAGACGCTGGACAT 401

RESULT 96 .  
 US-09-543-681A-1128  
 ; Sequence 1128, Application US/09543681A  
 ; Patent No. 6605709  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GARY BRETON  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID S  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.1002-001  
 ; CURRENT APPLICATION NUMBER: US/09/543.681A  
 ; CURRENT FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,706  
 ; PRIOR FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 8344  
 ; SEQ ID NO 1128  
 ; LENGTH: 603  
 ; TYPE: DNA  
 ; ORGANISM: Proteus mirabilis  
 US-09-543-681A-1128

Alignment Scores:	
Pred. No.:	325
Score:	38.00
Percent Similarity:	100.00%
Length:	603
Matches:	6
Conservative:	0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-543-681A-1128 (1-603)

Qy 3 GlyHisAspAlaGlyHis 8  
Db 474 GCCCATGATGCTGAGTCAC 491

## RESULT 97

US-09-252-991A-4810/c  
; Sequence 4810, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 4810  
; LENGTH: 624  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4810

Alignment Scores:  
Pred. No.: 338 Length: 624  
Score: 38.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-252-991A-4810 (1-624)

Qy 3 GlyHisAspAlaGlyHis 8  
Db 142 GCCCAGCAGCTGGCCAT 125

## RESULT 98

US-09-252-991A-7908  
; Sequence 7908, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 7908  
; LENGTH: 699  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7908

Alignment Scores:  
Pred. No.: 382 Length: 699  
Score: 38.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-252-991A-7908 (1-699)

Qy 3 GlyHisAspAlaGlyHis 8  
Db 654 GCCCATGATGCTGGCAT 671

## RESULT 99

US-09-270-767-11527/c  
; Sequence 11527, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11527  
; LENGTH: 737  
; TYPE: DNA  
; ORGANISM: *Drosophila melanogaster*  
US-09-270-767-11527

Alignment Scores:  
Pred. No.: 404 Length: 737  
Score: 38.00 Matches: 5  
Percent Similarity: 75.00% Conservative: 1  
Best Local Similarity: 62.50% Mismatches: 2  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-270-767-11527 (1-737)

Qy 1 TtpIleGlyHisAspAlaGlyHis 8  
Db 191 TGGCTTGGCCATGCCAGGCCAC 168

## RESULT 100

US-09-902-540-5908  
; Sequence 5908, Application US/09902540  
; Patent No. 8833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR FILING DATE: 60/217,883  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5908  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: *Myxococcus xanthus*  
US-09-902-540-5908

Alignment Scores:  
Pred. No.: 414 Length: 753  
Score: 38.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.70% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-5908 (1-753)

Qy 3 GlyHisepAlaGlyHis 8  
|||||  
Db 588 GCCCATGACGCTGCCAC 605

Search completed: June 8, 2005, 15:28:08  
Job time : 1074.11 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 09:39:06 ; Search time 1648.42 Seconds

(without alignments)  
235.159 Million cell updates/sec

Title: US-10-029-756-6

Perfect score: 53

Sequence: 1 WIGHDAGH 8

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool.p/US10029756/runat\_07062005.122750.28779/app\_query.fasta\_1.597  
-DB=GenEmbl -QWIT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATTRIX=biosum62 -TRANS=human40.cdi -LIST=1000  
-DOCALIGN=200 -THR SCORES=ptc -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10029756@cgn.1.1.5965@runat\_07062005.122750.28779 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_on:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pt:\*  
10: gb\_ro:\*  
11: gb\_ats:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	1450	8	AY055118 Echium pi
2	53	100.0	1478	8	AY055117 Echium ge
3	53	100.0	1684	6	AR076814 Sequence
4	53	100.0	1684	6	AR084177 Sequence

5	53	100.0	1684	6	BD062571	A sunflow
6	53	100.0	1684	6	BD070919	An oleosi
7	53	100.0	1685	6	AR020904	Sequence 4
8	53	100.0	1685	6	I38430	Sequence
9	53	100.0	1685	6	AR200408	Sequence
10	53	100.0	1685	6	AR455421	Sequence
11	53	100.0	1685	8	AF007561	Borago of
12	53	100.0	1687	6	AX951561	Sequence
13	53	100.0	1687	6	BOU79010	U79010 Borago offi
14	50	94.3	1362	6	AX824969	Sequence
15	50	94.3	1362	6	AX824971	Sequence
16	50	94.3	1410	8	AY234125	Primula f
17	50	94.3	1618	8	AY234127	Primula v
18	50	94.3	1788	8	AF031194	Triticum
19	50	94.3	1856	8	AF005096	Ricinus c
20	50	94.3	1972	8	BT009556	Triticum
21	49	92.5	140990	10	AC142257	Mus muscu
22	49	92.5	174714	2	AC107366	Mus muscu
23	49	92.5	183187	10	AC104328	Mus muscu
24	48	90.6	1347	8	AY131238	Argania s
25	48	90.6	1385	8	AY234126	Primula v
26	48	90.6	1681	8	AY234124	Primula f
27	47	88.7	1798	8	AK058543	Oryza sat
28	47	88.7	83296	2	AC022588	Homo sapi
29	47	88.7	95161	8	AP005554	Oryza sat
30	47	88.7	139537	9	AC021039	Homo sapi
31	47	88.7	158262	2	AC013757	Homo sapi
32	46	86.8	649	6	AX320439	Sequence
33	46	86.8	1570	3	AB127388	Haemaphys
34	46	86.8	42208	9	AL589989	Human DNA
35	46	86.8	42601	9	AC004210	Homo sapi
36	46	86.8	43003	9	AL845556	Human DNA
37	46	86.8	100000	9	AP000508	Homo sapi
38	46	86.8	102821	2	CR759828	Homo sapi
39	46	86.8	138102	9	AC004866	Homo sapi
40	46	86.8	160147	9	AC146233	Pan trogl
41	46	86.8	166079	9	AC090151	Homo sapi
42	46	86.8	166335	2	AC012461	Homo sapi
43	46	86.8	178168	2	AC012350	Homo sapi
44	46	86.8	181727	2	AC036232	Homo sapi
45	46	86.8	182152	2	AC067929	Homo sapi
46	46	86.8	184852	2	AC026032	Homo sapi
47	46	86.8	209452	2	AC108778	Mus muscu
48	46	86.8	211237	10	AC126280	Mus muscu
49	46	86.8	236822	9	DB4394	Homo sapien
50	46	86.8	244928	2	AC097177	Rattus no
51	46	86.8	245125	2	AC133759	Rattus no
52	46	86.8	256373	2	AC128269	Rattus no
53	46	86.8	333800	1	SME591792	Sinorhizo
54	46	86.8	338579	1	AP003004	Mesorhizo
55	45	84.9	1258	10	BC008166	Mus muscu
56	45	84.9	1623	10	AB069965	Mus muscu
57	45	84.9	1910	10	BC024119	Mus muscu
58	45	84.9	1927	10	BC013474	Mus muscu
59	45	84.9	1951	10	BC026598	Mus muscu
60	45	84.9	1976	10	BC026597	Mus muscu
61	45	84.9	99059	10	AL929383	Mouse DNA
62	45	84.9	101937	9	AC010221	Homo sapi
63	45	84.9	127121	2	AC008874	Homo sapi
64	45	84.9	165176	2	AC022199	Homo sapi
65	45	84.9	167322	2	AC016788	Homo sapi
66	45	84.9	190032	9	AP003462	Homo sapi
67	45	84.9	193415	2	AC074180	Homo sapi
68	45	84.9	197591	9	AC113404	Homo sapi
69	45	84.9	197997	6	AX663810	Sequence
70	45	84.9	200232	9	AC026783	Homo sapi
71	45	84.9	208710	10	AC126262	Mus muscu
72	45	84.9	218575	2	AL844841	Mus muscu
73	45	84.9	220283	2	AC103391	Mus muscu
74	45	84.9	224037	10	AL670399	Mouse DNA
75	45	84.9	231770	2	AC109171	Mus muscu
76	45	84.9	235505	2	AC133422	Rattus no
77	45	84.9	238637	2	AC092254	Mus muscu

78	45	84.9	245515	2	AC151275	AC151275 Mus muscu	151	43	81.1	266766	2	AC094770	AC094770 Rattus no
79	45	84.9	245515	2	AC151275	AC151275 Mus muscu	152	43	81.1	275555	2	AC097204	AC097204 Rattus no
80	45	84.9	251564	2	AC125698	AC125698 Rattus no	c 153	43	81.1	299750	1	AP005964	AP005964 Bradyrhiz
81	44	83.0	162	6	AR524799	AR524799 Sequence	c 154	43	81.1	300400	1	AP005943	AP005943 Bradyrhiz
82	84	83.0	833	6	AR508777	AR508777 Sequence	c 155	43	81.1	301675	1	AP005027	AP005027 Streptomy
83	44	83.0	2734	6	CQ590748	CQ590748 Sequence	c 156	43	81.1	309050	1	SC0939117	AL939117 Streptomy
84	44	83.0	5679	6	CQ590747	CQ590747 Sequence	c 157	43	81.1	311050	1	BX294133	BX294133 Pirellula
85	44	83.0	33443	2	AC014332	AC014332 Sequence	c 158	42	79.2	385	10	S66658	S66658 alpha-globi
86	44	83.0	160817	3	AC008316	AC008316 Drosophil	c 159	42	79.2	393	10	RATAGLO28X	M94075 Rat alpha-g
87	44	83.0	167230	8	AP003275	AP003275 Oryza sat	c 160	42	79.2	424	10	S5233753	S52345 OSF-1-pleio
88	44	83.0	172704	10	AC121531	AC121531 Mus muscu	c 161	42	79.2	517	10	BC048363	BC048363 Mus muscu
89	44	83.0	177028	3	AC008315	AC008315 Drosophil	c 162	42	79.2	522	6	AX577903	AX577903 Sequence
90	44	83.0	211153	2	AC136636	AC136636 Mus muscu	c 163	42	79.2	533	11	G90099	G90099 S208P6678FC
91	44	83.0	224124	2	AC098578	AC098578 Rattus no	c 164	42	79.2	650	6	AR307081	AR307081 Sequence
92	44	83.0	227182	2	AC111765	AC111765 Rattus no	c 165	42	79.2	650	6	AX154831	AX154831 Sequence
93	44	83.0	236198	2	AC108547	AC108547 Rattus no	c 166	42	79.2	672	6	CQ718202	CQ718202 Sequence
94	44	83.0	238323	3	AE003684	AE003684 Drosophil	c 167	42	79.2	734	6	BD147575	BD147575 Primer fo
95	44	83.0	239808	2	AC126585	AC126585 Rattus no	c 168	42	79.2	734	6	AX867513	AX867513 Sequence
96	44	83.0	246850	1	AP005346	AP005346 Vibrio vu	c 169	42	79.2	816	6	AR508169	AR508169 Sequence
97	44	83.0	301936	1	AE018808	AE018808 Vibrio vu	c 170	42	79.2	1167	8	AK109032	AK109032 Oryza sat
98	44	83.0	344321	1	BX640429	BX640429 Bordetell	c 171	42	79.2	1249	10	RNU622315	U62315 Rattus norv
99	44	83.0	346274	1	BX640443	BX640443 Bordetell	c 172	42	79.2	1331	10	BC002064	BC002064 Mus muscu
100	44	83.0	349354	1	BX640416	BX640416 Bordetell	c 173	42	79.2	1452	6	CQ733333	CQ733333 Sequence
101	43	81.1	24453	9	HS404P13	AL035069 Human DNA	c 174	42	79.2	1514	6	AX305712	AX305712 Sequence
102	43	81.1	33766	2	AC103836	AC103836 Homo sapi	c 175	42	79.2	1514	10	MUSOSF1	D90225 Mus musculu
103	43	81.1	39338	9	AC004644	AC004644 Homo sapi	c 176	42	79.2	1542	6	E03564	E03564 CDNA encodi
104	43	81.1	51240	2	AC104999	AC104999 Homo sapi	c 177	42	79.2	1591	8	HACVTBERN	H87143 Helianthus
105	43	81.1	59271	10	AL929456	AL929456 Mouse DNA	c 178	42	79.2	1603	10	BC061695	BC061695 Mus muscu
106	43	81.1	66917	2	AC104368	AC104368 Homo sapi	c 179	42	79.2	1606	6	AX007273	AX007273 Sequence
107	43	81.1	87099	2	AC151336	AC151336 Xenopus t	c 180	42	79.2	1638	10	BC078828	BC078828 Rattus no
108	43	81.1	110000	2	AC140815	Continuation (2 of	c 181	42	79.2	1866	6	BD157966	BD157966 Primer fo
109	43	81.1	114521	9	AL159985	AL159985 Human DNA	c 182	42	79.2	1866	6	AX879681	AX879681 Sequence
110	43	81.1	123153	2	AC149083	AC149083 Pan trogl	c 183	42	79.2	1866	9	AC022726	AC022726 Homo sapi
111	43	81.1	133786	9	AC091839	AC091839 Homo sapi	c 184	42	79.2	1917	9	BC033824	BC033824 Homo sapi
112	43	81.1	135407	2	AC124114	AC124114 Mus muscu	c 185	42	79.2	1974	3	BT001527	BT001527 Drosophil
113	43	81.1	136155	8	GNS08C80	AL731751 Oryza sat	c 186	42	79.2	2077	8	CR533565	CR533565 Homo sapi
114	43	81.1	140531	2	AC105341	AC105341 Homo sapi	c 187	42	79.2	2077	8	SCYNR012W	Z71627 S. cerevisia
115	43	81.1	150649	2	AC142157	AC142157 Rattus no	c 188	42	79.2	2188	5	CR760964	CR760964 Xenopus t
116	43	81.1	155937	2	AC016341	AC016341 Homo sapi	c 189	42	79.2	2238	6	BD206377	BD206377 Human nuc
117	43	81.1	160378	2	AC090076	AC090076 Homo sapi	c 190	42	79.2	2238	6	AR400692	AR400692 Sequence
118	43	81.1	166344	2	AL162577	AL162577 Homo sapi	c 191	42	79.2	2238	6	AX013196	AX013196 Sequence
119	43	81.1	167789	2	AC084260	AC084260 Homo sapi	c 192	42	79.2	2305	6	CQ718453	CQ718453 Sequence
120	43	81.1	167794	9	AC092472	AC092472 Homo sapi	c 193	42	79.2	2307	6	AR060049	AR060049 Sequence
121	43	81.1	170973	9	AC090097	AC090097 Homo sapi	c 194	42	79.2	2307	6	AR087204	AR087204 Sequence
122	43	81.1	172551	9	AC008518	AC008518 Homo sapi	c 195	42	79.2	2307	6	AR134391	AR134391 Sequence
123	43	81.1	172927	2	AC119701	AC119701 Rattus no	c 196	42	79.2	2307	6	AR144492	AR144492 Sequence
124	43	81.1	173888	9	AC105091	AC105091 Homo sapi	c 197	42	79.2	2307	6	AR256663	AR256663 Sequence
125	43	81.1	174741	2	AC024280	AC024280 Homo sapi	c 198	42	79.2	2307	6	AR372547	AR372547 Sequence
126	43	81.1	175838	9	AC026427	AC026427 Homo sapi	c 199	42	79.2	2307	9	HUMORFC	L40393 Homo sapien
127	43	81.1	176116	2	AC138590	AC138590 Mus muscu	c 200	42	79.2	2307	11	G27111	G27111 human STS S
128	43	81.1	176889	9	AC090274	AC090274 Homo sapi	c 201	42	79.2	2395	8	AB126085	AB126085 Oryza sat
129	43	81.1	176902	9	AF280813	AF280813 Homo sapi	c 202	42	79.2	2395	8	AK068159	AK068159 Oryza sat
130	43	81.1	185010	2	AC022514	AC022514 Mus muscu	c 203	42	79.2	2486	6	AX747833	AX747833 Sequence
131	43	81.1	186340	2	AC016684	AC016684 Homo sapi	c 204	42	79.2	2486	9	AK092975	AK092975 Homo sapi
132	43	81.1	190814	9	AC006111	AC006111 Homo sapi	c 205	42	79.2	2702	6	CQ493997	CQ493997 Sequence
133	43	81.1	198475	2	AC150880	AC150880 Bos tauru	c 206	42	79.2	2707	8	SCURK1	XS1998 S. cerevisia
134	43	81.1	203083	2	AC069459	AC069459 Mus muscu	c 207	42	79.2	2741	6	CQ603213	CQ603213 Sequence
135	43	81.1	204430	2	AC118027	AC118027 Mus muscu	c 208	42	79.2	2818	9	AB040911	AB040911 Homo sapi
136	43	81.1	207364	2	AC120564	AC120564 Rattus no	c 209	42	79.2	2846	6	AX321399	AX321399 Sequence
137	43	81.1	210643	9	AC137723	AC137723 Homo sapi	c 210	42	79.2	2995	6	AB4104	AB4104 Sequence 8
138	43	81.1	214382	10	AC098733	AC098733 Mus muscu	c 211	42	79.2	2995	9	AF015040	AF015040 Homo sapi
139	43	81.1	217584	2	AC113299	AC113299 Mus muscu	c 212	42	79.2	3045	9	BC024144	BC024144 Homo sapi
140	43	81.1	220737	2	AC128459	AC128459 Rattus no	c 213	42	79.2	3050	6	AX342026	AX342026 Sequence
141	43	81.1	223877	2	AC098923	AC098923 Rattus no	c 214	42	79.2	3050	6	AX342529	AX342529 Sequence
142	43	81.1	228998	2	AC112472	AC112472 Rattus no	c 215	42	79.2	3050	6	AX590316	AX590316 Sequence
143	43	81.1	232535	2	AC110702	AC110702 Rattus no	c 216	42	79.2	3050	9	AB030251	AB030251 Homo sapi
144	43	81.1	233882	2	AC112119	AC112119 Rattus no	c 217	42	79.2	3079	6	AX321395	AX321395 Sequence
145	43	81.1	234182	10	AL603707	AL603707 Mouse DNA	c 218	42	79.2	3079	9	AK000733	AK000733 Homo sapi
146	43	81.1	235276	10	AC102334	AC102334 Mus muscu	c 219	42	79.2	3079	9	BC032754	BC032754 Homo sapi
147	43	81.1	239030	2	AC135695	AC135695 Rattus no	c 220	42	79.2	3144	6	AR339606	AR339606 Sequence
148	43	81.1	251002	3	CNS07EGI	AL590451 chromosome	c 221	42	79.2	3155	6	CQ590060	CQ590060 Sequence
149	43	81.1	261587	2	AC126139	AC126139 Rattus no	c 222	42	79.2	3237	6	AX086632	AX086632 Sequence
150	43	81.1	261968	2	AC120289	AC120289 Rattus no	c 223	42	79.2	3270	9	AF108092	AF108092 Homo sapi

C 224	42	79.2	3336	6	C0586230	Sequence	C0586230	Sequence	297	42	79.2	188774	2	AC116853	Mus muscu
C 225	42	79.2	3370	6	AX281755	Homo sapi	AX281755	Homo sapi	c 298	42	79.2	190630	9	AC145773	Pan trogl
C 226	42	79.2	3429	9	AF171941	Homo sapi	AF171941	Homo sapi	299	42	79.2	191606	10	AC126272	Mus muscu
C 227	42	79.2	3462	9	AF171939	Homo sapi	AF171939	Homo sapi	c 300	42	79.2	191655	2	AC139828	Homo sapi
C 228	42	79.2	3479	9	HSM807281	Homo sapi	BX647137	Homo sapi	c 301	42	79.2	193700	2	AC139472	Homo sapi
C 229	42	79.2	3509	9	BC068476	Homo sapi	BC068476	Homo sapi	302	42	79.2	194454	2	AC140176	Homo sapi
C 230	42	79.2	3573	9	AF171940	Homo sapi	AF171940	Homo sapi	303	42	79.2	194866	2	AC142140	Rattus no
C 231	42	79.2	3606	9	AF171938	Homo sapi	AF171938	Homo sapi	304	42	79.2	194897	3	AC007697	Drosophi
C 232	42	79.2	4741	6	C0603212	Sequence	C0603212	Sequence	305	42	79.2	195768	9	AC022034	Homo sapi
C 233	42	79.2	6005	6	C0586229	Sequence	C0586229	Sequence	c 306	42	79.2	198141	2	AC138893	Homo sapi
C 234	42	79.2	12869	1	AE015268	Shigella	AE015268	Shigella	c 307	42	79.2	199016	9	HS480G12	Human DNA
C 235	42	79.2	23901	8	SCN201952	S cerevisia	X77395	S cerevisia	308	42	79.2	203046	2	AC006342	Homo sapi
C 236	42	79.2	39835	2	AC014355	Drosophi	AC014355	Drosophi	309	42	79.2	203256	2	AC117787	Mus muscu
C 237	42	79.2	41839	9	AC104815	Homo sapi	AC104815	Homo sapi	310	42	79.2	203980	2	AC134058	Rattus no
C 238	42	79.2	62327	9	AL365226	Human DNA	AL365226	Human DNA	311	42	79.2	209284	2	AC107589	Rattus no
C 239	42	79.2	62327	9	AL365226	Human DNA	AL365226	Human DNA	312	42	79.2	209539	2	AC139802	Homo sapi
C 240	42	79.2	74994	2	AP000651	Homo sapi	AP000651	Homo sapi	c 313	42	79.2	210000	2	AC110556	Mus muscu
C 241	42	79.2	84102	9	AY498860	Homo sapi	AY498860	Homo sapi	c 314	42	79.2	211927	2	AC150462	Callithri
C 242	42	79.2	103606	9	AC005004	Homo sapi	AC005004	Homo sapi	c 315	42	79.2	212332	5	BX294395	Zebrafish
C 243	42	79.2	110000	1	AE017354_08	Continuation (9 of	Continuation (9 of	Continuation (9 of	c 316	42	79.2	214895	10	AL845313	Mouse DNA
C 244	42	79.2	110000	1	AE017354_09	Continuation (10 of	Continuation (10 of	Continuation (10 of	c 317	42	79.2	216194	10	AC096051	Rattus no
C 245	42	79.2	110000	1	CR628336_09	Continuation (10 o	Continuation (10 o	Continuation (10 o	c 318	42	79.2	216387	9	AF109907	Homo sapi
C 246	42	79.2	110000	1	CR628336_10	Continuation (11 o	Continuation (11 o	Continuation (11 o	c 319	42	79.2	222386	2	AC138852	Homo sapi
C 247	42	79.2	110000	1	CR628337_09	Continuation (10 o	Continuation (10 o	Continuation (10 o	c 320	42	79.2	223363	2	AC120700	Rattus no
C 248	42	79.2	110000	2	AC115960_0	Continuation (2 of	Continuation (2 of	Continuation (2 of	c 321	42	79.2	228657	2	AC112333	Rattus no
C 249	42	79.2	110000	2	AC138524_1	Continuation (4 of	Continuation (4 of	Continuation (4 of	c 322	42	79.2	229923	2	AC125666	Rattus no
C 250	42	79.2	110000	2	AC139486_3	Continuation (3 of	Continuation (3 of	Continuation (3 of	c 323	42	79.2	230800	10	AL831742	Mouse DNA
C 251	42	79.2	110000	2	AC139487_2	Continuation (4 of	Continuation (4 of	Continuation (4 of	c 324	42	79.2	230800	10	AL831742	Mouse DNA
C 252	42	79.2	110000	2	AC139489_3	Continuation (4 of	Continuation (4 of	Continuation (4 of	c 325	42	79.2	231134	2	AC115520	Rattus no
C 253	42	79.2	11655	2	AC010239	Homo sapi	AC010239	Homo sapi	c 326	42	79.2	240645	2	AC131537	Rattus no
C 254	42	79.2	119393	9	AC003658	Homo sapi	AC003658	Homo sapi	c 327	42	79.2	241912	2	AC106197	Rattus no
C 255	42	79.2	122105	2	AL355998	Homo sapi	AL355998	Homo sapi	c 328	42	79.2	243648	2	AC128576	Rattus no
C 256	42	79.2	122912	2	AL355998	Homo sapi	AL355998	Homo sapi	c 329	42	79.2	246095	3	AE003802	Drosophi
C 257	42	79.2	124441	2	AC027098	Homo sapi	AC027098	Homo sapi	c 330	42	79.2	246109	2	AC127914	Rattus no
C 258	42	79.2	132077	9	AC005589	Homo sapi	AC005589	Homo sapi	c 331	42	79.2	249245	2	AC110695	Rattus no
C 259	42	79.2	135978	10	AL645582	Mouse DNA	AL645582	Mouse DNA	c 332	42	79.2	249565	2	AC097125	Rattus no
C 260	42	79.2	140096	9	AC092617	Homo sapi	AC092617	Homo sapi	c 333	42	79.2	250064	2	AC103494	Rattus no
C 261	42	79.2	140626	9	AC008127	Homo sapi	AC008127	Homo sapi	c 334	42	79.2	251769	2	AC117913	Rattus no
C 262	42	79.2	148232	2	AC121068	Pan trogl	AC121068	Pan trogl	c 335	42	79.2	251947	2	AC138849	Homo sapi
C 263	42	79.2	151262	9	AC093824	Homo sapi	AC093824	Homo sapi	c 336	42	79.2	252968	2	AC112300	Rattus no
C 264	42	79.2	151498	9	AL357835	Human DNA	AL357835	Human DNA	c 337	42	79.2	262198	2	AC106703	Rattus no
C 265	42	79.2	153863	2	AC025361	Homo sapi	AC025361	Homo sapi	c 338	42	79.2	268850	2	AC110949	Rattus no
C 266	42	79.2	154616	9	AC004846	Homo sapi	AC004846	Homo sapi	c 339	42	79.2	276008	2	AC112310	Rattus no
C 267	42	79.2	157734	8	OSJN00058	Oryza sat	AL606624	Oryza sat	c 340	42	79.2	287344	3	AE003816	Drosophi
C 268	42	79.2	160438	2	AC024971	Homo sapi	AC024971	Homo sapi	c 341	42	79.2	289103	2	AC126288	Rattus no
C 269	42	79.2	160869	2	AC026378	Mus muscu	AC026378	Mus muscu	c 342	42	79.2	292088	1	AE016986	Shigella
C 270	42	79.2	161500	9	AC103778	Homo sapi	AC103778	Homo sapi	c 343	42	79.2	309677	2	AC128863	Rattus no
C 271	42	79.2	161540	2	AC024229	Homo sapi	AC024229	Homo sapi	c 344	42	79.2	313518	1	AE016856	Pseudomon
C 272	42	79.2	162361	2	AC138967	Homo sapi	AC138967	Homo sapi	c 345	42	79.2	335598	2	AC133302	Rattus no
C 273	42	79.2	162493	2	AC138967	Homo sapi	AC138967	Homo sapi	c 346	42	79.2	340750	1	BX294135	Pirellula
C 274	42	79.2	164813	9	AC025154	Homo sapi	AC025154	Homo sapi	c 347	42	79.2	341944	2	AC079158	Homo sapi
C 275	42	79.2	165350	2	AC134958	Rattus no	AC134958	Rattus no	c 348	41.5	78.3	231285	2	AC097867	Rattus no
C 276	42	79.2	165848	2	AC138813	Homo sapi	AC138813	Homo sapi	c 349	41	77.4	339	6	CQ744270	Sequence
C 277	42	79.2	166347	9	AC098810	Papio anu	AC098810	Papio anu	c 350	41	77.4	342	1	XM342	X. maltophi
C 278	42	79.2	167408	2	AC025526	Homo sapi	AC025526	Homo sapi	c 351	41	77.4	380	8	AF358778	Oryza sat
C 279	42	79.2	168683	2	AC102348	Mus muscu	AC102348	Mus muscu	c 352	41	77.4	532	3	AF526232	Argopecte
C 280	42	79.2	172617	9	AC138816	Homo sapi	AC138816	Homo sapi	c 353	41	77.4	544	6	CQ775970	Sequence
C 281	42	79.2	173607	9	AC139493	Homo sapi	AC139493	Homo sapi	c 354	41	77.4	544	6	CQ790567	Sequence
C 282	42	79.2	173856	8	AP003203	Oryza sat	AP003203	Oryza sat	c 355	41	77.4	742	8	AF466103	Theobroma
C 283	42	79.2	175222	2	AC130641	Rattus no	AC130641	Rattus no	c 356	41	77.4	816	1	AB003685	Bacillus
C 284	42	79.2	175272	2	AC140809	Homo sapi	AC140809	Homo sapi	c 357	41	77.4	816	6	B50428	Process for
C 285	42	79.2	175357	9	AC138956	Homo sapi	AC138956	Homo sapi	c 358	41	77.4	955	6	AX065567	Sequence
C 286	42	79.2	176199	9	AC093307	Homo sapi	AC093307	Homo sapi	c 359	41	77.4	1058	4	ECIL12P40	Equus cabal
C 287	42	79.2	176421	9	AC096888	Homo sapi	AC096888	Homo sapi	c 360	41	77.4	1069	8	SP1ASCPER	Sequence
C 288	42	79.2	176740	2	AC102471	Mus muscu	AC102471	Mus muscu	c 361	41	77.4	1077	1	AB127053	Bacillus
C 289	42	79.2	177816	2	AC017643	Drosophi	AC017643	Drosophi	c 362	41	77.4	1083	8	SP1CAP	Spincia ol
C 290	42	79.2	177819	9	AC100771	Homo sapi	AC100771	Homo sapi	c 363	41	77.4	1143	6	AX653423	Sequence
C 291	42	79.2	178051	2	AC141333	Rattus no	AC141333	Rattus no	c 364	41	77.4	1312	5	BC064281	Danio rer
C 292	42	79.2	182295	2	AP001501	Homo sapi	AP001501	Homo sapi	c 365	41	77.4	1329	1	AJ842019	Streptoco
C 293	42	79.2	183161	3	AP0017851	Drosophi	AP0017851	Drosophi	c 366	41	77.4	1329	1	AJ842020	Streptoco
C 294	42	79.2	183641	2	AC118666	Rattus no	AC118666	Rattus no	c 367	41	77.4	1329	1	AJ842021	Streptoco
C 295	42	79.2	185379	2	AC138918	Homo sapi	AC138918	Homo sapi	c 368	41	77.4	1350	6	AX505863	Sequence
C 296	42	79.2	187877	2	AC023251	Homo sapi	AC023251	Homo sapi	c 369	41	77.4	1453	1	ANPRRNAB	A. abactocia

c 370	41	77.4	1461	6	BD016516	BD016516 Genes and	c 443	41	77.4	4694	9	HSM807133	BSX40976 Homo sapi
371	41	77.4	1491	8	BT003379	BT003379 Arabidops	444	41	77.4	4750	6	CQ873929	CQ873929 Sequence
372	41	77.4	1534	8	AB031546	AB031546 Chlamydom	445	41	77.4	4750	9	AF220263	AF220263 Homo sapi
c 373	41	77.4	1626	12	AF401989	AF401989 Synthetic	c 446	41	77.4	4965	6	CQ789052	CQ789052 Sequence
374	41	77.4	1633	8	AF001394	AF001394 Arabidops	c 447	41	77.4	4965	6	AR218911	AR218911 Sequence
375	41	77.4	1652	8	AY087345	AY087345 Arabidops	c 448	41	77.4	4965	6	BD003823	BD003823 Polynucle
376	41	77.4	1678	6	AK007241	AK007241 Sequence	c 449	41	77.4	5095	6	I18513	I18513 Sequence 3
377	41	77.4	1704	8	AF428420	AF428420 Arabidops	c 450	41	77.4	5095	6	AR204074	AR204074 Sequence
378	41	77.4	1705	8	ATAJ4161	ATAJ4161 Arabidops	c 451	41	77.4	5095	6	AR482544	AR482544 Sequence
c 379	41	77.4	1736	8	AK065299	AK065299 Oryza sat	c 452	41	77.4	5095	6	BD094050	BD094050 Shear str
380	41	77.4	1743	8	BT000442	BT000442 Arabidops	c 453	41	77.4	5175	6	CQ882057	CQ882057 Sequence
c 381	41	77.4	1815	10	AF170709	AF170709 Mus muscu	c 454	41	77.4	5356	9	BSX48281	BSX48281 Homo sapi
c 382	41	77.4	1929	10	AF169191	AF169191 Mus muscu	c 455	41	77.4	5382	6	BD141296	BD141296 Method of
c 383	41	77.4	1962	10	AF169192	AF169192 Mus muscu	c 456	41	77.4	5591	1	AY032955	AY032955 Methyloco
c 384	41	77.4	2000	6	AK656740	AK656740 Sequence	c 457	41	77.4	5851	6	BD171148	BD171148 Novel gen
c 385	41	77.4	2258	9	AK054685	AK054685 Homo sapi	c 458	41	77.4	5851	6	BD183308	BD183308 Novel gen
386	41	77.4	2338	5	BC066589	BC066589 Danio rer	c 459	41	77.4	5851	9	AB051435	AB051435 Homo sapi
387	41	77.4	2463	1	AB119810	AB119810 Streptoco	c 460	41	77.4	10029	9	AB008555	AB008555 Streptoco
388	41	77.4	2463	1	AB119812	AB119812 Streptoco	c 461	41	77.4	10595	1	AB031319	AB031319 Nocardioid
389	41	77.4	2463	1	AB119814	AB119814 Streptoco	c 462	41	77.4	10826	1	AE005947	AE005947 Caulobact
390	41	77.4	2463	1	AB119824	AB119824 Streptoco	c 463	41	77.4	11216	1	AE007498	AE007498 Streptoco
391	41	77.4	2463	6	AK480654	AK480654 Sequence	c 464	41	77.4	11821	1	AY165002	AY165002 Pigmentip
392	41	77.4	2466	1	AB119793	AB119793 Streptoco	c 465	41	77.4	19824	1	RHMOTB	L49337 Snorhizob
393	41	77.4	2466	1	AB119794	AB119794 Streptoco	c 466	41	77.4	29112	6	CQ363821	CQ363821 Sequence
394	41	77.4	2466	1	AB119795	AB119795 Streptoco	c 467	41	77.4	29180	2	AC019819	AC019819 Drosophil
395	41	77.4	2466	1	AB119796	AB119796 Streptoco	c 468	41	77.4	37719	10	BSX294108	BSX294108 Mouse DNA
396	41	77.4	2466	1	AB119797	AB119797 Streptoco	c 469	41	77.4	42805	9	AC004221	AC004221 Homo sapi
397	41	77.4	2466	1	AB119798	AB119798 Streptoco	c 470	41	77.4	44665	9	HSB107C2	ALU08724 Human DNA
398	41	77.4	2466	1	AB119799	AB119799 Streptoco	c 471	41	77.4	48600	9	AY324609	AY324609 Homo sapi
399	41	77.4	2466	1	AB119800	AB119800 Streptoco	c 472	41	77.4	49736	1	AF319998	AF319998 Stigmatel
400	41	77.4	2466	1	AB119801	AB119801 Streptoco	c 473	41	77.4	52777	9	AP000268	AP000268 Homo sapi
401	41	77.4	2466	1	AB119802	AB119802 Streptoco	c 474	41	77.4	52993	2	AC101518	AC101518 Mus muscu
402	41	77.4	2466	1	AB119803	AB119803 Streptoco	c 475	41	77.4	60733	2	AC131946	AC131946 Homo sapi
403	41	77.4	2466	1	AB119804	AB119804 Streptoco	c 476	41	77.4	64347	2	AC151337	AC151337 Xenopus t
404	41	77.4	2466	1	AB119805	AB119805 Streptoco	c 477	41	77.4	68662	9	AL133293	AL133293 Human DNA
405	41	77.4	2466	1	AB119806	AB119806 Streptoco	c 478	41	77.4	74165	8	BSX97678	BSX97678 Neurospor
406	41	77.4	2466	1	AB119807	AB119807 Streptoco	c 479	41	77.4	77207	2	AC074067	AC074067 Homo sapi
407	41	77.4	2466	1	AB119808	AB119808 Streptoco	c 480	41	77.4	87840	2	AC149900	AC149900 Xenopus t
408	41	77.4	2466	1	AB119809	AB119809 Streptoco	c 481	41	77.4	88892	9	AC096758	AC096758 Homo sapi
409	41	77.4	2466	1	AB119811	AB119811 Streptoco	c 482	41	77.4	89003	1	BSZ75208	Z75208 B.subtilis
410	41	77.4	2466	1	AB119813	AB119813 Streptoco	c 483	41	77.4	95993	8	ATF2A19	ALU32962 Arabidops
411	41	77.4	2466	1	AB119815	AB119815 Streptoco	c 484	41	77.4	100000	9	AP000033	AP000033 Homo sapi
412	41	77.4	2466	1	AB119816	AB119816 Streptoco	c 485	41	77.4	100000	9	AP000102	AP000102 Homo sapi
413	41	77.4	2466	1	AB119817	AB119817 Streptoco	c 486	41	77.4	100000	9	AP000178	AP000178 Homo sapi
414	41	77.4	2466	1	AB119818	AB119818 Streptoco	c 487	41	77.4	103804	9	AP003472	AP003472 Homo sapi
415	41	77.4	2466	1	AB119819	AB119819 Streptoco	c 488	41	77.4	103973	8	AP004028	AP004028 Oryza sat
416	41	77.4	2466	1	AB119820	AB119820 Streptoco	c 489	41	77.4	108930	9	AL513122	AL513122 Human DNA
417	41	77.4	2466	1	AB119821	AB119821 Streptoco	c 490	41	77.4	109022	8	AP004926	AP004926 Lotus cor
418	41	77.4	2466	1	AB119822	AB119822 Streptoco	c 491	41	77.4	110000	1	AE017282	Continuation (2 of
419	41	77.4	2466	1	AB119823	AB119823 Streptoco	c 492	41	77.4	110000	2	AE017283	Continuation (9 of
420	41	77.4	2466	1	AB119825	AB119825 Streptoco	c 493	41	77.4	110000	2	AE017283	Continuation (3 of
421	41	77.4	2466	1	AB119826	AB119826 Streptoco	c 494	41	77.4	110000	2	BSX25276	Continuation (9 of
422	41	77.4	2466	1	AB119827	AB119827 Streptoco	c 495	41	77.4	110000	2	BSX11197	Continuation (28 o
423	41	77.4	2466	1	AB119828	AB119828 Streptoco	c 496	41	77.4	110000	8	CR382132	Continuation (28 o
424	41	77.4	2466	1	AB119829	AB119829 Streptoco	c 497	41	77.4	114600	9	HS477H23	ALU351323 Human DNA
425	41	77.4	2466	1	AB119830	AB119830 Streptoco	c 498	41	77.4	116704	10	AL591921	AL591921 Mouse DNA
426	41	77.4	2466	1	AB119831	AB119831 Streptoco	c 499	41	77.4	128618	9	AC011485	AC011485 Homo sapi
427	41	77.4	2466	1	AB119832	AB119832 Streptoco	c 500	41	77.4	129921	8	AC146568	AC146568 Medicago
428	41	77.4	2466	1	AF101781	AF101781 Streptoco	c 501	41	77.4	132049	9	AL954207	AL954207 Pan trogl
429	41	77.4	2466	6	BD223944	BD223944 Nucleic a	c 502	41	77.4	132981	8	AC147802	AC147802 Oryza sat
430	41	77.4	2475	6	AK571171	AK571171 Sequence	c 503	41	77.4	135527	2	CR391995	CR391995 Danio rer
431	41	77.4	2511	1	SPAJ7291	SPAJ7291 Streptoco	c 504	41	77.4	137952	2	SPNEU1909	AL449931 Streptoco
c 432	41	77.4	2550	6	AK658183	AK658183 Sequence	c 505	41	77.4	139111	9	AC008768	AC008768 Homo sapi
c 433	41	77.4	2550	9	HUMDLR18	L00352 Human low d	c 506	41	77.4	142294	2	AP002352	AP002352 Homo sapi
434	41	77.4	3057	6	BD165200	BD165200 Novel pol	c 507	41	77.4	145014	8	AP004048	AP004048 Oryza sat
435	41	77.4	3057	6	AX123083	AX123083 Sequence	c 508	41	77.4	148567	10	AC128738	AC128738 Mus muscu
c 436	41	77.4	3070	10	BC013893	BC013893 Mus muscu	c 509	41	77.4	148811	9	AC073857	AC073857 Homo sapi
437	41	77.4	3187	6	AX813957	AX813957 Sequence	c 510	41	77.4	150900	9	AC068075	AC068075 Homo sapi
c 438	41	77.4	3331	10	MMU70674	U70674 Mus musculu	c 511	41	77.4	152426	9	AC145724	AC145724 Pan trogl
c 439	41	77.4	3495	10	BC033459	BC033459 Mus muscu	c 512	41	77.4	153753	9	AL954206	AL954206 Pan trogl
c 440	41	77.4	3522	9	BC014514	BC014514 Homo sapi	c 513	41	77.4	156539	9	AC091736	AC091736 Homo sapi
441	41	77.4	3549	6	AX411489	AX411489 Sequence	c 514	41	77.4	156603	2	BSX27116	BSX27116 Danio rer
c 442	41	77.4	4131	5	AY070261	AY070261 Danio rer	c 515	41	77.4	158134	5	BSX548006	BSX548006 Zebrafish

C 516	41	77.4	158219	9	AC005534	AC005534 Homo sapi	589	41	77.4	25463	2	AC139169	AC139169 Oryza sat
C 517	41	77.4	158580	4	AC150916	Bos taurus	C 590	41	77.4	252767	2	AC095931	AC095931 Rattus no
C 518	41	77.4	160118	10	AC132954	Mus muscu	C 591	41	77.4	252821	2	AC109758	AC109758 Rattus no
C 519	41	77.4	161737	8	AC090512	Homo sapi	C 592	41	77.4	254671	2	AC133377	AC133377 Rattus no
C 520	41	77.4	162545	8	AP004274	Homo sapi	C 593	41	77.4	257453	2	AC125972	AC125972 Rattus no
C 521	41	77.4	163120	9	AC011454	Homo sapi	C 594	41	77.4	260386	2	AC099464	AC099464 Rattus no
C 522	41	77.4	163319	2	AC110512	Mus muscu	C 595	41	77.4	265341	3	AB003634	AB003634 Drosophill
C 523	41	77.4	163802	10	AL831774	Muscu DNA	C 596	41	77.4	265816	2	AC106286	AC106286 Rattus no
C 524	41	77.4	163884	9	AC146388	Pan trogl	C 597	41	77.4	267692	2	AC135138	AC135138 Rattus no
C 525	41	77.4	165589	9	AL356584	Human DNA	C 598	41	77.4	267692	2	AC135138	AC135138 Rattus no
C 526	41	77.4	167543	8	AC107974	Homo sapi	C 599	41	77.4	268692	2	AC135138	AC135138 Rattus no
C 527	41	77.4	167895	8	OSJN00001	Homo sapi	C 600	41	77.4	283050	1	AC135138	AC135138 Rattus no
C 528	41	77.4	168098	2	AC138064	Homo sapi	C 601	41	77.4	283050	1	AC135138	AC135138 Rattus no
C 529	41	77.4	169199	2	AC109292	Mus muscu	C 602	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 530	41	77.4	169459	5	AL929274	Zebrafish	C 603	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 531	41	77.4	169522	2	AC147286	Homo sapi	C 604	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 532	41	77.4	170056	3	AC006240	Drosophill	C 605	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 533	41	77.4	170494	2	AC135687	Rattus no	C 606	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 534	41	77.4	174559	9	AC015720	Rattus no	C 607	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 535	41	77.4	177466	1	AE001826	Rattus no	C 608	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 536	41	77.4	181103	3	AC011065	AB001826	C 609	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 537	41	77.4	183330	2	AC008159	Homo sapi	C 610	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 538	41	77.4	184012	9	AC0117080	Homo sapi	C 611	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 539	41	77.4	184967	9	AC133299	Rattus no	C 612	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 540	41	77.4	186403	9	AC022358	Rattus no	C 613	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 541	41	77.4	187641	2	AC139844	Mus muscu	C 614	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 542	41	77.4	188508	2	AC130479	Mus muscu	C 615	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 543	41	77.4	191521	10	AC147232	AC147232 Muscu	C 616	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 544	41	77.4	191560	2	AC145530	Callithrix	C 617	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 545	41	77.4	193168	2	AC011969	AC011969 Homo sapi	C 618	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 546	41	77.4	193860	10	BL119959	BL119959 Mouse DNA	C 619	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 547	41	77.4	196187	4	AC149679	AC149679 Bos taurus	C 620	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 548	41	77.4	196355	2	BR510944	BR510944 Danio rer	C 621	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 549	41	77.4	196547	2	CR759803	Danio rer	C 622	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 550	41	77.4	197837	9	AC093107	AC093107 Homo sapi	C 623	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 551	41	77.4	200690	9	AC068714	AC068714 Homo sapi	C 624	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 552	41	77.4	200707	1	BSU00015	Z99118 Bacillus su	C 625	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 553	41	77.4	201201	2	AC015043	AC015043 Colobus g	C 626	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 554	41	77.4	202392	2	AC021018	AC021018 Homo sapi	C 627	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 555	41	77.4	202614	2	AC138765	AC138765 Mus muscu	C 628	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 556	41	77.4	204296	2	AC145823	AC145823 Pan trogl	C 629	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 557	41	77.4	204493	9	AC099489	AC099489 Homo sapi	C 630	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 558	41	77.4	204597	2	AC133019	AC133019 Rattus no	C 631	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 559	41	77.4	204666	2	AC118837	AC118837 Rattus no	C 632	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 560	41	77.4	206840	2	AC147743	AC147743 Mus muscu	C 633	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 561	41	77.4	207392	2	AC006558	AC006558 Homo sapi	C 634	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 562	41	77.4	209048	2	AC104690	AC104690 Mus muscu	C 635	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 563	41	77.4	210320	9	AC093873	AC093873 Homo sapi	C 636	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 564	41	77.4	212714	2	AC118846	AC118846 Homo sapi	C 637	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 565	41	77.4	213558	2	AC149587	AC149587 Mus muscu	C 638	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 566	41	77.4	214387	2	AC137537	AC137537 Canis fam	C 639	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 567	41	77.4	216328	2	AC102247	AC102247 Mus muscu	C 640	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 568	41	77.4	219026	2	AC144655	AC144655 Callicebu	C 641	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 569	41	77.4	220026	2	AC133613	AC133613 Rattus no	C 642	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 570	41	77.4	222107	2	AC146467	AC146467 Salmir b	C 643	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 571	41	77.4	223102	2	AC094457	AC094457 Rattus no	C 644	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 572	41	77.4	223151	2	AC098029	AC098029 Rattus no	C 645	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 573	41	77.4	223437	2	AC110660	AC110660 Rattus no	C 646	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 574	41	77.4	224344	10	AL606969	AL606969 Mouse DNA	C 647	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 575	41	77.4	224592	2	AC095943	AC095943 Rattus no	C 648	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 576	41	77.4	226047	2	AC129649	AC129649 Rattus no	C 649	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 577	41	77.4	226047	2	AC128392	AC128392 Rattus no	C 650	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 578	41	77.4	228074	2	AC131035	AC131035 Rattus no	C 651	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 579	41	77.4	232227	2	AC137468	AC137468 Rattus no	C 652	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 580	41	77.4	233428	2	AC096161	AC096161 Rattus no	C 653	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 581	41	77.4	233988	2	AC128806	AC128806 Rattus no	C 654	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 582	41	77.4	234302	2	AC098958	AC098958 Rattus no	C 655	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 583	41	77.4	235850	2	AC098211	AC098211 Rattus no	C 656	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 584	41	77.4	239008	2	AC022460	AC022460 Homo sapi	C 657	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 585	41	77.4	239172	2	AC095885	AC095885 Rattus no	C 658	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 586	41	77.4	243792	2	AC135947	AC135947 Rattus no	C 659	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 587	41	77.4	245135	2	AC111565	AC111565 Rattus no	C 660	41	77.4	302050	1	AP006568	AP006568 Gloebac
C 588	41	77.4	252026	2	AC098978	AC098978 Rattus no	C 661	41	77.4	302050	1	AP006568	AP006568 Gloebac

c 662	40	75.5	2843	8	MESBRNA	X77012 M. esculenta	735	40	75.5	110000	1	AE017180_34	Continuation (35 o
c 663	40	75.5	2927	5	BC077822	BC077822 Xenopus l	736	40	75.5	110000	1	AE017283_21	Continuation (22 o
c 664	40	75.5	3248	6	BD156510	BD156510 Primer fo	c 737	40	75.5	110000	3	AC119568_3	Continuation (4 of
c 665	40	75.5	3248	6	CQ721025	CQ721025 Sequence	c 738	40	75.5	110000	2	AC138332_3	Continuation (4 of
c 666	40	75.5	3248	6	AX877148	AX877148 Sequence	c 739	40	75.5	110000	2	LMFCH331_00	AL499621 Leishmani
c 667	40	75.5	3248	6	AK001629	AK001629 Homo sapi	c 740	40	75.5	110000	8	CR382125_17	Continuation (18 o
c 668	40	75.5	3296	6	CQ411989	CQ411989 Sequence	c 741	40	75.5	110000	8	CR382129_12	Continuation (13 o
c 669	40	75.5	3344	3	DMU18307	U18307 Drosophila	c 742	40	75.5	110000	8	CR382129_13	Continuation (14 o
c 670	40	75.5	3491	9	BC006085	BC006085 Homo sapi	c 743	40	75.5	110000	8	CR382132_35	Continuation (36 o
c 671	40	75.5	3499	9	BC011876	BC011876 Homo sapi	c 744	40	75.5	110149	8	AC005397_	AC005397 Arabidops
c 672	40	75.5	3500	9	BC000786	BC000786 Homo sapi	c 745	40	75.5	111170	9	AL354766	AL354766 Human DNA
c 673	40	75.5	4269	8	NCCPC2	X81875 N. crassa cp	c 746	40	75.5	114491	9	AC010331	AC010331 Homo sapi
c 674	40	75.5	4540	6	AX472454	AX472454 Sequence	c 747	40	75.5	116351	8	AP005574	AP005574 Oryza sat
c 675	40	75.5	4559	1	TFEN1FHDK	M15238 T. ferrooxid	c 748	40	75.5	117333	8	AC113394	AC113394 Homo sapi
c 676	40	75.5	5057	6	CQ611588	CQ611588 Sequence	c 749	40	75.5	121337	8	OSJN00104	AL606653 Oryza sat
c 677	40	75.5	5353	1	AF204275	AF204275 Desulfito	c 750	40	75.5	121852	9	AP003965	AP003965 Homo sapi
c 678	40	75.5	6070	5	AB066588	AB066588 Xenopus l	c 751	40	75.5	127917	6	CQ861449	CQ861449 Sequence
c 679	40	75.5	6827	6	CQ788969	CQ788969 Sequence	c 752	40	75.5	127917	9	HS257A7	AL008729 Human DNA
c 680	40	75.5	6827	6	AR218828	AR218828 Sequence	c 753	40	75.5	128748	10	AL671732	AL671732 Mouse DNA
c 681	40	75.5	6827	6	BD003740	BD003740 Polynucle	c 754	40	75.5	130328	2	AC079622	AC079622 Homo sapi
c 682	40	75.5	7437	14	RHDVGN5	Z49271 Rabbit hemo	c 755	40	75.5	132644	9	AC104801	AC104801 Homo sapi
c 683	40	75.5	7655	8	UM040753	U40753 Ustilago ma	c 756	40	75.5	132644	2	AC120597	AC120597 Homo sapi
c 684	40	75.5	8600	1	AY129009	AY129009 Streptomy	c 757	40	75.5	139418	8	OSJN00149	AL663017 Oryza sat
c 685	40	75.5	9612	1	AE012312	AE012312 Xanthomon	c 758	40	75.5	141313	9	AC004943	AC004943 Homo sapi
c 686	40	75.5	10170	1	AE008122	AE008122 Agrobacte	c 759	40	75.5	141912	6	AX646791	AX646791 Sequence
c 687	40	75.5	10486	1	AE008400	AE008400 Streptoco	c 760	40	75.5	143411	8	AP004346	AP004346 Oryza sat
c 688	40	75.5	10542	1	AE010881	AE010881 Methanosa	c 761	40	75.5	144092	5	AC092081	AC092081 Gallus ga
c 689	40	75.5	10886	1	AE011955	AE011955 Xanthomon	c 762	40	75.5	144233	8	AP003240	AP003240 Oryza sat
c 690	40	75.5	11116	1	AE012408	AE012408 Xanthomon	c 763	40	75.5	144252	8	AP005399	AP005399 Oryza sat
c 691	40	75.5	11249	1	AE006095	AE006095 Pasteurel	c 764	40	75.5	146346	2	AC111120	AC111120 Mus muscu
c 692	40	75.5	11344	1	AE007333	AE007333 Streptoco	c 765	40	75.5	146408	8	AC130610	AC130610 Oryza sat
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c 699	40	75.5	14668	1	D90864	D90864 E.coli geno	c 772	40	75.5	149697	9	AC091162	AC091162 Homo sapi
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c 701	40	75.5	16748	1	D90865	D90865 E.coli geno	c 774	40	75.5	150803	2	AC073490	AC073490 Homo sapi
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c 703	40	75.5	26309	6	CQ363747	CQ363747 Sequence	c 776	40	75.5	151284	9	CR626880	CR626880 Human DNA
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c 726	40	75.5	87613	8	AP004857	AP004857 Oryza sat	c 799	40	75.5	161099	10	AC132624	AC132624 Homo sapi
c 727	40	75.5	88624	2	AC020676	AC020676 Homo sapi	c 800	40	75.5	161127	9	AC073592	AC073592 Homo sapi
c 728	40	75.5	89808	10	AL591703	AL591703 Mouse DNA	c 801	40	75.5	161278	3	AC009749	AC009749 Drosophil
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c 955	40	75.5	349306	1	BX842575	Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,
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c 978	39	73.6	496	6	AX401097	KFLLSLAQEVTDFAVFHSGSTWKLKDSFFTYLYKDYSVSESKDYRKLVPFNK
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c 980	39	73.6	577	8	AF145259	AGHYVMPNPKLAKMGLIVASNCISGISIGMWKNNHNAHIAACNSLDYDPLOQVIFPL
c 981	39	73.6	645	10	MMDH4	VWSKLSSTSHFYKKLTFDLSLRFVSHQHTFYFVWC SARVNNFVQSLIMLLTK
c 982	39	73.6	681	8	ATH532241	RNVFYRSQELLGVFWIWTYPLLVSLCPNNGERIMFVVASLVTGLQOVQFSLNHFAA
c 983	39	73.6	749	5	CR405758	SVTVQPKGIDDFEKCTLDISCPSPMDWFHGGLOFQVEHHLFPKLPKCHLRKISP
c 984	39	73.6	855	6	CO743578	FVMEKCKHNLNCSNCSFQANEMTLRLTALQARDLTAKPLPKNLWEALNTHG"
c 985	39	73.6	857	5	BX931651	
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c 991	39	73.6	1031	5	CF523357	
c 992	39	73.6	1112	10	RNO18571	
c 993	39	73.6	1192	10	RNMDHR	
c 994	39	73.6	1244	6	BD131673	
c 995	39	73.6	1244	10	MUSMDH	
c 996	39	73.6	1283	9	BC017963	
c 997	39	73.6	1297	10	BC023482	
c 998	39	73.6	1324	10	BC063165	
c 999	39	73.6	1341	8	AF406816	
1000	39	73.6	1341	8	AF536526	
RESULT 1	AY055118	1450 bp	DNA	linear	PLN 01-DEC-2001	
LOCUS	Echium pitardii var. pitardii	delta-6-desaturase (D6DES) gene,				
DEFINITION	complete cds.					
ACCESSION	AY055118					
VERSION	AY055118.1	GI:17223796				
KEYWORDS	Echium pitardii var. pitardii					
SOURCE	Echium pitardii var. pitardii					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Boraginaceae; Echium.					
REFERENCE	1 (bases 1 to 1450)					
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.					
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from					
JOURNAL	Echium: Functional Expression in Yeast and Tobacco					
REFERENCE	2 (bases 1 to 1450)					
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.					
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from					
JOURNAL	Echium: Functional Expression in Yeast and Tobacco					
REFERENCE	2 (bases 1 to 1450)					
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.					
ORIGIN	US-10-029-756-6 (1-8) x AY055118 (1-1450)					
Alignment Scores:	5.11	Length:	1450			
Pred. No.:	53.00	Matches:	8			
Score:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	8	Gaps:	0			
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Db	473	TGGATTGGGATGATGCTGGGCAT	496			
RESULT 2	AY055117	1478 bp	DNA	linear	PLN 01-DEC-2001	
LOCUS	Echium gentianoides	delta-6-desaturase (D6DES) gene, complete cds.				
DEFINITION	Echium gentianoides					
ACCESSION	AY055117					
VERSION	AY055117.1	GI:17223794				
KEYWORDS	Echium gentianoides					
SOURCE	Echium gentianoides					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Boraginaceae; Echium.					
REFERENCE	1 (bases 1 to 1478)					
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.					
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from					
JOURNAL	Echium: Functional Expression in Yeast and Tobacco					
REFERENCE	2 (bases 1 to 1478)					
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.					
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from					
JOURNAL	Echium: Functional Expression in Yeast and Tobacco					
REFERENCE	2 (bases 1 to 1478)					
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.					



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RNVFRSDELLAGLVFVETWYPLLVSCLPNWGERIMFVVASLSVTGMQOVQFSLNHFA
SVYVGQPKNDWFEKQCGTLDISCPNMDWPHGLOFQVEHHLFPKLPKCHLKISP
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Alignment Scores:
Pred. No.: 5, 2 Length: 1478
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AY055117 (1-1478)

Qy 1 TptileGlyHisAspAlaGlyHis 8
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RESULT 3
AR076814
LOCUS AR076814 1684 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 1 from patent US 5959175.
ACCESSION AR076814
VERSION AR076814.1 GI:10003560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS Thomas, T.L., Nunberg, A.N. and Beremand, P.D.
TITLE Sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition
JOURNAL Patent: US 5959175-A 1 28-SEP-1999;
FEATURES
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ORIGIN
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Pred. No.: 5, 91 Length: 1684
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US-10-029-756-6 (1-8) x AR076814 (1-1684)

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RESULT 4
AR084177
LOCUS AR084177 1684 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 1 from patent US 5977436.
ACCESSION AR084177
VERSION AR084177.1 GI:10010948
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS Thomas, T.L. and Li, Z.
TITLE Oleosin 5' regulatory region for the modification of plant seed
lipid composition
JOURNAL Patent: US 5977436-A 1 02-NOV-1999;
FEATURES
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Pred. No.: 5, 91 Length: 1684
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR084177 (1-1684)

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Db 508 TGGATTGGCATGATGCTGGGCAT 531

RESULT 5
BD062571
LOCUS BD062571 1684 bp DNA linear PAT 27-AUG-2002
DEFINITION A sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition.
ACCESSION BD062571
VERSION BD062571.1 GI:22608174
KEYWORDS JP 2001518795-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 1684)
AUTHORS Thomas, T.L., Beremand, P.D. and Nunberg, A.N.
TITLE A sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition
JOURNAL Patent: JP 2001518795-A 1 16-OCT-2001;
COMMENT RHONE-POULENC AGRO
PN JP 2001518795-A/1
PD 16-OCT-2001
PF 09-APR-1998 JP 1998543140
PR 09-APR-1997 US 08/831570
PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC
C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC Strandedness:
Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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Alignment Scores:
Pred. No.: 5.91 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x BD062571 (1-1684)

Qy 1 TtpileGlyHisAspAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGGCAT 531

RESULT 6
BD070919 LOCUS 1684 bp DNA linear PAT 27-AUG-2002
DEFINITION An oleosin 5'regulatory region for the modification of plant seed
lipid composition.
ACCESSION BD070919
VERSION BD070919.1 GI:22616522
KEYWORDS JP 2001519668-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1684)
AUTHORS Thomas,T.L. and Li,Z.
TITLE An oleosin 5'regulatory region for the modification of plant seed
lipid composition
JOURNAL RHONE POULENC AGRO
COMMENT OS Unidentified
PN JP 2001519668-A/1
PF 23-OCT-2001
PD 09-APR-1998 JP 1998543141
PI 09-APR-1997 US 08/831575
PR TERRY L THOMAS, ZHONGSEN LI
PC C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC
Strandedness: Double;
CC Topology: linear;
CC An oleosin 5'regulatory region for the modification of plant
seed lipid
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FH Key Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 5.91 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x BD070919 (1-1684)

Qy 1 TtpileGlyHisAspAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGGCAT 531

RESULT 7
AR020904 LOCUS 1685 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5789220.
ACCESSION AR020904
VERSION AR020904.1 GI:3975519
KEYWORDS
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freysinet,G.L.
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 5789220-A 4 04-AUG-1998;
FEATURES Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x I38430 (1-1685)

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Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 8
I38430 LOCUS 1685 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5614393.
ACCESSION I38430
VERSION I38430.1 GI:2084484
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freysinet,G.L.
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 5614393-A 4 25-MAR-1997;
FEATURES Location/Qualifiers
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Pred. No.: 5.91 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x I38430 (1-1685)

Qy 1 TtpileGlyHisAspAlaGlyHis 8
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 9
AR200408 LOCUS 1685 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6355861.
ACCESSION AR200408
VERSION AR200408.1 GI:20250482
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
KEYWORDS Unclassified.
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REFERENCE 1 (bases 1 to 1685)  
AUTHORS Thomas,T.L.  
TITLE Production of gamma linolenic acid by a .DELTA.6-desaturase  
JOURNAL Patent: US 6355861-A 4 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..1685  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Alignment Scores:  
Pred. No.: 5.91 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR200408 (1-1685)

Qy 1 TptlGlyHisAspAlaGlyHis 8  
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Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 10  
LOCUS AR455421 1685 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 4 from patent US 6683232.  
ACCESSION AR455421  
VERSION AR455421.1 GI:42689973  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1685)  
AUTHORS Thomas,T.L.  
TITLE Production of .gamma. linolenic acid by a .DELTA.6-desaturase  
JOURNAL Patent: US 6683232-A 4 27-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..1685  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.91 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR455421 (1-1685)

Qy 1 TptlGlyHisAspAlaGlyHis 8  
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Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 11  
LOCUS AF007561 1685 bp mRNA linear PLN 05-JAN-1999  
DEFINITION Borago officinalis delta 6-desaturase mRNA, complete cds.  
ACCESSION AF007561  
VERSION AF007561.1 GI:4102020  
KEYWORDS Borago officinalis  
SOURCE Borago officinalis  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Boraginaceae; Borago.

REFERENCE 1 (bases 1 to 1685)  
AUTHORS Nunberg,A.N., Beremand,P.D. and Thomas,T.L.  
TITLE Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid

(GLA)  
Unpublished  
2 (bases 1 to 1685)  
Nunberg,A.N., Beremand,P.D. and Thomas,T.L.  
TITLE Direct Submission  
JOURNAL Submitted (09-JUN-1997) Biology, Texas A&M University, College  
Station, TX 77843, USA  
FEATURES Location/Qualifiers  
source 1..1685  
/organism="Borago officinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:13363"  
/tissue\_type="seed"  
/dev\_stage="12 day post pollination"  
/note="membrane bound polyosomal RNA"  
44..1390  
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/function="produces gamma linolenic acid from linoleic  
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/function="produces octadecatetraenoic acid from alpha  
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/codon\_start=1  
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/protein\_id="AAD01410.1"  
/db\_xref="GI:4102021"  
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MGLYDKKGHTMFATLCPIAMLFAMSVGVLFCEGVLVHLPFGCLMGFLWIOSGWTGHD  
AGHYMVYDSRLNKFPMGIFANCLISGISIGWKNHNAHHIACNSLEYDPSLOIYIPL  
VVSSEFGSLTSHPEKRLTPDSLSPFVSQHKTEYPIMCAARLNMVYQSLIMLLTK  
RVSYRAQELGCLGVFSIWIPLVSLPNSWGERIMFVIASLSVTGMQVQPSLNHPSS  
SNVYKPKGNWFEKQTDGTDLDISCPMPDMFHGGLQFQIEHLLFPKPRCNLRKISP  
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ORIGIN  
Alignment Scores:  
Pred. No.: 5.91 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AF007561 (1-1685)

Qy 1 TptlGlyHisAspAlaGlyHis 8  
|||||  
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 12  
LOCUS AX951561 1687 bp DNA linear PAT 08-JAN-2004  
DEFINITION Sequence 1 from Patent WO03093482.  
ACCESSION AX951561  
VERSION AX951561.1 GI:40781919  
KEYWORDS Borago officinalis  
SOURCE Borago officinalis  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Boraginaceae; Borago.

REFERENCE 1  
AUTHORS Cirpus,P., Renz,A., Lerchl,J. and Kuijpers,A.M.  
TITLE Method for producing multiple unsaturated fatty acids in plants  
JOURNAL Patent: WO 03093482-A 1 13-NOV-2003;  
BASF Plant Science GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..1687  
/organism="Borago officinalis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:13363"  
42..1388  
/note="unnamed protein product; Delta-6-Desaturase"

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/db_xref="GI:40781920"
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AGHYMVVSDSLNFKMGIFANCLSGISIGWKNWNAHIAACNSLEYDPLQVLPFL
VWSSKFGSLTSHFYERKRLTFDLSLRFVSQHWTFYPIMCAARLNNVQSLMLLTG
RNVSYRAHELLGCLLVFSIWTPLLVSLCLPNWGERIMFVIALSVTGMQVQFSLNHFS
SVYVGRKGNWFFKQDGTLDISCPWMDWFGGLQFQIEHLLFPKPRCNLRKISP
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## ORIGIN

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Alignment Scores:
Pred. No.: 5.92 Length: 1687
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-10-029-756-6 (1-8) x AX951561 (1-1687)

Qy 1 TriPleGlyHisAspAlaGlyHis 8

Db 507 TGGATTGGACATGATGCTGGGCAT 530

## RESULT 13

BOU79010

LOCUS

DEFINITION Borago officinalis delta 6 desaturase mRNA, linear PLN 02-MAY-1997

ACCESSION U79010

VERSION U79010.1 GI:2062402

KEYWORDS

SOURCE

ORGANISM

Borago officinalis

Borago officinalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiales; Boraginaceae; Borago.

1 (bases 1 to 1687)

Sayanova,O., Smith,M.A., Lapinskas,P., Stobart,A.K., Dobson,G.,

Christie,W.W., Shewry,P.R. and Napier,J.A.

Expression of a borage desaturase cDNA containing an N-terminal

cytochrome b5 domain results in the accumulation of high levels of

delta6-desaturated fatty acids in transgenic tobacco

Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)

97268723

9108131

2 (bases 1 to 1687)

Sayanova,O., Smith,M.A., Shewry,P.R. and Napier,J.A.

Direct Submission

Submitted (20-NOV-1996) Cell Biology, IACR-Long Ashton Research

Station, Long Ashton, Bristol BS18 9AF, UK

Location/Qualifiers

1. .1687

/organism="Borago officinalis"

/mol\_type="mRNA"

/db\_xref="taxon:13363"

42. .1388

/function="haem-binding protein"

/codon\_start=1

/product="delta 6 desaturase"

/protein\_id="AAC49700.1"

/db\_xref="GI:2062403"

/translation="MAAQIKKIYTSDELKNHDKPGDLWISIQKAYDVSDWKDHPGG

SFLKSLAGQVTDFAVAFHPASTWKNLDRFPTGYLYKDYSEVSXDYRKLVPFEFSK

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AGHYMVVSDSLNFKMGIFANCLSGISIGWKNWNAHIAACNSLEYDPLQVLPFL

VWSSKFGSLTSHFYERKRLTFDLSLRFVSQHWTFYPIMCAARLNNVQSLMLLTG

RNVSYRAHELLGCLLVFSIWTPLLVSLCLPNWGERIMFVIALSVTGMQVQFSLNHFS

SVYVGRKGNWFFKQDGTLDISCPWMDWFGGLQFQIEHLLFPKPRCNLRKISP

YVIBLCKHNLPPNYASFSGKANEMTLRLNTALQARDITKPLPLVWEALHTHG"

## ORIGIN

## Alignment Scores:

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Pred. No.: 5.92 Length: 1687
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
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US-10-029-756-6 (1-8) x BOU79010 (1-1687)

Qy 1 TriPleGlyHisAspAlaGlyHis 8

Db 507 TGGATTGGACATGATGCTGGGCAT 530

## RESULT 14

AX824969

LOCUS

DEFINITION Sequence 1 from Patent WO03072784.

ACCESSION AX824969

VERSION AX824969.1 GI:39750752

KEYWORDS

SOURCE

ORGANISM

Primula farinosa

Primula farinosa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; Ericales; Primulaceae; Primula.

1

Napier,J.A. and Sayanova,O.

Delta 6minus;desaturases from primulaceae&comma; expressing plants

and pufaminus;containing oils

Patent: WO 03072784-A 1 04-SEP-2003;

Rothamsted Experimental Station (GB)

Location/Qualifiers

1. .1362

/organism="Primula farinosa"

/mol\_type="unassigned DNA"

/db\_xref="taxon:133892"

1. .1362

/notes="unnamed protein product"

/codon\_start=1

/protein\_id="CAE84827.1"

/db\_xref="GI:39750753"

/translation="MANKSPNPKTYITSSDLKSHNKGDLWISIHQVQVDSWAA

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WIGHSGHYRIMSDRKNWPAQILSTNCLQGISIGWKNWNAHIAACNSLEYDPLQ

YIPLVVSPPFNSLTSRFDYKKNLFDGVSRLFVYQHWTFYPMVCVARLNMLAQPSI

TLFSSREVCHRAQEVFLAVFWVFPPLLSCLPNWGERIMFVIALSVTGMQVQFSL

NHFSDDVYVGPVGNWDFKKQTATLNISCPAWMDWFGGLQFQIEHLLFPKPRGQF

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TLG"

## ORIGIN

## Alignment Scores:

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Pred. No.: 16.8 Length: 1362
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 6 Gaps: 0
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US-10-029-756-6 (1-8) x AX824969 (1-1362)

Qy 1 TriPleGlyHisAspAlaGlyHis 8

Db 481 TGCATAGCTCAGCTACTCTGGGCAT 504

## RESULT 15

AX824971

LOCUS

DEFINITION Sequence 3 from Patent WO03072784.

ACCESSION AX824971

```

VERSION      AX824971.1  GI:39750754
KEYWORDS
SOURCE       Primula vialii
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Primulaceae; Primula.
REFERENCE    Napier, J.A. and Sayanova, O.
AUTHORS      Delta 6&minus;desaturases from primulaceae comma, expressing plants
              and pufa&minus; containing oils
              Patent: WO 03072784-A 3 04-SEP-2003;
              Rothamsted Experimental Station (GB)
JOURNAL
FEATURES
source
1. .1362
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CDS
1. .1362
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   /db_xref="GI:39750755"
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WIGHDSGHRIMSDRKWNFAQILSTNCLQISIGWKWNHNAHIAACNSLDYDPDLQ
YIPLLVSPKPFNSLTSFYDKLNFQVSRFLVCYQHWTFYPMVCVARLNWIAQSPF
TLFSSREVGKAEIETGLAVFWVWFPILLSCLPNKRGERIMPELLASYSVTGIGHVQFSL
NHFSSDVYVGPVGNDFKQKTAGTLNISCFAWMDWFHGGLOFQVEHHLFPRMRGQF
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THG"
ORIGIN
Alignment Scores:
Pred. No.:      16.8      Length:      1362
Score:          50.00     Matches:      7
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 87.50%  Mismatches:  0
Query Match:    94.34%   Indels:       0
DB:             6       Gaps:       0

US-10-029-756-6 (1-8) x AX824971 (1-1362)

Oy      1  TtpileGlyHisAspAlaGlyHis 8
Db      481 TGGATAGTCACGACTCTGGGCAT 504

RESULT 16
AY234125
LOCUS     Primula farinosa      1410 bp      mRNA      linear      PLN 04-MAY-2003
DEFINITION Primula farinosa fatty acid delta-6 desaturase mRNA, complete cds.
ACCESSION AY234125
VERSION   AY234125.1  GI:30350276
KEYWORDS
SOURCE    Primula farinosa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Primulaceae; Primula.
REFERENCE Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and
AUTHORS   Napier, J.A.
          Identification of Primula fatty acid Delta(6)-desaturases with n-3
          substrate preferences(1)
          FEBS Lett. 542 (1-3), 100-104 (2003)
          JOURNAL MEDLINE 12729906
          PUBMED 22615586
REFERENCE Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and
AUTHORS   Napier, J.A.
          Direct Submission
          Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
          Research Station, Long Ashton, Bristol BS41 9AF, UK
          Location/Qualifiers
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             /db_xref="taxon:175103"
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             join(36..522,744..1618)
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             /mol_type="mRNA"
             /db_xref="taxon:133892"
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             for n-3 fatty acid substrates"
             /codon_start=1
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             /protein_id="AAP23034.1"
             /db_xref="GI:30350277"
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WIGHDSGHRIMSDRKWNFAQILSTNCLQISIGWKWNHNAHIAACNSLDYDPDLQ
YIPLLVSPKPFNSLTSFYDKLNFQVSRFLVCYQHWTFYPMVCVARLNWIAQSPF
TLFSSREVGKAEIETGLAVFWVWFPILLSCLPNKRGERIMPELLASYSVTGIGHVQFSL
NHFSSDVYVGPVGNDFKQKTAGTLNISCFAWMDWFHGGLOFQVEHHLFPRMRGQF
RKISPFVRDLCKKHNLPYNIASTKANVFTLTKLNTAIEARDLSNLPKNNWWEALH
TLG"
US-10-029-756-6 (1-8) x AY234125 (1-1410)

Oy      1  TtpileGlyHisAspAlaGlyHis 8
Db      529 TGGATAGTCACGACTCTGGGCAT 552

RESULT 17
AY234127
LOCUS     Primula vialii      1618 bp      DNA      linear      PLN 04-MAY-2003
DEFINITION Primula vialii fatty acid delta-6 desaturase gene, complete cds.
ACCESSION AY234127
VERSION   AY234127.1  GI:30350280
KEYWORDS
SOURCE    Primula vialii
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Primulaceae; Primula.
REFERENCE Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and
AUTHORS   Napier, J.A.
          Identification of Primula fatty acid Delta(6)-desaturases with n-3
          substrate preferences(1)
          FEBS Lett. 542 (1-3), 100-104 (2003)
          JOURNAL MEDLINE 12729906
          PUBMED 22615586
REFERENCE Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and
AUTHORS   Napier, J.A.
          Direct Submission
          Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
          Research Station, Long Ashton, Bristol BS41 9AF, UK
          Location/Qualifiers
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             join(36..522,744..1618)
             /note="cytochrome b5 fusion desaturase; has a preference"
          CDS
          1. .1410
             /organism="Primula farinosa"
             /mol_type="mRNA"
             /db_xref="taxon:133892"
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             /note="cytochrome b5 fusion desaturase; has a preference
             for n-3 fatty acid substrates"
             /codon_start=1
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WIGHDSGHRIMSDRKWNFAQILSTNCLQISIGWKWNHNAHIAACNSLDYDPDLQ
YIPLLVSPKPFNSLTSFYDKLNFQVSRFLVCYQHWTFYPMVCVARLNWIAQSPF
TLFSSREVGKAEIETGLAVFWVWFPILLSCLPNKRGERIMPELLASYSVTGIGHVQFSL
NHFSSDVYVGPVGNDFKQKTAGTLNISCFAWMDWFHGGLOFQVEHHLFPRMRGQF
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TLG"

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for n-3 fatty acid substrates"
/codon_start=1
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/protein_id="AAP23036.1"
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LHPGSAFLMAGHVDYDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSSDYRKLL
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WIGHDSHYRIMSRKNWFAQVLTSTNCLGISIGWKNHNAHIAACNSLDYDPLQ
YIPLLVSPKPFNSLTSRFDYDKLNFQVGRFLVYOHWTFFPVMCVARLNMIAQSF
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NHSSDYVGPVPVANDWFKQTAGTLNISCPAWMDWFGGLQFQVEHHLFPRMGOF
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intron
523..743
/note="similar to mobile genetic element"

ORIGIN
Alignment Scores:
Pred. No.: 19.9 Length: 1618
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AY234127 (1-1618)

Qy 1 TpileGlyHisAspAlaGlyHis 8
Db 737 TGGATAGTCACGACTCTGGGCAT 760

RESULT 18
AF031194 AF031194 1788 bp mRNA linear PLN 29-JAN-1999
LOCUS Triticum aestivum S276 (S276) mRNA, complete cds.
DEFINITION AF031194.1 GI:4104055
VERSION AF031194.1
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1788)
Delhaize,E., Hebb,D.M., Gardner,R.C. and Richards,K.D.
Aluminum tolerance in yeast conferred by over-expression of wheat
genes
Unpublished
2 (bases 1 to 1788)
Delhaize,E., Hebb,D.M., Gardner,R.C. and Richards,K.D.
Direct Submission
JOURNAL Submitted (23-OCT-1997) Plant Industry, CSIRO, Canberra, ACT 2601,
Australia
FEATURES
source
1..1788 Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
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/db_xref="taxon:4565"
1..1788
/gene="S276"
121..1530
/gene="S276"
/note="similar to Borago officinalis delta 6 desaturase,
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/codon_start=1
/product="S276"
/protein_id="AAD10250.1"
/db_xref="GI:4104056"

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CDS
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WISISGDVDTVWLRHHPGGEVPLITLAGQDATDAFMAYHPSVPLLRFFVGRIT
DVTVPASADPRLLAQLSAGLPERVGHPTPKFLLVANSVLFCIALYCVLACSSTGAH
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 09:24:10 ; Search time 385.263 Seconds

(without alignments)  
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Title: US-10-029-756-6

Perfect score: 53

Sequence: 1 WIGHDAGH 8

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Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/usPTO\_epool\_p/US10029756/runat\_07062005\_122750\_28771/app\_query.fasta\_1.597  
-DB=N\_Geneseq\_16Dec04 -QWTF=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=1000 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10029756 @CGN 1 1 1063 @runat\_07062005\_122750\_28771 -NCPU=6 -ICPU=3  
-NO.MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980as:\*

2: Geneseqn1990as:\*

3: Geneseqn2000as:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	1684	2 AAX34398	Aax34398 Borage de
2	53	100.0	1684	2 AAX24917	Aax24917 Borage de
3	53	100.0	1685	2 AAT30395	Aat30395 Borage de
4	53	100.0	1685	6 ABK49502	Abk49502 DNA encod
5	53	100.0	1685	8 ABX15366	Abx15366 Borage de

6	53	100.0	1685	12 ADO15534	Ado15534 Borage CD
7	53	100.0	1685	12 ADN49362	Adn49362 Borage de
8	50	94.3	880	3 AAD01351	Aad01351 Soybean s
9	50	94.3	1362	10 ADI26234	Adi26234 Primula v
10	50	94.3	1362	10 ADI26232	Adi26232 Aletris f
11	50	94.3	1503	13 ADR60098	Adr60098 Cotton CD
12	50	94.3	1972	3 AAD01353	Aad01353 Wheat sph
13	47	88.7	1764	3 AAD01350	Aad01350 Corn sphl
14	47	88.7	2054	12 ADJ48284	Adj48284 Maize oil
15	46	86.8	649	4 AAS46880	Aas46880 Human G p
16	46	86.8	649	6 ABK81658	Abk81658 cDNA enco
17	45	84.9	533	11 ADP65987	Adp65987 Mouse EST
18	45	84.9	1697	4 AAC83979	Aac83979 Murine or
19	45	84.9	197997	10 AAL54074	Aal54074 Human tra
20	44	83.0	2734	4 ABL14177	Ab114177 Drosophil
21	44	83.0	5679	4 ABL14176	Ab114176 Drosophil
22	43	81.1	472	10 ABT41186	Abt41186 Toxicity
23	42.5	80.2	1152	11 ABD06890	Abd06890 Pseudomon
24	42	79.2	475	12 ACH87364	Ach87364 Human gen
25	42	79.2	487	12 ACH82639	Ach82639 Human gen
26	42	79.2	498	6 ABQ60110	Abq60110 Human col
27	42	79.2	521	12 ACH77282	Ach77282 Human gen
28	42	79.2	522	8 ABZ34667	Abz34667 Coding se
29	42	79.2	539	10 ADB57297	Adb57297 Toxicity-
30	42	79.2	539	10 ABT41439	Abt41439 Toxicity
31	42	79.2	565	12 ACH73652	Ach73652 Human gen
32	42	79.2	571	12 ACH90983	Ach90983 Human gen
33	42	79.2	589	12 ACH68939	Ach68939 Human gen
34	42	79.2	650	5 AAS05580	Aas05580 Mammalian
35	42	79.2	734	4 AAH05583	Aah05583 Human CDN
36	42	79.2	1514	6 AB199493	Ab199493 Mouse isc
37	42	79.2	1542	2 AAQ20695	Aaq20695 Mouse OSF
38	42	79.2	1606	3 AAZ44851	Aaz44851 Sphingoli
39	42	79.2	1771	6 ABT11029	Abt11029 Human bre
40	42	79.2	1833	8 ACA37407	Act37407 Prokaryot
41	42	79.2	1866	4 AAH15974	Aah15974 Human CDN
42	42	79.2	1923	12 ADO07820	Ado07820 Human pol
43	42	79.2	1996	5 AAS74417	Aas74417 DNA encod
44	42	79.2	2238	2 AAZ42116	Aaz42116 Human end
45	42	79.2	2307	6 ABK83895	Abk83895 Human CDN
46	42	79.2	2458	10 ADD12700	Add12700 Human CDN
47	42	79.2	2486	10 ADB63204	Adb63204 Human CDN
48	42	79.2	2702	5 ABV25875	Abv25875 Human pro
49	42	79.2	2741	4 ABL22487	Ab122487 Drosophil
50	42	79.2	2804	3 AAC77708	Aac77708 Human can
51	42	79.2	2846	6 AAS61862	Aas61862 Lung smal
52	42	79.2	2893	10 ADE56172	Ade56172 Rat gene
53	42	79.2	2984	6 ABQ54696	Abq54696 Human ova
54	42	79.2	2995	2 AAV70355	Aav70355 Human h-N
55	42	79.2	3050	13 ADR25565	Adr25565 Breast ca
56	42	79.2	3079	6 AAS61859	Aas61859 Lung smal
57	42	79.2	3144	4 AAI59203	Aai59203 Human pol
58	42	79.2	3144	5 ADQ99427	Adq99427 DNA encod
59	42	79.2	3144	9 ADB43187	Adb43187 Novel hum
60	42	79.2	3155	4 ABL13718	Ab113718 Drosophil
61	42	79.2	3237	5 ABX71357	Abx71357 Human sig
62	42	79.2	3237	11 ADP64967	Adp64967 Human Rac
63	42	79.2	3237	11 ADP65420	Adp65420 Human mRN
64	42	79.2	3237	12 ADO20213	Ado20213 Human PRO
65	42	79.2	3237	13 ACN39430	Acn39430 Tumour-as
66	42	79.2	3259	5 AAS84091	Aas84091 DNA encod
67	42	79.2	3336	6 ABL11165	Ab111165 Drosophil
68	42	79.2	3355	6 ABK35882	Abk35882 cDNA sequ
69	42	79.2	3370	5 AAS94909	Aas94909 Human DNA
70	42	79.2	3419	5 AAS78145	Aas78145 DNA encod
71	42	79.2	3470	8 ACC46735	Acc46735 Human dit
72	42	79.2	4023	10 ADE31423	Ade31423 Human dia
73	42	79.2	4741	4 ABL22486	Ab122486 Drosophil
74	42	79.2	6005	4 ABL11164	Ab111164 Drosophil
75	42	79.2	8335	5 AAS78974	Aas78974 DNA encod
76	42	79.2	100762	12 ADQ59518	Adq59518 Human can
77	41	77.4	418	9 ACH20392	Ach20392 Human adu
78	41	77.4	476	6 ABL93274	Ab193274 Arabidops

c 79	41	77.4	514	12	ACH78188	Ach78188 Human gen	c 152	40	75.5	723	13	ADS56787	Ads56787 Bacterial
c 80	41	77.4	544	12	ADJ84393	Adj84393 Human phe	c 153	40	75.5	780	4	AAH06798	Aah06798 Human cDN
c 81	41	77.4	564	4	AAK63843	Aak63843 Human imm	c 154	40	75.5	828	13	ADR93383	Adr93383 Novel S.
c 82	41	77.4	656	13	ADS60395	Ads60395 Bacterial	c 155	40	75.5	843	13	ADS57548	Ads57548 Bacterial
c 83	41	77.4	658	4	AAH36243	Aah36243 Human col	c 156	40	75.5	856	3	AAC75808	Aac75808 Human ORF
c 84	41	77.4	775	6	ADG32419	Adg32419 Cocoa ole	c 157	40	75.5	858	12	ADQ1379	Adq1379 Human sof
c 85	41	77.4	780	13	ADS49622	Ads49622 Bacterial	c 158	40	75.5	942	10	ABX05802	Abx05802 S. pneumo
c 86	41	77.4	816	13	ADS55132	Ads55132 Bacterial	c 159	40	75.5	960	8	ABZ42364	Abz42364 Streptoco
c 87	41	77.4	921	10	AAF82258	Aaf82258 Bacillus	c 160	40	75.5	1176	13	ADS56580	Ads56580 Bacterial
c 88	41	77.4	955	4	AAE81200	Aae81200 Orf14 cod	c 161	40	75.5	1274	13	ADS48415	Ads48415 Bacterial
c 89	41	77.4	955	4	AAF71706	Aaf71706 Corynebac	c 162	40	75.5	1305	12	ADJ40265	Adj40265 Plant cDN
c 90	41	77.4	1143	8	ADA69970	Ada69970 Rice gene	c 163	40	75.5	1311	5	AAS45093	Aas45093 cDNA enco
c 91	41	77.4	1161	4	AAK86046	Aak86046 Human imm	c 164	40	75.5	1460	4	AAC84336	Aac84336 C. soroki
c 92	41	77.4	1311	2	AAZ96369	Aaz96369 S. pneumo	c 165	40	75.5	1460	4	AAC84338	Aac84338 C. soroki
c 93	41	77.4	1350	6	ABZ12753	Abz12753 Arabidops	c 166	40	75.5	1465	3	AAC42244	Aac42244 Arabidops
c 94	41	77.4	1461	6	ABA01201	Aba01201 Aldehyde-	c 167	40	75.5	1471	3	AAD01349	Aad01349 Florida b
c 95	41	77.4	1650	3	AAC51462	Aac51462 Arabidops	c 168	40	75.5	1523	3	AAZ39020	Aaz39020 Mouse nov
c 96	41	77.4	1650	3	AAZ33846	Aaz33846 Arabidops	c 169	40	75.5	1594	3	AAZ44832	Aaz44832 B. napus
c 97	41	77.4	1678	3	AAZ44833	Aaz44833 A. thalia	c 170	40	75.5	1696	12	ADO15558	Ado15558 Evening p
c 98	41	77.4	1756	4	AAK86044	Aak86044 Human imm	c 171	40	75.5	1702	6	ABK49503	Abk49503 DNA encod
c 99	41	77.4	1757	4	AAK86045	Aak86045 Human imm	c 172	40	75.5	1702	8	ABX15367	Abx15367 Evening p
c 100	41	77.4	1962	12	ADO07822	Ado07822 Mouse pol	c 173	40	75.5	1702	12	ADO15556	Ado15556 Evening p
c 101	41	77.4	2000	8	ADA73284	Ada73284 Rice gene	c 174	40	75.5	1702	12	ADN49384	Adn49384 Evening p
c 102	41	77.4	2466	3	AAZ91853	Aaz91853 Streptoco	c 175	40	75.5	1934	3	AAD01352	Aad01352 Soybean s
c 103	41	77.4	2466	12	ADG67565	Adg67565 Streptoco	c 176	40	75.5	2541	4	ABL28071	AbL28071 Drosophil
c 104	41	77.4	2466	12	ADG67567	Adg67567 Streptoco	c 177	40	75.5	2568	8	ACA40424	Aca40424 Prokaryot
c 105	41	77.4	2475	10	ABX07903	Abx07903 S. pneumo	c 178	40	75.5	2680	6	AAS62282	Aas62282 cDNA equ
c 106	41	77.4	2505	13	ADR93522	Adr93522 Novel S.	c 179	40	75.5	3248	4	AAH14518	Aah14518 Human cDN
c 107	41	77.4	2550	10	ADL24770	Adl24770 Intestina	c 180	40	75.5	3248	13	ACN40824	Acn40824 Tumour-as
c 108	41	77.4	3057	5	AAH67964	Aah67964 C. glutami	c 181	40	75.5	3296	5	ADL45170	Adl45170 Human ova
c 109	41	77.4	3187	11	ADL65624	Adl65624 C. glutam	c 182	40	75.5	4540	6	ABS56604	Abs56604 S. macros
c 110	41	77.4	3549	6	ABL58732	AbL58732 Coryneb	c 183	40	75.5	5057	4	ABL28070	AbL28070 Drosophil
c 111	41	77.4	4530	4	AAH99553	Aah99553 Human pro	c 184	40	75.5	6825	10	ADF55397	Adf55397 Human DNA
c 112	41	77.4	4750	13	ADR83446	Adr83446 Human MOS	c 185	40	75.5	6827	2	AAV52193	Av52193 Streptoco
c 113	41	77.4	4763	13	ACN38958	Acn38958 Tumour-as	c 186	40	75.5	26309	4	AAS59535	Aas59535 Propionib
c 114	41	77.4	4965	2	AAV52276	Av52276 Streptoco	c 187	40	75.5	26309	8	ACF64464	Acf64464 Propionib
c 115	41	77.4	5095	4	AAH02884	Aah02884 Human she	c 188	40	75.5	110000	4	AAI99682_11	Contiuation (11 o
c 116	41	77.4	5108	1	AAH60388	Aah60388 Sequence	c 189	40	75.5	110000	4	AAI99682_11	Contiuation (11 o
c 117	41	77.4	5174	12	ADQ83539	Adq83539 Human tum	c 190	40	75.5	110000	4	AAI99683_10	Contiuation (12 o
c 118	41	77.4	5174	13	ADQ84718	Adq84718 Human tum	c 191	40	75.5	110000	4	AAI99683_11	Contiuation (12 o
c 119	41	77.4	5174	13	ACN40463	Acn40463 Tumour-as	c 192	40	75.5	110000	10	ABS56454_00	Ab56454 Streptoco
c 120	41	77.4	5175	12	ADFA5426	Adf45426 Human vas	c 193	40	75.5	127917	13	ADRS2731	Adrs2731 Drug ther
c 121	41	77.4	5175	12	ADI28823	Adi28823 Human mod	c 194	40	75.5	141912	10	ACN86530	Acn86530 Human GPC
c 122	41	77.4	5175	12	ADK70429	Adk70429 Respirato	c 195	40	75.5	233380	11	ACN44282	Acn44282 Human gen
c 123	41	77.4	5175	12	ADN03813	Adn03813 Antipsori	c 196	39	73.6	262	4	AAK83296	Aak83296 Human imm
c 124	41	77.4	5175	12	ADO19241	Ado19241 Human PRO	c 197	39	73.6	273	10	ADD49985	Add49985 Mammalian
c 125	41	77.4	5194	4	ABA09043	Aba09043 Human LDL	c 198	39	73.6	334	3	AAC71797	Aac71797 Single nu
c 126	41	77.4	5201	4	AAH98389	Aah98389 Human EST	c 199	39	73.6	334	3	AAC71734	Aac71734 Single nu
c 127	41	77.4	5214	12	ADK70381	Adk70381 Respirato	c 200	39	73.6	334	3	AAC71743	Aac71743 Single nu
c 128	41	77.4	5343	12	ADQ22368	Adq22368 Human sof	c 201	39	73.6	415	3	AAC04445	Aac04445 Human sec
c 129	41	77.4	5382	6	ABL91141	AbL91141 Hominidae	c 202	39	73.6	418	9	ACH47722	Ach47722 Human inf
c 130	41	77.4	5468	2	AAQ06540	Aaq06540 Human low	c 203	39	73.6	425	9	ACH47830	Ach47830 Human inf
c 131	41	77.4	5851	6	ABN83957	Abn83957 Human gen	c 204	39	73.6	426	9	ACH46760	Ach46760 Human inf
c 132	41	77.4	24167	5	ABA16132	Aba16132 Human ner	c 205	39	73.6	437	10	ADE85546	Ade85546 Farnesyl
c 133	41	77.4	29112	4	AA559609	Aas59609 Propionib	c 206	39	73.6	454	5	AAK87901	Aak87901 Human dig
c 134	41	77.4	29112	8	ACF64538	Acf64538 Propionib	c 207	39	73.6	454	5	AAS31717	Aas31717 Human liv
c 135	41	77.4	5999	13	ADR28249	Adr28249 Human low	c 208	39	73.6	454	5	ABN90072	Abn90072 Human liv
c 136	41	77.4	72149	10	ADE81173	Ade81173 ML-2368 s	c 209	39	73.6	454	11	ADJ14839	Adj14839 Human liv
c 137	41	77.4	110000	10	ABS56454_18	Contiuation (19 o	c 210	39	73.6	477	9	ACH43182	Ach43182 Human foe
c 138	41	77.4	110000	10	ABS56454_19	Contiuation (20 o	c 211	39	73.6	496	6	ABK62866	Abk62866 Rat seque
c 139	41	77.4	34980	5	AAH68533	Aah68533 C glutami	c 212	39	73.6	496	10	ADS56864	Ads56864 Toxicity-
c 140	40.5	76.4	942	10	ABQ80365	Abq80365 A. fumiga	c 213	39	73.6	496	12	ADP72150	Adp72150 Renal tox
c 141	40.5	76.4	1002	10	ABQ80365	Abq80365 A. fumiga	c 214	39	73.6	521	3	AAC32639	Aac32639 Arabidops
c 142	40	75.5	384	4	AAL13439	Aal13439 Human bre	c 215	39	73.6	567	6	ABN68155	Abn68155 Streptoco
c 143	40	75.5	390	11	ACN91287	Acn91287 Breast ca	c 216	39	73.6	580	5	AAS70360	Aas70360 DNA encod
c 144	40	75.5	393	4	AAL22309	Aal22309 Human bre	c 217	39	73.6	662	13	ADQ52982	Adq52982 Novel can
c 145	40	75.5	413	5	AA545281	Aas45281 cDNA enco	c 218	39	73.6	685	10	ACD94064	Acd94064 Human col
c 146	40	75.5	427	5	ADI73727	Adi73727 Human ova	c 219	39	73.6	796	4	AAK89367	Aak89367 Human dig
c 147	40	75.5	427	5	ADI67330	Adi67330 Human ova	c 220	39	73.6	796	5	AAS31900	Aas31900 Human liv
c 148	40	75.5	464	9	ACH42387	Ach42387 Human foe	c 221	39	73.6	796	6	ABN90255	Abn90255 Human liv
c 149	40	75.5	468	5	ADL38964	Adl38964 Human ova	c 222	39	73.6	796	11	ADJ15168	Adj15168 Human liv
c 150	40	75.5	575	11	ACN83525	Acn83525 Breast ca	c 223	39	73.6	902	4	AAI94202	Aai94202 Human neu
c 151	40	75.5	595	3	AAF11470	Aaf11470 Aspergill	c 224	39	73.6	943	10	ADC87054	Adc87054 Human GPC



c 225	39	73.6	1192	10	ADBS3230	Adbs3230 Primary r	c 298	38	71.7	367	4	AAI92907	Aai92907 Human pol
c 226	39	73.6	1244	2	AAV72448	Aav72448 Mouse MDH	c 299	38	71.7	371	8	ABZ36849	Abz36849 Human GEN
c 227	39	73.6	1390	6	AAI42599	Aai42599 Human eer	c 300	38	71.7	373	6	ABN96255	Abn96255 Gene #275
c 228	39	73.6	1669	8	ABZ24267	Abz24267 Human SLC	c 301	38	71.7	379	3	AACT79312	Aac79312 Human lun
c 229	39	73.6	1674	8	ABZ24266	Abz24266 Human SLC	c 302	38	71.7	379	3	AAD23388	Aad23388 Human lun
c 230	39	73.6	1692	2	AAT60974	Aat60974 NLERK2 cD	c 303	38	71.7	379	10	ADD66662	Add66662 Human lun
c 231	39	73.6	1705	13	ACN37636	Acn37636 Tumour-as	c 304	38	71.7	379	10	ADE87916	Ade87916 Human lun
c 232	39	73.6	1821	3	AAA62004	Aaa62004 Hydrophob	c 305	38	71.7	384	5	AAS80296	Aas80296 DNA enco
c 233	39	73.6	1829	8	ABZ24263	Abz24263 Human SLC	c 306	38	71.7	400	4	AAI81281	Aai81281 Human pol
c 234	39	73.6	1831	13	ADQ84960	Adq84960 Human tum	c 307	38	71.7	404	4	AAI81570	Aai81570 CDNA enco
c 235	39	73.6	1832	8	ABZ24265	Abz24265 Human SLC	c 308	38	71.7	404	4	AAI01153	Aai01153 Human rep
c 236	39	73.6	1864	8	ABZ24268	Abz24268 Human SLC	c 309	38	71.7	404	4	ABL96615	Abi96615 Human tes
c 237	39	73.6	1866	10	ACF67850	Acf67850 Phototrab	c 310	38	71.7	405	2	AAV63618	Aav63618 Synthetic
c 238	39	73.6	1950	5	AAAC85821	Aac85821 hOAT2B DN	c 311	38	71.7	405	2	AAZ09860	Aaz09860 Synthetic
c 239	39	73.6	2000	12	ADJ41525	Adj41525 Plant cDN	c 312	38	71.7	406	2	AAQ60129	Aaq60129 Human bra
c 240	39	73.6	2052	4	ABL07785	Abi07785 Drosophi	c 313	38	71.7	420	2	AAQ34090	Aaq34090 Mycobacte
c 241	39	73.6	2112	3	AAA62014	Aaa62014 Hydrophob	c 314	38	71.7	431	6	ABQ57922	Abq57922 Human col
c 242	39	73.6	2136	8	ABZ24264	Abz24264 Human SLC	c 315	38	71.7	435	6	ABN17451	Abn17451 Human ORF
c 243	39	73.6	2153	6	AAH17179	Aah17179 Human cDN	c 316	38	71.7	459	3	RAC08555	Rac08555 Human sec
c 244	39	73.6	2235	6	ABZ13084	Abz13084 Arabidops	c 317	38	71.7	462	9	ACH28524	Ach28524 Human adu
c 245	39	73.6	2380	2	AAV06355	Aav06355 AL-2-shor	c 318	38	71.7	486	2	AAQ34091	Aaq34091 Mycobacte
c 246	39	73.6	2493	3	AAA75034	Aaa75034 DNA enco	c 319	38	71.7	486	3	RAC01882	Rac01882 Human sec
c 247	39	73.6	2501	5	RAC85820	Rac85820 hOAT2A DN	c 320	38	71.7	505	6	ABN65709	Abn65709 Human can
c 248	39	73.6	2502	3	AAA75035	Aaa75035 DNA enco	c 321	38	71.7	507	8	ABZ53370	Abz53370 Aspergill
c 249	39	73.6	2704	12	ADQ64839	Adq64839 Novel hum	c 322	38	71.7	520	4	AAH72956	Aah72956 Human cer
c 250	39	73.6	2788	6	AAI71438	Aai71438 Human exc	c 323	38	71.7	528	6	ABN65938	Abn65938 Human can
c 251	39	73.6	2855	13	ADS09787	Ads09787 Human the	c 324	38	71.7	537	11	ADR69872	Adr69872 Synthetic
c 252	39	73.6	2952	8	ADA70942	Ada70942 Rice gene	c 325	38	71.7	552	5	AAH75734	Aah75734 DNA enco
c 253	39	73.6	2965	4	ABA09274	Aba09274 Human liv	c 326	38	71.7	564	9	ACH38770	Ach38770 Human foe
c 254	39	73.6	2987	8	ABX12546	Abx12546 cDNA enco	c 327	38	71.7	579	6	ABN64307	Abn64307 Human can
c 255	39	73.6	3259	12	ADQ25284	Adq25284 Human sof	c 328	38	71.7	589	5	AAH75735	Aah75735 DNA enco
c 256	39	73.6	3394	6	ABL67235	Abi67235 Thyroid c	c 329	38	71.7	603	10	ADF00843	Adf00843 Bacterial
c 257	39	73.6	3401	8	ABZ34869	Abz34869 Coding se	c 330	38	71.7	621	4	AAH42564	Aah42564 Prokaryot
c 258	39	73.6	3494	10	ADD49973	Add49973 Mammalian	c 331	38	71.7	621	8	ACA42564	Aca42564 Prokaryot
c 259	39	73.6	3575	11	ADN95705	Adn95705 Human BEC	c 332	38	71.7	622	10	ADB50941	Adb50941 Primary r
c 260	39	73.6	3575	13	ADR25499	Adr25499 Breast ca	c 333	38	71.7	624	11	ABD06206	Abd06206 Pseudomon
c 261	39	73.6	4437	4	ABL07784	Abi07784 Drosophi	c 334	38	71.7	645	4	ABL14295	Abi14295 Drosophi
c 262	39	73.6	7016	4	AAH57552	Aah57552 Human bra	c 335	38	71.7	650	13	ADS051198	Ads051198 Novel can
c 263	39	73.6	7016	4	AAH57552	Aah57552 Human bra	c 336	38	71.7	655	4	AAH32307	Aah32307 DNA enco
c 264	39	73.6	7443	13	ADR84285	Adr84285 Aspergill	c 337	38	71.7	679	13	ADS88642	Ads88642 Human hou
c 265	39	73.6	12595	4	AAH342100	Aah342100 Geomic s	c 338	38	71.7	699	11	ABD09304	Abd09304 Pseudomon
c 266	39	73.6	16607	4	AAH04678	Aah04678 Human rep	c 339	38	71.7	724	4	AAH03782	Aah03782 Human cDN
c 267	39	73.6	16607	4	ABL97585	Abi97585 Human tes	c 340	38	71.7	730	3	AAA02336	Aaa02336 Human col
c 268	39	73.6	16607	5	ABA18349	Aba18349 Human ner	c 341	38	71.7	747	13	ADS56559	Ads56559 Bacterial
c 269	39	73.6	22651	4	AAK78202	Aak78202 Human imm	c 342	38	71.7	753	13	ADS92665	Ads92665 Chitinase
c 270	39	73.6	38596	9	ADA02957	Ada02957 Mouse Dad	c 343	38	71.7	753	13	ADS92693	Ads92693 Chitinase
c 271	39	73.6	38596	10	ADB72695	Adb72695 Mouse Dad	c 344	38	71.7	754	3	AAF12578	Aaf12578 Aspergill
c 272	39	73.6	38596	10	ADC85437	Adc85437 Mouse Dad	c 345	38	71.7	754	9	ADA09917	Ada09917 Human rec
c 273	39	73.6	38596	12	ADM74552	Adm74552 Murine ca	c 346	38	71.7	776	4	AAH08301	Aah08301 Human cDN
c 274	39	73.6	48853	13	ABD33472	Abd33472 Murine ca	c 347	38	71.7	780	13	ADS92691	Ads92691 Chitinase
c 275	39	73.6	60203	10	ACF65383	Acf65383 Continuation (5 of	c 348	38	71.7	795	10	ADE28260	Ade28260 Human MDD
c 276	39	73.6	110000	2	AAV30458	Aav30458 Continuation (5 of	c 349	38	71.7	833	9	ADA03021	Ada03021 Human RAC
c 277	39	73.6	110000	2	AAV30458	Aav30458 Continuation (5 of	c 350	38	71.7	833	10	ADB72759	Adb72759 Human RAC
c 278	39	73.6	110000	8	ADS3223	Ads3223 Continuation (6 of	c 351	38	71.7	833	10	ADC85501	Adc85501 Human RAC
c 279	39	73.6	110000	10	ACF67367	Acf67367 Human can	c 352	38	71.7	833	12	ADM74616	Adm74616 Human car
c 280	39	73.6	110000	13	ABD32968	Abd32968 Human can	c 353	38	71.7	834	11	ABD09039	Abd09039 Pseudomon
c 281	39	73.6	112414	6	ABL59091	Abi59091 Nucleotid	c 354	38	71.7	859	12	ADP13582	Adp13582 Renal cel
c 282	39	73.6	129722	6	ABQ88117	Abq88117 Human ost	c 355	38	71.7	862	12	ADQ84286	Adq84286 Human tum
c 283	39	73.6	129722	12	ADQ18027	Adq18027 Human sof	c 356	38	71.7	862	12	ADQ83607	Adq83607 Human tum
c 284	39	73.6	137049	11	ACN44646	Acn44646 Human gen	c 357	38	71.7	862	13	ADQ84033	Adq84033 Human tum
c 285	39	73.6	157875	6	ABK99972	Abk99972 Human CAD	c 358	38	71.7	862	13	ADQ85751	Adq85751 Human tum
c 286	39	73.6	167163	10	ADB82948	Adb82948 Human pvt	c 359	38	71.7	862	13	ADQ86826	Adq86826 Human tum
c 287	39	73.6	313287	13	ABD33100	Abd33100 Human can	c 360	38	71.7	862	13	ACN40555	Acn40555 Tumour-as
c 288	39	73.6	349980	6	ABQ81846	Abq81846 Bifidobac	c 361	38	71.7	863	12	ADP03024	Adp03024 Human hou
c 289	39	73.6	349980	6	ABQ81844	Abq81844 Bifidobac	c 362	38	71.7	863	13	ADS88522	Ads88522 Human hou
c 290	38.5	72.6	38771	4	AAK81036	Aak81036 Human imm	c 363	38	71.7	894	11	ABD09237	Abd09237 Pseudomon
c 291	38	71.7	121	3	AAA45639	Aaa45639 Human sec	c 364	38	71.7	901	13	ADT07990	Adt07990 Chicken o
c 292	38	71.7	136	2	AAT20688	Aat20688 Human gen	c 365	38	71.7	901	13	ADS91448	Ads91448 Fragment
c 293	38	71.7	187	3	AAO2341	Aao2341 Human sec	c 366	38	71.7	902	12	ADT62577	Adt62577 Chicken o
c 294	38	71.7	300	3	AAO20352	Aao20352 Human col	c 367	38	71.7	902	13	ADI04138	Adi04138 Chicken o
c 295	38	71.7	317	6	ABV88166	Abv88166 Human col	c 368	38	71.7	912	5	AAH81092	Aah81092 DNA enco
c 296	38	71.7	347	11	ABD06085	Abd06085 Pseudomon	c 369	38	71.7	927	13	ADT47059	Adt47059 Bacterial
c 297	38	71.7	357	9	ACH50288	Ach50288 Human leu	c 370	38	71.7	939	3	RAC93489	Rac93489 Human sec

c 371	38	71.7	1010	5	AA575736	Aa875736 DNA encod	c 444	38	71.7	2686	13	ADP55714	Adp55714 Human PRO
372	38	71.7	1023	8	ACA45475	Aca45475 Prokaryot	445	38	71.7	2737	4	AAD05321	Aad05321 Human sec
c 373	38	71.7	1024	5	AA545057	Aa545057 cDNA enco	446	38	71.7	2814	10	ADB69912	Adb69912 C. neofor
c 374	38	71.7	1034	2	AAV13052	Aav13052 pBAR-EDN	c 447	38	71.7	2852	4	ABL14294	Ab114294 Drosophil
375	38	71.7	1041	13	ADT45349	Adt45349 Bacterial	448	38	71.7	2853	10	ADB69551	Adb69551 C. neofor
376	38	71.7	1050	13	ADT44326	Adt44326 Bacterial	c 449	38	71.7	2865	8	ACA45858	Aca45858 Prokaryot
c 377	38	71.7	1052	5	AA545245	Aa545245 cDNA enco	c 450	38	71.7	2879	4	ABL27160	Ab127160 Drosophil
378	38	71.7	1059	3	AAA15661	Aa11661 Human sec	c 451	38	71.7	3011	2	AAV64132	Aav64132 Drosophil
c 379	38	71.7	1134	4	ABL07379	Ab107379 Drosophil	452	38	71.7	3171	6	ABK92214	Abk92214 Prostata
c 380	38	71.7	1176	11	ABD08967	Abd08967 Pseudomon	453	38	71.7	3171	6	ABN89393	Abn89393 Human P-c
381	38	71.7	1197	5	AAH74574	Aah74574 Nucleotid	454	38	71.7	3171	6	ABT07755	Abt07755 Breast ca
382	38	71.7	1197	5	AAH74575	Aah74575 Nucleotid	455	38	71.7	3171	6	ABK52038	Abk52038 DNA encod
383	38	71.7	1197	5	AAH74548	Aah74548 Nucleotid	456	38	71.7	3171	6	ABN97264	Abn97264 Gene #376
384	38	71.7	1197	13	AD58238	Ad58238 Bacterial	457	38	71.7	3171	8	ABZ24736	Abz24736 Human P-c
385	38	71.7	1260	2	AAT50964	Aat50964 Pseudomon	458	38	71.7	3171	10	ADD14795	Add14795 Human src
386	38	71.7	1260	2	AA09009	Aa09009 Methionin	459	38	71.7	3171	10	ACA56750	Aca56750 Human sig
387	38	71.7	1279	2	AA084990	Aa084990 Human sec	460	38	71.7	3171	11	ADN39464	Adn39464 Cancer/an
388	38	71.7	1279	8	ACD18916	Acd18916 Novel hum	461	38	71.7	3171	11	ADN39577	Adn39577 Cancer/an
389	38	71.7	1279	12	ADG78307	Adg78307 Human sec	462	38	71.7	3171	11	ADN39544	Adn39544 Cancer/an
390	38	71.7	1279	12	ADN60598	Adn60598 Human sec	463	38	71.7	3171	11	ADN39481	Adn39481 Cancer/an
c 391	38	71.7	1299	2	AAV63620	Aav63620 Nucleic a	464	38	71.7	3171	12	ADJ56546	Adj56546 Human pol
c 392	38	71.7	1299	2	AAZ09862	Aaz09862 pET-11d-E	465	38	71.7	3171	12	ADL06487	Adl06487 Human tum
393	38	71.7	1320	2	AAT85643	Aat85643 DNA encod	466	38	71.7	3171	12	ADQ20014	Adq20014 Human sof
394	38	71.7	1338	8	AAD49078	Aad49078 Thraustoc	467	38	71.7	3171	13	ADR24808	Adr24808 Breast ca
395	38	71.7	1367	13	ABD33194	Abd33194 Murine ca	468	38	71.7	3183	12	ADO00912	Ado00912 Human hom
c 396	38	71.7	1369	2	AA511369	Aa511369 P. putida	c 469	38	71.7	3194	4	ABA09022	Ab09022 Human FGF
c 397	38	71.7	1369	2	AA511370	Aa511370 P. putida	c 470	38	71.7	3194	4	AAK52458	Aak52458 Human pol
398	38	71.7	1369	2	AA232211	Aax232211 P. putida	471	38	71.7	3205	6	ABQ81547	Abq81547 Gene up-r
399	38	71.7	1369	2	AA228097	Aax28097 Methionin	472	38	71.7	3205	8	ABX76155	Abx76155 Lung canc
400	38	71.7	1387	13	ADS48911	Ad48911 Bacterial	473	38	71.7	3205	8	ABX76399	Abx76399 Lung canc
401	38	71.7	1416	4	ABL30503	Ab130503 Drosophil	474	38	71.7	3205	10	ACC72821	Acc72821 Human can
c 402	38	71.7	1417	3	AAA26301	Aaa26301 Human sec	475	38	71.7	3205	11	ADN39711	Adn39711 Cancer/an
c 403	38	71.7	1417	8	ADA33975	Ada33975 Human sec	476	38	71.7	3205	11	ADN39019	Adn39019 Cancer/an
c 404	38	71.7	1417	8	ACC50537	Acc50537 Human sec	477	38	71.7	3205	12	ADL70220	Adl70220 Colon can
c 405	38	71.7	1417	10	ADC73600	Adc73600 Human sec	478	38	71.7	3205	12	ADN59612	Adn59612 Colon neo
c 406	38	71.7	1417	10	ADD37635	Add37635 Human sec	479	38	71.7	3205	12	ADN03947	Adn03947 Antipsori
c 407	38	71.7	1417	10	ADA56163	Ada56163 Gene enco	480	38	71.7	3205	12	ADO28656	Ado28656 Human CAD
c 408	38	71.7	1425	6	AAK24297	Aak24297 t(2;22) t	481	38	71.7	3205	12	ADP26910	Adp26910 Human P-c
409	38	71.7	1427	6	ABK34855	Abk34855 Human cDN	482	38	71.7	3206	4	AAH99681	Aah99681 Human pro
410	38	71.7	1427	6	ABK13115	Abk13115 Human sec	483	38	71.7	3219	6	AAD27637	Aad27637 Human col
c 411	38	71.7	1427	6	ABK13115	Abk13115 Human sec	484	38	71.7	3266	12	ADQ24084	Adq24084 Human sof
412	38	71.7	1461	10	ADD71204	Add71204 Human int	c 485	38	71.7	3281	2	AAV64133	Aav64133 Drosophil
413	38	71.7	1483	6	ABZ35390	Abz35390 Human enco	c 486	38	71.7	3578	4	ABL30502	Ab130502 Drosophil
414	38	71.7	1484	5	AA545022	Aa545022 cDNA enco	c 487	38	71.7	3599	4	AAD05638	Aad05638 Human sec
415	38	71.7	1516	11	ADN95655	Adn95655 Human BEC	488	38	71.7	3599	4	AD085058	Aad08508 Human sec
c 416	38	71.7	1520	2	AA34093	Aax34093 Mycobacte	489	38	71.7	3599	9	AD891447	Ad891447 Human sec
c 417	38	71.7	1608	4	AA523120	Aas23120 DNA encod	490	38	71.7	3599	10	ADA56704	Ada56704 Gene enco
418	38	71.7	1632	3	RAZ55789	Aaz55789 cDNA enco	491	38	71.7	3632	13	ADR44020	Adr44020 Human col
419	38	71.7	1686	9	ADB06255	Adb06255 Alloicoc	492	38	71.7	3665	4	AAD08490	Aad08490 Human sec
420	38	71.7	1753	2	AAV04456	Aav04456 Replicati	493	38	71.7	3763	4	AAH16650	Aah16650 Human cDN
c 421	38	71.7	1781	4	AA506728	Aa506728 Polynucle	c 494	38	71.7	3777	9	ACH03801	Ach03801 Human cDN
c 422	38	71.7	1901	3	AAZ44679	Aaz44679 Rat liver	c 495	38	71.7	3884	10	ADD24906	Add24906 DNA encod
c 423	38	71.7	1910	10	ADB57944	Adb57944 Toxicity-	496	38	71.7	3906	10	ADH69190	Adh69190 C. neofor
c 424	38	71.7	1910	10	ADB53450	Adb53450 Primary r	497	38	71.7	3986	5	ABV28780	Abv28780 Human pro
425	38	71.7	1959	8	ACA26531	Aca26531 Prokaryot	498	38	71.7	3986	5	ABV22948	Abv22948 Human pro
426	38	71.7	1992	8	ADA70741	Ada70741 Rice gene	499	38	71.7	3989	10	ADA53410	Ada53410 Human cod
427	38	71.7	1992	9	ADA48621	Ada48621 Rice gene	500	38	71.7	4100	4	AA527115	Aas27115 cDNA enco
428	38	71.7	2000	9	ABZ15274	Abz15274 Arabidops	501	38	71.7	4100	10	AD893293	Ad893293 Human cDN
429	38	71.7	2028	9	ADA48343	Ada48343 Rice gene	502	38	71.7	4112	6	ABZ11824	Abz11824 Human pol
430	38	71.7	2076	13	ADT48722	Adt48722 Bacterial	503	38	71.7	4112	12	ADM44342	Adm44342 Novel hum
431	38	71.7	2100	12	ADP28102	Adp28102 Human sec	504	38	71.7	4177	10	ADE54313	Ade54313 Human gen
432	38	71.7	2100	12	ADP28195	Adp28195 Human sec	505	38	71.7	4177	10	ADE54317	Ade54317 Human gen
c 433	38	71.7	2151	4	ABL03193	Ab103193 Drosophil	506	38	71.7	4217	6	ABT10142	Abt10142 Human bre
c 434	38	71.7	2316	11	ABD08346	Abd08346 Pseudomon	507	38	71.7	4217	10	ADD67641	Add67641 Human Ly6
c 435	38	71.7	2364	8	ABX63037	Abx63037 Human cDN	508	38	71.7	4217	12	ADQ21677	Adq21677 Human sof
436	38	71.7	2379	4	AAH15341	Aah15341 Human cDN	509	38	71.7	4217	13	ADR52722	Adr52722 Drug ther
437	38	71.7	2412	13	AD555593	Ad555593 Bacterial	c 510	38	71.7	4220	4	ABL03192	Ab103192 Drosophil
438	38	71.7	2412	13	AD555078	Ad555078 Bacterial	511	38	71.7	4441	6	ABX92073	Abx92073 Lung spec
439	38	71.7	2433	4	ABL04033	Ab104033 Drosophil	512	38	71.7	4458	4	AAI60755	Aai60755 Human pol
c 440	38	71.7	2451	8	ACA44102	Aca44102 Prokaryot	513	38	71.7	4492	3	AAI77245	Aai77245 Human ORF
441	38	71.7	2530	5	AA588011	Aa588011 DNA encod	514	38	71.7	4494	4	AAI58969	Aai58969 Human pol
442	38	71.7	2624	4	AAD13348	Ad113348 Human sec	515	38	71.7	4494	5	ADQ99191	Adq99191 DNA encod
c 443	38	71.7	2660	13	ADR14030	Adr14030 Human NF-	516	38	71.7	4494	9	ADB48951	Adb48951 Novel hum

517	38	71.7	4520	4	ABL09423	Ab109423 Drosophil	590	38	71.7	13255	8	ADA41522	Ada41522 Human sec
518	38	71.7	4559	4	AB118477	Ab118477 Drosophil	591	38	71.7	13255	10	ADA57647	Ada57647 BAC fragm
519	38	71.7	4603	4	AB104032	Ab104032 Drosophil	c 592	38	71.7	14919	4	AA163992	AA163992 Human pol
520	38	71.7	4615	2	AAQ070724	AaQ070724 TATA-bind	c 593	38	71.7	14919	4	AA331670	AA331670 Genomic s
521	38	71.7	4615	2	AAQ742210	AaQ742210 Drosophil	c 594	38	71.7	14919	12	ADM24707	Adm24707 Human PRO
522	38	71.7	4615	2	AAQ79604	AaQ79604 TATA-bind	c 595	38	71.7	17874	4	AAK71070	AAK71070 Human imm
523	38	71.7	4625	4	ABL07378	Ab107378 Drosophil	c 596	38	71.7	17874	4	AAK66943	AAK66943 Human imm
524	38	71.7	4934	5	ADL45192	AdL45192 Human ova	597	38	71.7	19632	4	ABL26670	Ab126670 Drosophil
525	38	71.7	4940	6	ABX92006	Abx92006 Lung spec	c 598	38	71.7	23416	4	ABL26670	Ab126670 Drosophil
526	38	71.7	5076	12	ADH56432	Adh56432 Human hyp	c 599	38	71.7	28564	11	ACN44866	Acn44866 Human gen
527	38	71.7	5140	6	AAZ29679	Aaz29679 N. tabacu	600	38	71.7	28564	13	ABD33193	Abd33193 Murine ca
528	38	71.7	5140	6	AAZ58338	Ab158338 N. tabacu	c 601	38	71.7	30001	2	AAK61016	AAK61016 Total DNA
529	38	71.7	5203	6	ABL60880	Ab160880 Human cyt	c 602	38	71.7	30001	2	AAK05110	AAK05110 S. aureof
530	38	71.7	5345	4	AAZ27696	Aaz27696 Human cyt	603	38	71.7	31422	3	AAA92302	AAa92302 S. averm
531	38	71.7	5345	4	ABK42842	Abk42842 Genomic s	604	38	71.7	31422	3	AAH79278	AAh79278 Streptomy
532	38	71.7	5345	5	ADM20212	Adm20212 Alternati	605	38	71.7	32199	4	AAK90296	AAK90296 Human dig
533	38	71.7	5345	9	ADB60998	Adb60998 Connectiv	606	38	71.7	32199	4	AAI57673	AAI57673 Human col
534	38	71.7	5345	10	ADB94499	Adb94499 Novel hum	607	38	71.7	32199	6	ABS99850	ABs99850 Genomic D
535	38	71.7	5385	12	ADQ23484	Adq23484 Human sof	608	38	71.7	32199	10	ADB93003	Abd93003 Human col
536	38	71.7	5748	3	AAQ76580	AaQ76580 Human ORF	609	38	71.7	33481	4	ABL04906	Ab104906 Drosophil
537	38	71.7	6132	10	ADQ07519	AdQ07519 Novel cod	610	38	71.7	38734	2	AAZ32020	Aaz32020 Human MET
538	38	71.7	6195	8	ABZ74127	Abz74127 Secreted	611	38	71.7	38734	5	AAQ90077	AaQ90077 AL021529
539	38	71.7	6195	8	ADA98554	Ada98554 Human sec	612	38	71.7	38764	9	ADA03020	Ada03020 Human RAC
540	38	71.7	6195	8	ADA44292	Ada44292 Human sec	613	38	71.7	38764	10	ADB72758	Adb72758 Human RAC
541	38	71.7	6195	10	ADC20671	Adc20671 Human sec	614	38	71.7	38764	10	ADC85500	Adc85500 Human Rac
542	38	71.7	6195	10	ADC20782	Adc20782 Human sec	615	38	71.7	38764	12	ADM74615	Adm74615 Human car
543	38	71.7	6195	10	ADF10864	Adf10864 Human sec	616	38	71.7	43633	12	ADQ59425	Adq59425 Human can
544	38	71.7	6234	2	AAV64131	Aav64131 St-H segm	617	38	71.7	44242	4	ABL19930	Ab119930 Drosophil
545	38	71.7	6240	4	AAH06443	AAh06443 Drosophil	c 618	38	71.7	46250	10	ABX13974	Abx13974 Human Ras
546	38	71.7	6248	4	AAH98460	AAh98460 Murine BS	c 619	38	71.7	46275	6	ABT10145	ABt10145 Human bre
547	38	71.7	6490	12	ADJ27244	Adj27244 Human TRI	c 620	38	71.7	46275	9	ADA02795	Ada02795 Mouse Tnf
548	38	71.7	6625	6	ABS67779	ABs67779 Human rec	c 621	38	71.7	52479	10	ADB72533	Adb72533 Mouse Tnf
549	38	71.7	6663	6	ABL92102	Ab192102 Human Tum	c 622	38	71.7	52479	10	ADC85275	Adc85275 Mouse Tnf
550	38	71.7	6702	10	ADA19207	Ada19207 Human ins	c 623	38	71.7	52479	10	ADC85275	Adc85275 Mouse Tnf
551	38	71.7	6702	10	ADN04791	Adn04791 Antipsoi	c 624	38	71.7	52479	11	ACN44396	Acn44396 Murine ca
552	38	71.7	6702	12	ADQ07978	AdQ07978 Human tum	c 625	38	71.7	54929	11	ACN44396	Acn44396 Mouse gen
553	38	71.7	6702	13	ACN38608	Acn38608 Tumour-as	c 626	38	71.7	66861	13	ABD33333	Abd33333 Murine ca
554	38	71.7	6702	13	ADP24833	Adp24833 PRO poly	c 627	38	71.7	68196	13	ABD32800	Abd32800 Human can
555	38	71.7	6729	4	AAQ05595	AaQ05595 Human sec	c 628	38	71.7	80557	6	ABX09142	Abx09142 Mycobacte
556	38	71.7	6729	9	ADB91309	Adb91309 Human sec	629	38	71.7	95001	12	ADH56439	Adh56439 Human hyp
557	38	71.7	6729	10	ADA56398	Ada56398 Gene enco	630	38	71.7	100608	13	ABD32769	Abd32769 Human can
558	38	71.7	6756	2	AAQ11174	AaQ11174 Sequence,	631	38	71.7	109453	13	ABD32728	Abd32728 Mouse can
559	38	71.7	6756	2	AAQ11174	AaQ11174 Aspergill	632	38	71.7	110000	4	AAI99682_18	AAI99682_18 o
560	38	71.7	6756	8	ABX13436	ABx13436 Plasmids	c 633	38	71.7	110000	4	AAI99682_18	AAI99682_18 o
561	38	71.7	6759	8	AAV63619	Aav63619 Nucleic a	c 634	38	71.7	110000	4	AAI99683_18	AAI99683_18 o
562	38	71.7	6799	2	AAZ09861	Aaz09861 pET-11d-E	c 635	38	71.7	110000	9	ADB12064_00	ADB12064_00 o
563	38	71.7	7080	2	AAV33621	Aav33621 Plasmid p	c 636	38	71.7	110000	11	ADM27081_13	ADM27081_13 o
564	38	71.7	7389	4	AAZ27788	Aaz27788 DNA enco	c 637	38	71.7	110000	11	ADN46845_10	ADN46845_10 o
565	38	71.7	7389	10	ADB94591	Adb94591 Novel hum	c 638	38	71.7	110000	12	ADN47591_10	ADN47591_10 o
566	38	71.7	7389	10	ADH09422	Adh09422 Drosophil	c 639	38	71.7	110000	12	ADN46123_10	ADN46123_10 o
567	38	71.7	9525	4	ABL04103	Ab104103 Vector pt	c 640	38	71.7	110000	12	ADN47205_10	ADN47205_10 o
568	38	71.7	9678	12	ADH04103	Adh04103 Vector pt	641	38	71.7	110000	12	ADN46464_10	ADN46464_10 o
569	38	71.7	9933	4	ABL06442	Ab106442 Drosophil	c 642	38	71.7	110000	12	ADN47960_10	ADN47960_10 o
570	38	71.7	10083	4	ABL18476	Ab118476 Drosophil	643	38	71.7	110000	12	ABD32721_0	ABD32721_0 o
571	38	71.7	10297	12	ADH04127	Adh04127 Vector pt	c 644	38	71.7	110000	13	ACN44998	Acn44998 Human gen
572	38	71.7	10297	13	ADT08018	Adt08018 Transposo	c 645	38	71.7	122614	11	ACN44074	Acn44074 Human gen
573	38	71.7	10401	12	ADJ81642	Adj81642 Human tyr	646	38	71.7	128668	11	ACN44074	Acn44074 Human sof
574	38	71.7	10512	12	ADH04129	Adh04129 Vector pt	c 647	38	71.7	131239	12	ADQ21179	AdQ21179 Human gen
575	38	71.7	10512	13	ADT08015	Adt08015 Transposo	c 648	38	71.7	144723	11	ACN44898	Acn44898 Human gen
576	38	71.7	11011	6	ABN83947	ABn83947 Human tra	c 649	38	71.7	212331	13	ACN44598	Acn44598 Human gen
577	38	71.7	11308	8	ACF64554	ACf64554 Propionib	650	38	71.7	247461	13	ABD33153	ABd33153 Murine ca
578	38	71.7	11332	12	ADH04141	Adh04141 Vector pt	c 651	38	71.7	299598	12	ADQ59380	Adq59380 Human can
579	38	71.7	11964	13	ADT62603	Adt62603 Transposo	652	38	71.7	312477	12	ADP69744	Adp69744 Human ROC
580	38	71.7	11964	13	ADT62603	Adt62603 Transposo	653	38	71.7	321491	11	ACN44202	Acn44202 Human gen
581	38	71.7	11964	13	ADT62603	Adt62603 Transposo	c 654	38	71.7	326002	13	ABD32843	ABd32843 Human can
582	38	71.7	11967	13	ADT62604	Adt62604 Transposo	c 655	37.5	70.8	777	6	ABQ55513	ABq55513 Human ova
583	38	71.7	12155	4	ABL06990	Ab106990 Drosophil	c 656	37.5	70.8	3624	12	ADO28604	Ado28604 Human myo
584	38	71.7	12339	13	ADT62607	Adt62607 Transposo	c 657	37.5	70.8	5043	10	ADC27727	Adc27727 Human col
585	38	71.7	12339	13	ADT62607	Adt62607 Transposo	c 658	37.5	70.8	5046	10	ADC27727	Adc27727 Human col
586	38	71.7	12342	13	ADT62607	Adt62607 Transposo	c 659	37.5	70.8	5046	10	ADC27727	Adc27727 Human col
587	38	71.7	12342	13	ADT62607	Adt62607 Transposo	660	37.5	70.8	321019	13	ABD36450	ABd36450 Human aut
588	38	71.7	12342	13	ADT62607	Adt62607 Transposo	661	37.5	70.8	329019	13	ABD36450	ABd36450 Human aut
589	38	71.7	12355	4	AAQ76842	AaQ76842 Human imm	c 662	37	69.8	55	2	AAQ41963	AAq41963 Ig delta

663	37	69.8	84	12	ADP22732	Adp22732 Human HAR	736	37	69.8	507	2	AAQ20697	Aa20697 OSF.1 gen
664	37	69.8	153	4	AAI22253	Aai22253 Probe #12	737	37	69.8	507	3	AAZ91785	Aaz91785 Human PTN
665	37	69.8	153	4	ABA67331	Aba67331 Human Foe	738	37	69.8	513	4	AAI70201	Aai70201 Human ple
666	37	69.8	153	4	AAI47545	Aai47545 Probe #16	739	37	69.8	513	5	AAF85304	Aaf85304 Nucleotid
667	37	69.8	153	4	ABA49419	Aba49419 Human bre	c 740	37	69.8	567	12	ACH69875	Ach69875 Human gen
668	37	69.8	153	4	ABA34422	Aba34422 Probe #12	c 741	37	69.8	582	4	AAI18338	Aai18338 Probe #82
669	37	69.8	153	4	AAK14505	Aak14505 Human bon	c 742	37	69.8	582	4	ABA63339	Aba63339 Human foe
670	37	69.8	153	4	AAK15764	Aak15764 Human bra	c 743	37	69.8	582	4	AAI43453	Aai43453 Probe #12
671	37	69.8	153	4	ABA41094	Aba41094 Human liv	c 744	37	69.8	582	4	ABA30543	Aba30543 Probe #90
672	37	69.8	153	5	AAI07950	Aai07950 Probe #79	c 745	37	69.8	582	4	AAK37582	Aak37582 Human bon
673	37	69.8	153	6	ABS15510	Abs15510 Human gen	c 746	37	69.8	582	4	AAK11881	Aak11881 Human bra
674	37	69.8	198	12	ACH85073	Ach85073 Human gen	c 747	37	69.8	582	4	ABS37242	Abs37242 Human liv
675	37	69.8	222	4	AAK44202	Aak44202 Human bon	c 748	37	69.8	582	6	ABS11567	Abs11567 Human gen
676	37	69.8	222	4	ABS43859	Abs43859 Human liv	749	37	69.8	583	12	ACH78772	Ach78772 Human gen
677	37	69.8	222	6	ABS18438	Abs18438 Human gen	c 750	37	69.8	595	5	AAH82488	Aah82488 Human ova
678	37	69.8	259	3	AAAI0181	Aaai0181 Rat liver	751	37	69.8	596	12	ACH71317	Ach71317 Human gen
679	37	69.8	280	10	ABX86931	Abx86931 Corn ear-	c 752	37	69.8	600	5	ADL44070	Adl44070 Human ova
c 680	37	69.8	287	9	ADA58057	Ada58057 Maize fru	c 753	37	69.8	603	6	ABQ55800	Abq55800 Human ova
c 681	37	69.8	297	12	ADP60854	Adp60854 Maize car	754	37	69.8	604	8	ABX71006	Abx71006 Novel hum
682	37	69.8	304	2	AAV63639	Aav63639 Contig 35	755	37	69.8	607	13	ACN47396	Acn47396 Cotton pr
683	37	69.8	304	2	AAK00906	Aak00906 Human des	756	37	69.8	618	5	AA891283	Aa891283 DNA encod
684	37	69.8	304	2	AAV82638	Aav82638 Contig 35	c 757	37	69.8	654	5	AA876099	Aa876099 DNA encod
685	37	69.8	304	3	AAA14590	Aaa14590 Nucleotid	c 758	37	69.8	665	5	ADI72547	Adi72547 Human ova
686	37	69.8	304	3	AAA09449	Aaa09449 Human con	c 759	37	69.8	665	5	ADL37686	Adl37686 Human ova
687	37	69.8	304	3	AAA49935	Aaa49935 Human del	c 760	37	69.8	696	8	ACF39378	Acf39378 Mycobacte
688	37	69.8	304	6	ABS76709	Abs76709 Human des	c 761	37	69.8	699	11	ABD12355	Abd12355 Pseudomon
689	37	69.8	304	6	ABS71822	Abs71822 Human del	c 762	37	69.8	705	8	ADA50534	Ada50534 Human pro
c 690	37	69.8	327	2	AAI68134	Aai68134 H. pylori	c 763	37	69.8	711	4	AAH04911	Aah04911 Human CDN
691	37	69.8	333	4	ABK41734	Abk41734 cDNA enco	c 764	37	69.8	714	2	AAZ06674	Aaz06674 Pig Facto
692	37	69.8	333	9	ADB59401	Adb59401 Connectiv	c 765	37	69.8	725	12	ACH867523	Ach867523 Human gen
693	37	69.8	392	2	AAV68572	Aav68572 Partial h	766	37	69.8	730	4	AAK82227	Aak82227 Human imm
c 694	37	69.8	394	5	AA866625	Aa866625 DNA encod	c 767	37	69.8	738	2	AAK30478	Aak30478 H. pylori
c 695	37	69.8	395	10	ADD13825	Add13825 Mouse mit	768	37	69.8	753	12	ACH92032	Ach92032 Human gen
696	37	69.8	401	6	ABN25585	Abn25585 Human ORF	769	37	69.8	760	4	AAK93705	Aak93705 Human CDN
697	37	69.8	401	12	ADP91287	Adp91287 Cotton ex	770	37	69.8	760	12	ADL30132	Adl30132 3' end of
c 698	37	69.8	410	9	ACH31241	Ach31241 Human bon	771	37	69.8	774	2	AAH05182	Aah05182 Human CDN
c 699	37	69.8	412	6	ABQ98404	Abq98404 Human ORF	772	37	69.8	783	2	AAV69512	Aav69512 Banana fr
700	37	69.8	414	9	ACH29878	Ach29878 Human tes	773	37	69.8	808	4	AAK93646	Aak93646 Human CDN
c 701	37	69.8	431	8	ABX44733	Abx44733 Bovine ES	774	37	69.8	808	4	AAK91979	Aak91979 Human CDN
702	37	69.8	447	4	AAI13015	Aai13015 Probe #29	775	37	69.8	808	12	ADL28406	Adl28406 5' end of
703	37	69.8	447	4	ABA54715	Aba54715 Human foe	776	37	69.8	816	3	AAA46661	Aaa46661 cDNA of a
704	37	69.8	447	4	AAI34369	Aai34369 Probe #30	777	37	69.8	816	3	AAA46661	Aaa46661 cDNA of a
705	37	69.8	447	4	ABA44265	Aba44265 Human bre	778	37	69.8	816	3	AAA46661	Aaa46661 cDNA of a
706	37	69.8	447	4	ABA24495	Aba24495 Probe #29	779	37	69.8	822	2	AAQ20696	Aaq20696 Human OSF
707	37	69.8	447	4	AAK28447	Aak28447 Human bon	c 780	37	69.8	828	2	AAV59796	Aav59796 Human sec
708	37	69.8	447	4	AAK02998	Aak02998 Human bra	c 781	37	69.8	828	6	ABS73790	Abs73790 Human CDN
709	37	69.8	447	4	ABS28042	Abs28042 Human liv	c 782	37	69.8	828	9	ACD82933	Acd82933 cDNA sequ
710	37	69.8	447	5	AAI02931	Aai02931 Probe #29	c 783	37	69.8	828	10	ADI23018	Adi23018 cDNA enco
711	37	69.8	447	6	ABS02955	Abs02955 Human gen	c 784	37	69.8	828	12	ADH74020	Adh74020 Human sec
712	37	69.8	453	9	ACH41883	Ach41883 Human foe	c 785	37	69.8	831	11	ABD12562	Abd12562 Pseudomon
c 713	37	69.8	455	3	AAK07014	Aak07014 Human sec	786	37	69.8	831	11	ABD12562	Abd12562 Pseudomon
c 714	37	69.8	475	3	AAI16336	Aai16336 Probe #62	787	37	69.8	832	4	AAK93707	Aak93707 Human CDN
c 715	37	69.8	475	4	ABA59160	Aba59160 Human foe	788	37	69.8	832	4	AAK92044	Aak92044 Human CDN
c 716	37	69.8	475	4	AAI38911	Aai38911 Probe #75	789	37	69.8	832	12	ADL30134	Adl30134 3' end of
c 717	37	69.8	475	4	ABA27933	Aba27933 Probe #63	790	37	69.8	832	12	ADL28471	Adl28471 5' end of
718	37	69.8	475	4	AAK31107	Aak31107 Human bon	c 791	37	69.8	834	13	ADS49928	Ads49928 Bacterial
c 719	37	69.8	475	4	AAK33116	Aak33116 Human bon	c 792	37	69.8	835	5	AAF94058	Aaf94058 Primer sp
c 720	37	69.8	475	4	AAK07348	Aak07348 Human bra	c 793	37	69.8	843	13	ADS55443	Ads55443 Bacterial
c 721	37	69.8	475	4	ABS32853	Abs32853 Human liv	c 794	37	69.8	852	8	ACA27078	Aca27078 Prokaryot
722	37	69.8	475	4	ABS30787	Abs30787 Human liv	795	37	69.8	864	3	AAA49944	Aaa49944 Putative
723	37	69.8	475	6	ABS07933	Abs07933 Human gen	796	37	69.8	864	6	ABS76714	Abs76714 Human CDN
724	37	69.8	475	6	ABS05859	Abs05859 Human gen	797	37	69.8	864	6	ABS71827	Abs71827 Human del
725	37	69.8	477	4	AAI98720	Aai98720 Human exc	798	37	69.8	890	4	AAK93978	Aak93978 Human CDN
c 726	37	69.8	477	5	AAI63116	Aai63116 Human kid	799	37	69.8	890	4	AAK91991	Aak91991 Human CDN
c 727	37	69.8	479	9	ACH13126	Ach13126 Human adu	800	37	69.8	890	12	ADL28418	Adl28418 5' end of
c 728	37	69.8	492	4	AA823930	Aa823930 Human ova	801	37	69.8	890	12	ADL30405	Adl30405 5' end of
729	37	69.8	493	6	ABS69532	Abs69532 Novel mur	802	37	69.8	900	8	ABZ52402	Abz52402 Aspergill
730	37	69.8	494	10	ADB50671	Adb50671 Primary r	803	37	69.8	912	5	AA870559	Aa870559 DNA encod
c 731	37	69.8	496	10	ADH28970	Adh28970 Human chr	c 804	37	69.8	913	5	AA866812	Aa866812 DNA encod
732	37	69.8	498	3	AAK62329	Aak62329 Contig HE	c 805	37	69.8	914	5	AA866812	Aa866812 DNA encod
c 733	37	69.8	500	6	ABA05271	Aba05271 Human lg-	c 806	37	69.8	914	5	AA866812	Aa866812 DNA encod
c 734	37	69.8	500	10	ADE97362	Ade97362 Human ger	807	37	69.8	918	2	AAK00907	Aak00907 Human des
c 735	37	69.8	500	12	ACH73812	Ach73812 Human gen	808	37	69.8	918	2	AAV82639	Aav82639 Contig 38

809	37	69.8	918	3	AAA14591	Aaa14591 Nucleotid	882	37	69.8	1575	6	ABL90108	Ab190108 Human pol
810	37	69.8	918	3	AAA09450	Aaa09450 Human con	c 883	37	69.8	1580	7	ADS31114	Ad31114 Human gen
811	37	69.8	918	3	AAA49936	Aaa49936 Human del	c 884	37	69.8	1590	8	ACA37980	Ac37980 Prokaryot
812	37	69.8	918	6	ABS76710	Ab576710 Human des	c 885	37	69.8	1606	10	ADA52622	Ad52622 Human cod
813	37	69.8	918	6	ABS71823	Ab571823 Human des	c 886	37	69.8	1621	10	ADF82405	Adf82405 Leukaemia
814	37	69.8	960	3	AAA49951	Aaa49951 Human del	c 887	37	69.8	1686	4	AAF63836	Aaf63836 Human sec
815	37	69.8	960	6	ABS76727	Ab576727 Human des	c 888	37	69.8	1686	13	ADR99928	Adr99928 Immune re
816	37	69.8	960	6	ABS71840	Ab571840 Human del	c 889	37	69.8	1692	6	ABQ90404	Abq90404 M. capseul
817	37	69.8	961	2	AAQ13151	Aaql3151 Heparin-b	c 890	37	69.8	1716	4	AAH17528	Aah17528 Human cDN
818	37	69.8	966	13	ADR96646	Adr96646 M. tuberc	c 891	37	69.8	1749	4	AAH161154	Aah161154 Human pol
819	37	69.8	981	6	ABK31789	Abk31789 DNA encod	c 892	37	69.8	1787	5	AA574236	Aa574236 DNA encod
820	37	69.8	981	6	ABS76726	Ab576726 Human cDN	c 893	37	69.8	1843	2	AAV63642	Aav63642 Contig 25
821	37	69.8	990	6	ABS71839	Ab571839 Human del	c 894	37	69.8	1843	2	AAV63642	Aav63642 Contig 25
822	37	69.8	999	13	ADT44325	Adt44325 Bacterial	c 895	37	69.8	1843	2	AAV63642	Aav63642 Contig 25
823	37	69.8	1001	2	AAQ67396	Aaql67396 HARP like	c 896	37	69.8	1843	2	AAV63642	Aav63642 Contig 25
824	37	69.8	1014	13	ADR99931	Adr99931 Immune re	c 897	37	69.8	1843	3	AAA14593	Aaa14593 Nucleotid
825	37	69.8	1020	13	AAFL16150	Aaf16150 Human pro	c 898	37	69.8	1843	3	AAA09452	Aaa09452 Human con
826	37	69.8	1029	6	ABL67217	Ab167217 Thyroid c	c 899	37	69.8	1843	3	AAA09452	Aaa09452 Human con
827	37	69.8	1029	6	ABT10913	Abt10913 Human bre	c 900	37	69.8	1843	3	AAA09452	Aaa09452 Human con
828	37	69.8	1029	12	ADQ19929	Adq19929 Human sof	c 901	37	69.8	1843	3	AAA09452	Aaa09452 Human con
829	37	69.8	1041	13	ADT45348	Adt45348 Bacterial	c 902	37	69.8	1843	3	AAA09452	Aaa09452 Human con
830	37	69.8	1056	13	ADS47995	Ad547995 Bacterial	c 903	37	69.8	1843	3	AAA09452	Aaa09452 Human con
831	37	69.8	1077	13	AD58792	Ad58792 Saprolegni	c 904	37	69.8	1843	3	AAA09452	Aaa09452 Human con
832	37	69.8	1077	13	ADR20168	Adr20168 Saprolegni	c 905	37	69.8	1843	3	AAA09452	Aaa09452 Human con
833	37	69.8	1080	13	ADS48002	Ad548002 Bacterial	c 906	37	69.8	1843	3	AAA09452	Aaa09452 Human con
834	37	69.8	1095	13	ADS58661	Ad558661 Bacterial	c 907	37	69.8	1843	3	AAA09452	Aaa09452 Human con
835	37	69.8	1115	3	AAFL16150	Aaf16150 Human pro	c 908	37	69.8	1843	3	AAA09452	Aaa09452 Human con
836	37	69.8	1131	11	ACF69599	Adf69599 C. elegans	c 909	37	69.8	1843	3	AAA09452	Aaa09452 Human con
837	37	69.8	1136	11	ACN88800	Acn88800 Breast ca	c 910	37	69.8	1843	3	AAA09452	Aaa09452 Human con
838	37	69.8	1137	2	AAV68561	Aav68561 Human hea	c 911	37	69.8	1843	3	AAA09452	Aaa09452 Human con
839	37	69.8	1137	10	ADT25556	Adt25556 Human LLP	c 912	37	69.8	1843	3	AAA09452	Aaa09452 Human con
840	37	69.8	1137	10	ADG14395	Adg14395 Human LLP	c 913	37	69.8	1843	3	AAA09452	Aaa09452 Human con
841	37	69.8	1146	2	AAV68562	Aav68562 Human hea	c 914	37	69.8	1843	3	AAA09452	Aaa09452 Human con
842	37	69.8	1233	2	AAV68566	Aav68566 Human hea	c 915	37	69.8	1843	3	AAA09452	Aaa09452 Human con
843	37	69.8	1236	2	AAV68566	Aav68566 Human hea	c 916	37	69.8	1843	3	AAA09452	Aaa09452 Human con
844	37	69.8	1238	5	ADL63377	Adl63377 Human ova	c 917	37	69.8	1843	3	AAA09452	Aaa09452 Human con
845	37	69.8	1242	2	AAV68565	Aav68565 Human kid	c 918	37	69.8	1843	3	AAA09452	Aaa09452 Human con
846	37	69.8	1250	6	ABK86148	Abk86148 cDNA enco	c 919	37	69.8	1843	3	AAA09452	Aaa09452 Human con
847	37	69.8	1269	8	ABT16045	Abt16045 NOVX rela	c 920	37	69.8	1843	3	AAA09452	Aaa09452 Human con
848	37	69.8	1269	8	ACA34666	Ac344666 Prokaryot	c 921	37	69.8	1843	3	AAA09452	Aaa09452 Human con
849	37	69.8	1269	12	ADO41691	Ado41691 Novel hum	c 922	37	69.8	1843	3	AAA09452	Aaa09452 Human con
850	37	69.8	1332	2	AAV68567	Aav68567 Human kid	c 923	37	69.8	1843	3	AAA09452	Aaa09452 Human con
851	37	69.8	1335	3	AAA49932	Aaa49932 Human del	c 924	37	69.8	1843	3	AAA09452	Aaa09452 Human con
852	37	69.8	1335	4	AAAD19402	Aad19402 Rat delta	c 925	37	69.8	1843	3	AAA09452	Aaa09452 Human con
853	37	69.8	1335	4	AAAD19403	Aad19403 Human del	c 926	37	69.8	1843	3	AAA09452	Aaa09452 Human con
854	37	69.8	1335	5	AAI66599	Aai66599 Rat fatty	c 927	37	69.8	1843	3	AAA09452	Aaa09452 Human con
855	37	69.8	1335	5	AAFL16150	Aaf16150 Nucleotid	c 928	37	69.8	1843	3	AAA09452	Aaa09452 Human con
856	37	69.8	1335	6	ABS76706	Ab576706 Human cDN	c 929	37	69.8	1843	3	AAA09452	Aaa09452 Human con
857	37	69.8	1335	6	ABS71819	Ab571819 Human del	c 930	37	69.8	1843	3	AAA09452	Aaa09452 Human con
858	37	69.8	1335	12	ADL35459	Adl35459 Human del	c 931	37	69.8	1843	3	AAA09452	Aaa09452 Human con
859	37	69.8	1344	6	AAAD19402	Aad19402 Rat delta	c 932	37	69.8	1843	3	AAA09452	Aaa09452 Human con
860	37	69.8	1383	2	AAQ38811	Aaq38811 Heparin-b	c 933	37	69.8	1843	3	AAA09452	Aaa09452 Human con
861	37	69.8	1383	2	AAQ61628	Aaq61628 HBNF gene	c 934	37	69.8	1843	3	AAA09452	Aaa09452 Human con
862	37	69.8	1383	2	AAAT12736	Aat12736 Human ple	c 935	37	69.8	1843	3	AAA09452	Aaa09452 Human con
863	37	69.8	1383	2	AAAT12736	Aat12736 Human ple	c 936	37	69.8	1843	3	AAA09452	Aaa09452 Human con
864	37	69.8	1383	3	AAZ38456	Aaz38456 Human ple	c 937	37	69.8	1843	3	AAA09452	Aaa09452 Human con
865	37	69.8	1398	6	ABZ14279	Abz14279 Arabidops	c 938	37	69.8	1843	3	AAA09452	Aaa09452 Human con
866	37	69.8	1398	12	ADN74696	Adn74696 Thale cre	c 939	37	69.8	1843	3	AAA09452	Aaa09452 Human con
867	37	69.8	1400	13	ADL14576	Adl14576 Human NF-	c 940	37	69.8	1843	3	AAA09452	Aaa09452 Human con
868	37	69.8	1442	6	ABK63626	Abk63626 Rat seque	c 941	37	69.8	1843	3	AAA09452	Aaa09452 Human con
869	37	69.8	1442	10	ADB58034	Adb58034 Toxicity-	c 942	37	69.8	1843	3	AAA09452	Aaa09452 Human con
870	37	69.8	1442	10	ADB52506	Adb52506 Primary r	c 943	37	69.8	1843	3	AAA09452	Aaa09452 Human con
871	37	69.8	1442	10	ADB79828	Adb79828 Rat aldol	c 944	37	69.8	1843	3	AAA09452	Aaa09452 Human con
872	37	69.8	1442	10	ABT41789	Abt41789 Toxicity	c 945	37	69.8	1843	3	AAA09452	Aaa09452 Human con
873	37	69.8	1442	12	ADP72631	Adp72631 Renal tox	c 946	37	69.8	1843	3	AAA09452	Aaa09452 Human con
874	37	69.8	1442	13	ADSS1471	Ad551471 Bacterial	c 947	37	69.8	1843	3	AAA09452	Aaa09452 Human con
875	37	69.8	1464	4	AAAF60969	Aaf60969 P. putida	c 948	37	69.8	1843	3	AAA09452	Aaa09452 Human con
876	37	69.8	1474	3	AAFL16150	Aaf16150 Human bre	c 949	37	69.8	1843	3	AAA09452	Aaa09452 Human con
877	37	69.8	1489	10	AAAD53959	Aad53959 Synchocy	c 950	37	69.8	1843	3	AAA09452	Aaa09452 Human con
878	37	69.8	1533	3	AAAC42592	Aac42592 Arabidops	c 951	37	69.8	1843	3	AAA09452	Aaa09452 Human con
879	37	69.8	1550	11	ADL30775	Adl30775 Human cDN	c 952	37	69.8	1843	3	AAA09452	Aaa09452 Human con
880	37	69.8	1554	4	ABL12149	Ab112149 Drosophil	c 953	37	69.8	1843	3	AAA09452	Aaa09452 Human con
881	37	69.8	1575	4	AAAF60968	Aaf60968 P. putida	c 954	37	69.8	1843	3	AAA09452	Aaa09452 Human con



PI Thomas TL, Li Z;  
XX WPI; 1999-180333/15.  
DR P-PSDB; AAW98130.  
XX  
PT Nucleic acid containing oleosin 5'-regulatory region - useful for  
PT modulating fatty acid synthesis and lipid metabolism in plants,  
PT particularly to increase content of gamma-linolenic acid.  
XX  
PS Example 2; Page 59-61; 101pp; English.  
XX  
CC The present sequence encodes borage delta-6 desaturase (see AAW98130), an  
CC enzyme that catalyses the conversion of linoleic acid to gamma-linolenic  
CC acid (GLA). Delta-6 desaturase cDNA was isolated from a borage membrane-  
CC bound polysomal cDNA library using a partial clone, obtained from an EST  
CC database search, as probe. The borage delta-6 desaturase nucleic acid can  
CC be operably linked to the seed-specific 5' regulatory region (see  
CC AAX24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed  
CC expression cassettes of the invention. Transgenic plants, e.g. sunflower,  
CC soybean, maize, tobacco, cotton, peanut, oilseed rape or Arabidopsis are  
CC obtained that show increased levels of GLA or octadecatetraenoic acid.  
CC The levels of desirable fatty acids in oilseed crops can be manipulated  
CC to provide seed oils of use in human health and industrial applications  
XX  
SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.11 Length: 1684  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-029-756-6 (1-8) x AAX24917 (1-1684)  
  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 508 TGGATTGGACATGATGCTGGGCAT 531  
  
RESULT 3  
AAT30395  
ID AAT30395 standard; DNA; 1685 BP.  
XX  
AC AAT30395;  
XX  
DT 15-SEP-1996 (first entry)  
XX  
DE Borage delta-6-desaturase gene.  
XX  
KW Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;  
KW polyunsaturated fatty acid; octadecatetraenoic acid; chilling resistance;  
KW oilseed; ss; ds.  
XX  
OS Borage officinalis.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..1390  
FT /\*tag= a  
FT  
XX WO9621022-A2.  
XX  
PD 11-JUL-1996.  
XX  
PP 28-DEC-1995; 95WO-IB001167.  
XX  
PR 30-DEC-1994; 94US-00366779.  
XX  
PA (RHON ) RHONE POULENC AGROCHIMIE.  
XX  
PI Thomas TL, Reddy AS, Nuccio M, Nunberg AN, Freysinet GL;  
XX WPI; 1996-333997/33.  
XX  
  
DR P-PSDB; AAR98455.  
XX  
PT Transgenic plants comprising the borage delta-6-desaturase gene - show  
PT increased production of gamma linolenic acid and having increased  
PT resistance to chilling.  
XX  
PS Claim 2; Page 51-52; 75pp; English.  
XX  
CC A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455),  
CC which catalyses the conversion of linoleic acid to gamma-linolenic acid  
CC (GLA). It was isolated from a borage membrane-bound polysomal library  
CC using probes based on abundantly expressed seed storage protein cDNAs and  
CC with an isolated partial cDNA clone. The gene can be incorporated into a  
CC vector, pref. incorporating a tissue-specific promoter, for the  
CC expression of delta-6-desaturase in transgenic plants, esp. sunflower,  
CC soybean, maize, tobacco, peanut, carrot or oilseed rape, resulting in  
CC increased GLA prodn. Alteration of plant lipids may also lead to improved  
CC chilling resistance  
XX  
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.11 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-029-756-6 (1-8) x AAT30395 (1-1685)  
  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
  
RESULT 4  
ABK49502  
ID ABK49502 standard; DNA; 1685 BP.  
XX  
AC ABK49502;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE DNA encoding Borage officinalis delta6-desaturase.  
XX  
KW delta6-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot;  
KW oil seed rape; gamma linolenic acid; GLA; chilling tolerance; gene; ds;  
KW borage.  
XX  
OS Borage officinalis.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..1390  
FT /\*tag= a  
FT /product= "delta6-desaturase"  
FT /transl\_except= (pos:1151..1153, aa:Ser)  
XX  
PN US6355861-B1.  
XX  
PD 12-MAR-2002.  
XX  
PP 19-SEP-1997; 97US-00934254.  
XX  
PR 10-OCT-1991; 91US-00774475.  
PR 08-JAN-1992; 92US-00817919.  
PR 13-OCT-1992; 92US-00959952.  
PR 14-SEP-1994; 94US-00307382.  
PR 28-JAN-1997; 97US-00789936.  
XX  
PA (RHON ) RHONE-POULENC AGROCHIMIE.  
XX  
PI Thomas TL;  
XX

DR WPI; 2002-380944/41.  
DR P-PSDB; AAU79830.  
XX  
PT Novel nucleic acid encoding evening primrose delta6-desaturase which  
PT converts linoleic acid to gamma linolenic acid useful for producing gamma  
PT linolenic acid in transgenic plant or bacteria.  
XX  
PS Example 9; Col 29-32; 53pp; English.  
XX  
CC The invention describes an isolated nucleic acid encoding an evening  
CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the  
CC nucleic acid are useful for producing a plant such as sunflower, soybean,  
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased  
CC gamma linolenic acid (GLA) content, and also for inducing or increasing  
CC production of GLA in a bacteria or plant deficient, lacking in or  
CC producing low levels of GLA. The nucleic acid is also useful for inducing  
CC chilling tolerance in plants. This sequence encodes the borage delta6  
CC desaturase involved in the production of gamma linoleic acid  
XX  
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;  
XX  
Alignment Scores: Pred. No.: 6.11 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-029-756-6 (1-8) x ABK49502 (1-1685)  
Qy 1 TtpIleGlyHisAspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
RESULT 5  
ABX15366  
ID ABX15366 standard; cDNA; 1685 BP.  
XX  
AC ABX15366;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE Borage delta-6-desaturase #1 cDNA.  
XX  
KW Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;  
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;  
KW octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;  
KW borage.  
XX  
OS Borage officinalis.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..1390  
FT /\*tag= a  
FT /product= "Borage delta-6-desaturase #1"  
FT /trans\_except= (pos:1151..1153, aa:Ser)  
XX  
XX US2002108147-A1.  
XX  
XX 08-AUG-2002.  
XX  
XX 21-DEC-2001; 2001US-00029756.  
XX  
XX 10-OCT-1991; 91US-00774475.  
XX 08-JAN-1992; 92US-00817919.  
XX 13-OCT-1992; 92US-00959952.  
XX 14-SEP-1994; 94US-00307382.  
XX 28-JAN-1997; 97US-00789936.  
XX 19-SEP-1997; 97US-00934254.  
XX  
XX (THOM/) THOMAS T L.  
XX

PI Thomas TL;  
XX  
DR WPI; 2003-066659/06.  
DR P-PSDB; ABG73095.  
XX  
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful  
PT for producing plant with increased gamma linolenic acid content, and for  
PT inducing octadecatetraenoic acid production in plant.  
XX  
PS Example 9; Fig 5A; 55pp; English.  
XX  
CC The invention relates to a nucleic acid encoding an evening primrose  
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the  
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful  
CC for producing a plant (such as sunflower, soybean, maize, tobacco,  
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic  
CC acid (GLA) content by transforming a plant cell with the nucleic acid or  
CC vector and generating a plant with increased GLA content from the plant  
CC cell, for inducing or increasing production of GLA in an organism lacking  
CC in or producing low levels of GLA and for inducing production of  
CC octadecatetraenoic acid in at least one of a plant deficient or lacking  
CC in or producing low levels of octadecatetraenoic acid, a bacterium which  
CC produces alpha-linolenic acid or a bacterium which exhibits a delta-15-  
CC desaturase activity on a GLA substrate. This sequence represents cDNA  
CC encoding a borage delta-6-desaturase polypeptide  
XX  
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;  
XX  
Alignment Scores: Pred. No.: 6.11 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0  
US-10-029-756-6 (1-8) x ABX15366 (1-1685)  
Qy 1 TtpIleGlyHisAspAlaGlyHis 8  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
RESULT 6  
AD015534  
ID AD015534 standard; cDNA; 1685 BP.  
XX  
AC AD015534;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Borage cDNA encoding delta6-desaturase.  
XX  
KW Delta6-desaturase; ss; gene; linolenic acid; gamma linolenic acid;  
KW essential fatty acid; arachidonic acid; prostaglandin;  
KW hypercholesterolaemia; atherosclerosis; coronary disease;  
KW delta12-desaturase; borage; plant.  
XX  
OS Borage officinalis.  
XX  
XX US6683232-B1.  
XX  
XX 27-JAN-2004.  
XX  
XX 10-OCT-2000; 2000US-00685775.  
XX  
XX 10-OCT-1991; 91US-00774475.  
XX 08-JAN-1992; 92US-00817919.  
XX 13-OCT-1992; 92US-00959952.  
XX 14-SEP-1994; 94US-00307382.  
XX 28-JAN-1997; 97US-00789936.  
XX 19-SEP-1997; 97US-00934254.  
XX  
XX (RHON ) RHONE-POULENC AGROCHIMIE.  
XX



XX Thomas TL;  
XX WPI; 2004-118584/12.  
DR P-PSDB; ADO15535.  
XX  
PT Inducing production of gamma linolenic acid (GLA) in plants, plant cells  
PT or microorganisms by transforming the plants, plant cells or  
PT microorganisms with a nucleic acid encoding bacterial delta 6-desaturase  
PT or delta 12-desaturase.  
XX  
XX Example 9; SEQ ID NO 4; 52pp; English.  
XX  
CC The invention relates to inducing production of gamma linolenic acid  
CC (GLA) in plants, plant cells or microorganisms that are deficient or  
CC lacking in or producing low levels of GLA and linolenic acid (LA)  
CC comprising transforming the plants, plant cells or microorganisms with an  
CC isolated nucleic acid that encodes bacterial delta6-desaturase and an  
CC isolated nucleic acid encoding delta12-desaturase. The delta6-desaturase  
CC is from *Synechocystis* sp., Borage or evening primrose. GLA is a precursor  
CC of arachidonic acid, essential for the production of mammalian  
CC prostaglandin. Consumption of dietary GLA may have a beneficial effect on  
CC hypercholesterolaemia, atherosclerosis and coronary disease. The plants  
CC transformed with the desaturase genes are crop plants comprising  
CC sunflower, soybean, oil seed rape, maize, peanut or tobacco plants. The  
CC present sequence encodes Borage delta6-desaturase.  
XX  
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.11 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0  
  
US-10-029-756-6 (1-8) x ADO15534 (1-1685)  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
  
RESULT 7  
ADNA9362  
ID ADNA9362 standard; cDNA; 1685 BP.  
XX  
AC ADNA9362;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
XX Borage delta 6-desaturase cDNA.  
XX  
XX Delta 6-desaturase; chilling tolerance; plant growth regulatant; plant;  
XX borage; gene; ss.  
XX  
XX Borage officinalis.  
XX  
XX Key Location/Qualifiers  
XX CDS 44..1390  
FT /\*tag= a  
FT /product= "Borage delta 6-desaturase protein"  
FT /transl\_except= (pos:1151..1153,aa:Ser)  
XX  
XX US2004078845-A1.  
XX  
XX 22-APR-2004.  
XX  
XX 06-NOV-2003; 2003US-00702777.  
XX  
XX 10-OCT-1991; 91US-00774475.  
XX 08-JAN-1992; 92US-00817919.  
PR 13-OCT-1992; 92US-00959952.

PR 14-SEP-1994; 94US-00307382.  
PR 28-JAN-1997; 97US-00789936.  
PR 19-SEP-1997; 97US-00934254.  
PR 10-OCT-2000; 2000US-00685775.  
XX  
XX (THOM/) THOMAS T L.  
XX  
XX Thomas TL;  
XX  
XX WPI; 2004-340086/31.  
DR P-PSDB; ADN49363.  
XX  
XX New nucleic acid encoding an evening primrose delta-6-desaturase, useful  
XX in inducing or increasing production of gamma linolenic acid in an  
XX organism or inducing production of octadecatetraenoic acid in a plant.  
XX Example 9; SEQ ID NO 4; 54pp; English.  
XX  
CC The present invention relates to delta 6-desaturase polypeptides and the  
CC encoding polynucleotides. The invention is useful in inducing or  
CC increasing production of gamma linolenic acid (GLA) in an organism or  
CC inducing production of octadecatetraenoic acid in a plant. The invention  
CC is also useful in inducing chilling tolerance in plants. The invention  
CC acts as a plant growth regulating agent. The present sequence is borage  
CC delta 6-desaturase cDNA.  
XX  
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.11 Length: 1685  
Score: 53.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0  
  
US-10-029-756-6 (1-8) x ADN49362 (1-1685)  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||  
Db 509 TGGATTGGACATGATGCTGGGCAT 532  
  
RESULT 8  
AAD01351  
ID AAD01351 standard; cDNA; 880 BP.  
XX  
AC AAD01351;  
XX  
XX 12-OCT-2000 (first entry)  
XX  
XX Soybean sphingolipid desaturase cDNA #1.  
XX  
XX Soybean; sphingolipid desaturase; membrane-bound desaturase;  
XX transgenic plant; fatty acid; ss.  
XX  
XX Glycine max.  
XX  
XX Key Location/Qualifiers  
XX CDS 15..818  
FT /\*tag= a  
FT /product= "Sphingolipid desaturase"  
FT /transl\_except= (pos:651..652,aa:Leu)  
FT /transl\_except= (pos:692..743,aa:Phe-Leu)  
FT /transl\_except= (pos:495..497,aa:Xaa)  
FT /transl\_except= (pos:510..512,aa:Xaa)  
FT /transl\_except= (pos:522..524,aa:Xaa)  
FT /transl\_except= (pos:531..533,aa:Xaa)  
FT /transl\_except= (pos:630..632,aa:Xaa)  
FT /transl\_except= (pos:813..815,aa:Xaa)  
FT /note= "Xaa is an unknown amino acid; the CDS does not  
FT include start and stop codons"  
FT /partial  
XX

```

PN WO200032790-A2.
XX
PD 08-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US028589.
XX PF
XX 03-DEC-1998; 98US-0110784P.
XX PR
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PA
XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
XX PI
XX WPI: 2000-412336/35.
XX DR
XX P-PSDB; RAY71553.
XX DR
XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
XX PT transgenic plants and for producing antibodies specific to which is
XX PT useful for screening cDNA expression libraries.
XX PT
XX Claim 2; Page 44-45; 57pp; English.
XX PS
XX The present sequence is a cDNA encoding sphingolipid desaturase derived
XX CC from a contig of clones sf11.pk0012.c5 and sf11.pk0031.d11 isolated from
XX CC soybean immature flower cDNA library. sf11. The present sequence is
XX CC useful for producing transgenic plants having altered levels of
XX CC sphingolipid desaturase which in turn would alter the fatty acid
XX CC composition. The enzyme is useful for producing polyclonal or monoclonal
XX CC antibodies. The polynucleotide is also useful as a primer or probe for
XX CC screening cDNA libraries to isolate desired full-length cDNA clones
XX CC
XX SQ Sequence 880 BP; 162 A; 267 C; 184 G; 251 T; 0 U; 16 Other;

Alignment Scores:
Pred. No.: 10.6 Length: 880
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAD01351 (1-880)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 267 TGGATAGCCACGACTCGGCCAT 290

RESULT 9
ADI26234
ID ADI26234 standard; DNA; 1362 BP.
XX
AC ADI26234;
XX
XX 06-MAY-2004 (first entry)
XX DT
XX Primula vialii delta6-desaturase gene SeqID3.
XX DE
XX delta6-desaturase; omega3-fatty acid; oil; lipid; free fatty acid;
XX KW animal feed; food; cosmetic; pharmaceutical; arachidonic acid;
XX KW omega-6 family; gene; ds; plant.
XX KW
XX OS Primula vialii.
XX
XX Key Location/Qualifiers
XX FH 1..1362
XX FT /*tag= a
XX FT /product= "Aleruritia farinosa delta6-desaturase"
XX
XX GB2385852-A.
XX
XX 03-SEP-2003.
XX PD
XX
XX 27-FEB-2002; 2002GB-00004676.
XX PF
XX

PR 27-FEB-2002; 2002GB-00004676.
XX
XX (ROTH-) ROTHAMSTED EXPERIMENTAL STATION.
XX
XX Napier JA, Sayanova O;
XX PI
XX WPI: 2003-699784/67.
XX DR
XX P-PSDB; ADI26235.
XX DR
XX New nucleic acid encoding delta6-desaturase and the encoded enzyme,
XX PT useful for preparing transgenic plants with increased production of omega
XX PT -3 fatty acids.
XX
XX Claim 2; SEQ ID NO 3; 51pp; English.
XX PS
XX This invention relates to a novel DNA sequence that encodes a protein
XX CC with delta6-desaturase activity that specifically converts omega3-fatty
XX CC acids. Transgenic organisms, specifically plants, that contain the DNA of
XX CC the invention are used for production of omega-3 fatty acids, as oils,
XX CC lipids or free fatty acids, useful in animal feeds, foods, cosmetics and
XX CC pharmaceuticals. The invention can also be used in homology screening to
XX CC isolate other genomic sequences, and as antisense reagents, ribozymes or
XX CC other inhibitory molecules to prevent expression of delta6-desaturase,
XX CC for example where oils of higher saturated fatty acid contents are
XX CC required. Plants that express the DNA of the invention have an increased
XX CC content of omega-3 fatty acids, without formation of unwanted by-products
XX CC (particularly arachidonic acid or other members of the omega-6 family).
XX CC The protein has activity towards omega-3 acids at least 1.5, particularly
XX CC 5, times greater than against omega-6 acids. The present sequence is that
XX CC of a delta6-desaturase gene of the invention.
XX
XX SQ Sequence 1362 BP; 300 A; 385 C; 338 G; 339 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 17 Length: 1362
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADI26234 (1-1362)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 481 TGGATAGGTCCAGCTCTGGCCAT 504

RESULT 10
ADI26232
ID ADI26232 standard; DNA; 1362 BP.
XX
AC ADI26232;
XX
XX 06-MAY-2004 (first entry)
XX DT
XX Aletris farinosa delta6-desaturase gene SeqID1.
XX DE
XX delta6-desaturase; omega3-fatty acid; oil; lipid; free fatty acid;
XX KW animal feed; food; cosmetic; pharmaceutical; arachidonic acid;
XX KW omega-6 family; gene; ds; plant.
XX KW
XX OS Aletris farinosa.
XX
XX Key Location/Qualifiers
XX FH 1..1362
XX FT /*tag= a
XX FT /product= "Aleruritia farinosa delta6-desaturase"
XX
XX GB2385852-A.
XX
XX 03-SEP-2003.
XX PD
XX
XX 27-FEB-2002; 2002GB-00004676.
XX PF
XX

```



KW Wheat; sphingolipid desaturase; membrane-bound desaturase;  
 KW transgenic plant; fatty acid; ss.

OS Triticum aestivum.

XX Key Location/Qualifiers  
 XX CDS 124..1533

FT /\*tag= a  
 FT /product= "Sphingolipid desaturase"

XX WO200032790-A2.

XX PN 08-JUN-2000.

XX 02-DEC-1999; 99WO-US028589.

XX 03-DEC-1998; 98US-0110784P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX WPI; 2000-412336/35.

XX P-PSDB; AAY71555.

XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing  
 PT transgenic plants and for producing antibodies specific to which is  
 PT useful for screening cDNA expression libraries.

XX Disclosure; Page 48-49; 57pp; English.

XX The present sequence is a cDNA encoding sphingolipid desaturase from  
 CC clone wrel.pk0004.c7.fis isolated from wheat etiolated seedling root cDNA  
 CC library, wrel. The present sequence is useful for producing transgenic  
 CC plants having altered levels of sphingolipid desaturase which in turn  
 CC would alter the fatty acid composition. The enzyme is useful for  
 CC producing polyclonal or monoclonal antibodies. The polynucleotide is also  
 CC useful as primer or probe for screening cDNA libraries to isolate desired  
 CC full-length cDNA clones

XX SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 25.4 Length: 1972  
 Score: 50.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 87.50% Mismatches: 0  
 Query Match: 94.34% Indels: 0  
 DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAD01353 (1-1972)

Qy 1 TptlGlyHisAspAlaGlyHis 8

Db 649 TGGATTGGCCATGACTCGGCCAC 672

RESULT 13

AAD01350

ID AAD01350 standard; cDNA; 1764 BP.

XX AAD01350;

XX 12-OCT-2000 (first entry)

XX Corn sphingolipid desaturase cDNA.

XX Corn; sphingolipid desaturase; membrane-bound desaturase;

XX transgenic plant; fatty acid; ss.

XX Zea mays.

XX Key Location/Qualifiers

XX CDS 89..1477

FT /\*tag= a  
 FT /product= "Sphingolipid desaturase"

XX WO200032790-A2.

XX PN 08-JUN-2000.

XX 02-DEC-1999; 99WO-US028589.

XX 03-DEC-1998; 98US-0110784P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX WPI; 2000-412336/35.

XX P-PSDB; AAY71552.

XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing  
 PT transgenic plants and for producing antibodies specific to which is  
 PT useful for screening cDNA expression libraries.

XX Claim 2; Page 41-42; 57pp; English.

XX The present sequence is a cDNA encoding sphingolipid desaturase from  
 CC clone cdelc.pk001.o8.fis isolated from corn developing embryo cDNA  
 CC library, cdelc. The present sequence is useful for producing transgenic  
 CC plants having altered levels of sphingolipid desaturase which in turn  
 CC would alter the fatty acid composition. The enzyme is useful for  
 CC producing polyclonal or monoclonal antibodies. The polynucleotide is also  
 CC useful as primer or probe for screening cDNA libraries to isolate desired  
 CC full-length cDNA clones

XX SQ Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 78.7 Length: 1764  
 Score: 47.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 2  
 Best Local Similarity: 75.00% Mismatches: 0  
 Query Match: 88.68% Indels: 0  
 DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAD01350 (1-1764)

Qy 1 TptlGlyHisAspAlaGlyHis 8

Db 593 TGGATGGGCCACGACTCGGCCAC 616

RESULT 14

ADJ48284

ID ADJ48284 standard; DNA; 2054 BP.

XX AC ADJ48284;

XX DT 06-MAY-2004 (first entry)

XX DE Maize oil-associated gene #102.

XX ds; maize; plant; oil-associated gene; transgenic; enhanced seed oil;  
 KW vegetable oil.

XX OS Zea mays.

XX US2004025202-A1.

XX 05-FEB-2004.

XX 14-MAR-2003; 2003US-00389566.

XX 15-MAR-2002; 2002US-0365301P.

XX 26-JUN-2002; 2002US-0391786P.

XX 26-JUN-2002; 2002US-0392018P.

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XX (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
XX
XX Laurie CC, Ravanello M, Savage T, Ledoux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX
XX Example 1; SEQ ID NO 288; 22pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents a maize oil-
XX associated gene.
XX
XX SQ Sequence 2054 BP; 343 A; 692 C; 538 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 92.8 Length: 2054
Score: 47.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 88.68% Indels: 0
DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ADJ48284 (1-2054)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||:::|||||:::|||||
Db 667 TGGATGGGCCACGACTCGGGCCAC 690

RESULT 15
AAS46880
ID AAS46880 standard; cDNA; 649 BP.
XX
XX AAS46880;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human G protein-coupled receptor (GPCR) cDNA #62.
DE
XX
XX Human; G protein-coupled receptor; GPCR; mental disorder; schizophrenia;
XX neurological disorder; metabolic disorder; cancer; rheumatoid arthritis;
XX thyroid disorder; neurodegenerative disorder; cardiovascular disorder;
XX renal failure; autoimmune disorder; hyperproliferative disorder; HIV; ss;
XX human immunodeficiency virus; viral infection; neuroprotective;
XX immunostimulant; neuroleptic; nootropic; tranquilizer; antidepressant;
XX anorectic; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200168858-A2.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 16-MAR-2001; 2001WO-US008456.
PF
XX
XX 16-MAR-2000; 2000US-0187783P.
PR
XX
XX 16-MAR-2000; 2000US-0189907P.
PR
XX
XX 16-MAR-2000; 2000US-0189917P.
PR
XX
XX 16-MAR-2000; 2000US-0189918P.
PR

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PR 16-MAR-2000; 2000US-0189960P.
PR 29-MAR-2000; 2000US-0192155P.
PR 29-MAR-2000; 2000US-0192234P.
PR 29-MAR-2000; 2000US-0192830P.
PR 29-MAR-2000; 2000US-0192916P.
PR 29-MAR-2000; 2000US-0192933P.
PR 29-MAR-2000; 2000US-0192945P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Vogeli G;
XX WPI; 2001-607458/69.
XX P-PSDB; AAU29441.
XX
XX Nucleic acid encoding G-protein coupled receptors, useful for the
XX prevention, diagnosis and treatment of mental disorders.
XX
XX Claim 4; Page 80; 274pp; English.
XX
XX Sequences AAS46819-AAS46946 represent cDNA molecules encoding human G
XX protein-coupled receptor (GPCR) polypeptides. The protein and DNA
XX sequences of the invention can be used to identify compounds which bind
XX to GPCR polypeptides and in screening for compounds that modulate GPCR
XX activity. By screening a human subject for the presence of mutations in
XX GPCR DNA, a GPCR-related disorder or a genetic predisposition can be
XX diagnosed. The sequences can also be used for treatment and prevention of
XX mental disorders such as schizophrenia, neurological disorders such as
XX manic depression, metabolic disorders such as obesity, cancer, rheumatoid
XX arthritis, thyroid disorders such as myxoedema, neurodegenerative
XX disorders such as Parkinson's disease, cardiovascular disorders such as
XX atherosclerosis, renal failure, autoimmune disorders, hyperproliferative
XX disorders such as psoriasis and viral infections such as those caused by
XX HIV
XX
XX SQ Sequence 649 BP; 197 A; 122 C; 166 G; 164 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 40.6 Length: 649
Score: 46.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 86.79% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAS46880 (1-649)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||:::|||||:::|||||
Db 428 TGGGTAGGTTATGATCTGGGCAT 451

RESULT 16
ABK81658
ID ABK81658 standard; DNA; 649 BP.
XX
XX ABK81658;
AC
XX
XX 13-AUG-2002 (first entry)
DT
XX
XX cDNA encoding novel G protein coupled receptor (nGCPR-x) #62.
DE
XX
XX G protein coupled receptor; nGCPR-x; immune response; thyroid disorder;
XX mental disorder; thyrotoxicosis; myxoedema; inflammatory condition;
XX Crohn's disease; cell differentiation; homeostasis; rheumatoid arthritis;
XX renal failure; autoimmune disorder; movement disorder; CNS disorder;
XX viral infection; human immunodeficiency virus; HIV; metabolic disorder;
XX cardiovascular disorder; diabetes; obesity; anorexia; cardiomyopathy;
XX poriferative disease; cancer; psoriasis; lung cancer; hormonal disorder;
XX sexual dysfunction; gene; ss.
XX
XX Homo sapiens.
OS
XX

```

PN US2002058306-A1.  
 XX 16-MAY-2002.  
 PD  
 XX  
 XX 16-MAR-2001; 2001US-00811284.  
 XX  
 XX 16-MAR-2000; 2000US-0189783P.  
 PR 16-MAR-2000; 2000US-0189907P.  
 PR 16-MAR-2000; 2000US-0189917P.  
 PR 16-MAR-2000; 2000US-0189918P.  
 PR 16-MAR-2000; 2000US-0189960P.  
 PR 24-MAR-2000; 2000US-01921155P.  
 PR 27-MAR-2000; 2000US-0192234P.  
 PR 29-MAR-2000; 2000US-0192830P.  
 PR 29-MAR-2000; 2000US-0192916P.  
 PR 29-MAR-2000; 2000US-0192923P.  
 PR 29-MAR-2000; 2000US-0192933P.  
 PR 29-MAR-2000; 2000US-0192935P.  
 PR 29-MAR-2000; 2000US-0192945P.  
 XX  
 XX (VOGE/) VOGELI G.  
 PA  
 XX  
 XX Vogel G;  
 PI  
 XX  
 XX WPI; 2002-434856/46.  
 DR P-PSDB; ABG60729.  
 DR  
 XX  
 XX New isolated nucleic acid encoding a G protein coupled receptor for  
 PT producing the receptor which can induce an immune response in a mammal.  
 PT  
 XX  
 XX Claim 4; Page 53; 216pp; English.  
 PS  
 XX  
 CC The invention describes an isolated nucleic acid (I) comprising a  
 CC sequence encoding a portion of a G protein coupled receptor (ngPCR-x).  
 CC (I) is used to produce a recombinant ngPCR-x polypeptide. A polypeptide  
 CC encoded by (I) is used to induce an immune response in a mammal. ngPCR-x  
 CC is used to identify a compound that binds to it and/or modulates it's  
 CC activity. (I) is used to identify animal homologues of ngPCR-x. (I) can  
 CC be used to diagnose a human subject as having a brain or genetic  
 CC predisposition disorder, such as a mental disorder. (I) is used to screen  
 CC for an ngPCR-x related disorder including thyroid disorders (e.g.  
 CC thyrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g.  
 CC Crohn's disease), diseases related to cell differentiation and  
 CC homeostasis, rheumatoid arthritis, autoimmune disorders, movement  
 CC disorders, CNS disorders, viral infections (e.g. Human immunodeficiency  
 CC virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity,  
 CC anorexia, cardiomyopathies), proliferative diseases and cancers (e.g.  
 CC psoriasis, lung cancer), hormonal disorders, sexual dysfunction and  
 CC hereditary mental disorders in a human patient. A host cell comprising  
 CC (I) is used to screen for a modulator of ngPCR-x activity. ngPCR-x is  
 CC used to identify compounds that can treat mental disorders. The  
 CC polypeptide encoded by (I) is used to purify a G protein from a sample.  
 CC This sequence encodes a novel G protein coupled receptor (ngPCR-x)  
 CC protein described in the invention  
 XX  
 XX Sequence 649 BP; 197 A; 122 C; 166 G; 164 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 40.6 Length: 649  
 Score: 46.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 2  
 Best Local Similarity: 75.00% Mismatches: 0  
 Query Match: 86.79% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-029-756-6 (1-8) x ABK81658 (1-649)  
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
 Db 428 TGGGTAGGATGATGATCGGGCAT 451  
 RESULT 17  
 ADP65987

ID ADP65987 standard; DNA; 533 BP.  
 XX  
 AC ADP65987;  
 XX  
 XX 12-AUG-2004 (first entry)  
 DT  
 XX  
 DE Mouse EST sequence #145 DNA.  
 XX  
 XX autoimmune disease; arthritis; gene expression analysis;  
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
 KW antirheumatic; osteopathic; antigout; antinflammatory; dermatological;  
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KW immune; ds; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 XX W02003072827-A1.  
 FN  
 XX  
 XX 04-SEP-2003.  
 PD  
 XX  
 XX 31-OCT-2002; 2002WO-US035433.  
 PF  
 XX  
 XX 31-OCT-2001; 2001US-0336220P.  
 PR  
 XX  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PA  
 XX  
 XX Hirsch R, Thorton SL;  
 PI  
 XX  
 XX WPI; 2003-712740/67.  
 DR  
 XX GENBANK; AI893697.  
 DR  
 XX  
 XX Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.  
 XX  
 XX Disclosure; Page: 56pp; English.  
 PS  
 XX The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
 CC antigout, antinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This polynucleotide  
 CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.  
 XX  
 XX Sequence 533 BP; 121 A; 135 C; 151 G; 126 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 49.8 Length: 533  
 Score: 45.00 Matches: 6  
 Percent Similarity: 87.50% Conservative: 1  
 Best Local Similarity: 75.00% Mismatches: 1



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FT replace(11136,C)
FT /*tag= ap
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11364,G)
FT /*tag= aq
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11471,G)
FT /*tag= ar
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11628,G)
FT /*tag= as
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12029,G)
FT /*tag= at
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12349,C)
FT /*tag= au
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12579,G)
FT /*tag= av
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12663,G)
FT /*tag= aw
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12891,T)
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FT /standard_name= "Single nucleotide polymorphism"
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FT /standard_name= "Single nucleotide polymorphism"
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FT replace(13352,G)
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FT replace(13474,R)
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FT replace(13899,G)
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FT replace(14334,C)
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FT replace(14980,T)
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FT replace(21114,C)
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FT replace(21566,A)
FT /*tag= bl
FT /standard_name= "Single nucleotide polymorphism"
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FT replace(22637,C)
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FT replace(24154,A)
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FT replace(30468,G)
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Alignment Scores:
Pred. No.: 2.97e+04 Length: 197997
Score: 45.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 84.91% Indels: 0
DB: 10 Gaps: 0
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US-10-029-756-6 (1-8) x AAL54074 (1-197997)

```
Oy 1 TrpIleGlyHisaspAlaGlyHis 8
Db 185026 TGGGTCGGGCATGATGCTGGAAT 185049
RESULT 20
ABL14177/c
ID ABL14177 standard; CDNA; 2734 BP.
```



XX AC ABL14177;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37013.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical; gene; ss.  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX WI; 2001-656860/75.  
 XX DR P-PSDB; ABB70074.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX PT interactions.  
 XX PS Claim 1; SEQ ID NO 37013; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX CC useful in developmental biology and in elucidating cell signalling and  
 XX CC cell-cell interactions in higher eukaryotes for the development of  
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 XX CC ABB72072). The sequence data for this patent did not form part of the  
 XX CC printed specification, but was obtained in electronic format directly  
 XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 2734 BP; 719 A; 760 C; 749 G; 506 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 442 Length: 2734  
 Score: 44.00 Matches: 6  
 Percent Similarity: 87.50% Conservative: 1  
 Best Local Similarity: 75.00% Mismatches: 1  
 Query Match: 83.02% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-029-756-6 (1-8) x ABL14177 (1-2734)  
 QY 1 TptileGlyHisAspAlaGlyHis 8  
 DB 704 TGGATGGGGCATTTCAGCTGGGCAT 681  
 RESULT 21  
 ABL14176/c  
 ID ABL14176 standard; cDNA; 5679 BP.  
 XX AC ABL14176;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37010.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX WI; 2001-656860/75.  
 XX DR P-PSDB; ABB70073.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX PT interactions.  
 XX PS Claim 1; SEQ ID NO 37010; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX CC useful in developmental biology and in elucidating cell signalling and  
 XX CC cell-cell interactions in higher eukaryotes for the development of  
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 XX CC ABB72072). The sequence data for this patent did not form part of the  
 XX CC printed specification, but was obtained in electronic format directly  
 XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 5679 BP; 1627 A; 1375 C; 1297 G; 1380 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 974 Length: 5679  
 Score: 44.00 Matches: 6  
 Percent Similarity: 87.50% Conservative: 1  
 Best Local Similarity: 75.00% Mismatches: 1  
 Query Match: 83.02% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-029-756-6 (1-8) x ABL14176 (1-5679)  
 QY 1 TptileGlyHisAspAlaGlyHis 8  
 DB 2023 TGGATGGGGCATTTCAGCTGGGCAT 2000  
 RESULT 22  
 ABL1186/c  
 ID ABL1186 standard; DNA; 472 BP.  
 XX AC ABL1186;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE Toxicity modelling related rat gene SEQ ID No 888.  
 XX KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
 XX KW database; drug screening; toxicity assay; rat; ds.  
 XX OS Rattus norvegicus.  
 XX PN WO200295000-A2.  
 XX PD 28-NOV-2002.  
 XX PF 22-MAY-2002; 2002WO-US016173.  
 XX



XX Human genome derived single exon probe #20559.  
 DE Human; probe; ss; gene expression; single exon probe; microarray;  
 XX alternative splicing event; genomic alteration.  
 KW Homo sapiens.  
 OS  
 XX  
 XX US2003194704-A1.  
 PN 16-OCT-2003.  
 PD  
 XX  
 XX 03-APR-2002; 2002US-00029386.  
 PF  
 XX 03-APR-2002; 2002US-00029386.  
 PR  
 XX (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 XX Penn SG, Rank DR, Hanzel DK;  
 XX WPI; 2004-119264/12.  
 DR  
 XX  
 XX New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 XX Claim 1; SEQ ID NO 20559; 80pp; English.  
 PS  
 XX  
 XX The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030194704  
 XX  
 XX Sequence 475 BP; 106 A; 107 C; 164 G; 98 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 154 Length: 475  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-029-756-6 (1-8) x ACH87364 (1-475)  
 QY 1 TrpIleGlyHisAspAlaGlyHis 8  
 DB 356 TGGATAGGCGCATTCATTGGCCAC 379  
 RESULT 25  
 ACH82639  
 ID ACH82639 standard; DNA; 487 BP.  
 XX  
 AC ACH82639;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 XX Human genome derived single exon probe #15834.  
 XX Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003194704-A1.  
 XX  
 XX 16-OCT-2003.  
 XX  
 XX 03-APR-2002; 2002US-00029386.  
 XX  
 XX 03-APR-2002; 2002US-00029386.  
 XX (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 XX Penn SG, Rank DR, Hanzel DK;  
 XX WPI; 2004-119264/12.  
 XX  
 XX New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 XX Claim 1; SEQ ID NO 15834; 80pp; English.  
 PS  
 XX The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030194704  
 XX



CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subsequence, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterizing  
CC alternative splicing events, in detecting and characterizing gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence is a human  
CC single exon probe of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
XX  
SQ Sequence 521 BP; 118 A; 165 C; 119 G; 119 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 170 Length: 521  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ACH77282 (1-521)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||||  
Db 69 TGGATAGGCGCATTCATTGGCCAC 46

RESULT 28  
ABZ34667  
ID ABZ34667 standard; cDNA; 522 BP.  
XX  
AC ABZ34667;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Coding sequence SEQ ID 25, downregulated in osteogenesis.  
XX  
KW Osteopathic; osteogenesis modulator; gene therapy; osteogenesis;  
XX osteoporosis; bone disease; downregulator; human; ss.  
XX Homo sapiens.  
XX  
FN WO200281745-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 05-APR-2002; 2002WO-IB002211.  
XX  
PR 05-APR-2001; 2001US-0281400P.  
XX  
PA (AVET ) AVENTIS PHARMA SA.

XX Garcia T, Roman Roman S, Baron R, Call K, Theilhaber J;  
PI Connolly T, Jackson A, Bushnell SE, Rawadi G;  
XX WPI; 2003-058567/05.  
XX Novel isolated nucleic acid upregulated/downregulated in osteogenesis,  
PT useful for bone disease therapy in subject.  
XX

PS Claim 27; Page 93; 237pp; English.

XX The present invention relates to novel nucleotide sequences, which are  
XX differentially expressed in models of osteogenesis upon being put in  
XX contact with a stimulator of osteogenesis. The present sequence is one  
XX such sequence. This sequence can be used for diagnosing osteoporosis/bone  
XX disease in a patient, promoting osteogenesis and/or preventing  
XX osteoporosis/bone disease. The present sequence encodes a secreted  
XX protein

SQ Sequence 522 BP; 154 A; 120 C; 153 G; 95 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 170 Length: 522  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x ABZ34667 (1-522)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||||  
Db 194 TGGATTGGGCACCCGGGAGGCAC 217

RESULT 29  
ADB57297  
ID ADB57297 standard; DNA; 539 BP.  
XX  
AC ADB57297;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Toxicity-related gene, SEQ ID 2323.  
XX  
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
XX drug screening; toxicity assay; ds.  
XX Unidentified.

XX WO2003064624-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-US003194.  
XX  
PR 31-JAN-2002; 2002US-00060087.  
XX  
PR 15-MAR-2002; 2002US-0364045P.  
XX  
PR 15-MAR-2002; 2002US-0364055P.  
XX  
PR 30-DEC-2002; 2002US-0436643P.  
XX  
PA (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
PI WPI; 2003-689530/65.  
XX  
PT Predicting a toxic effect of a compound, useful in identifying toxicity  
XX markers in liver tissues or cells for drug screening and toxicity assays,  
XX comprises preparing gene expression profile of tissue or cells exposed to  
XX the compound.  
XX  
PS Claim 1; SEQ ID NO 2323; 1156pp; English.

XX The present invention relates to a method for predicting a toxic effect  
XX of a compound. The method comprises preparing a gene expression profile  
XX of a tissue or cell sample exposed to the compound, and comparing the  
XX gene expression profile to a database comprising SEQ ID 1-4925, where  
XX differential expression of the gene indicates at least one toxic effect.  
XX The method is useful for predicting at least one toxic effect of a  
XX compound, predicting hepatotoxicity or the progression of a toxic effect  
XX of a compound, identifying an agent that modulates the onset or

CC progression of a toxic response, predicting the cellular pathways that a  
CC compound modulates in a cell, and identifying an agent that modulates at  
CC least one activity of a protein. The method and compositions of the  
CC present invention using a database of genes having liver toxin-induced  
CC differential expression, are useful in identifying toxicity markers in  
CC liver tissues or cells for drug screening and toxicity assays. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 539 BP; 126 A; 123 C; 158 G; 132 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 176 Length: 539  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADB57297 (1-539)

Qy 1 TrrpIleGlyHisAspAlaGlyHis 8

Db 274 TGGACAGGGCACCAGGCGAGTTCAT 297

RESULT 30

ABT41439

ID ABT41439 standard; DNA; 539 BP.

XX AC ABT41439;

XX DT 26-JUN-2003 (first entry)

XX DE Toxicity modelling related rat gene SEQ ID No 1141.

XX KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
KW database; drug screening; toxicity assay; rat; ds.

XX OS Rattus norvegicus.

XX FN WO200295000-A2.

XX PD 28-NOV-2002.

XX PF 22-MAY-2002; 2002WO-US016173.

XX PR 22-MAY-2001; 2001US-0292335P.

XX PR 13-JUN-2001; 2001US-0297523P.

XX PR 19-JUN-2001; 2001US-0298925P.

XX PR 10-JUL-2001; 2001US-0303807P.

XX PR 10-JUL-2001; 2001US-0303808P.

XX PR 10-JUL-2001; 2001US-0303810P.

XX PR 28-AUG-2001; 2001US-0315047P.

XX PR 27-SEP-2001; 2001US-0324928P.

XX PR 22-OCT-2001; 2001US-0330462P.

XX PR 01-NOV-2001; 2001US-0330867P.

XX PR 21-NOV-2001; 2001US-0331805P.

XX PR 06-DEC-2001; 2001US-0336144P.

XX PR 19-DEC-2001; 2001US-0340873P.

XX PR 21-FEB-2002; 2002US-0357842P.

XX PR 21-FEB-2002; 2002US-0357843P.

XX PR 21-FEB-2002; 2002US-0357844P.

XX PR 15-MAR-2002; 2002US-0364134P.

XX PR 08-APR-2002; 2002US-0370144P.

XX PR 08-APR-2002; 2002US-0370206P.

XX PR 17-APR-2002; 2002US-0370247P.

XX PR 21-APR-2002; 2002US-0372794P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;

XX DR WPI; 2003-148464/14.

XX PT Predicting at least one toxic effect of a compound, useful for toxicity  
PT modeling, comprises preparing a gene expression profile of a tissue or  
PT cell sample exposed to the compound, and comparing the gene expression  
PT profile to a database.

XX PS Example 4; Page; 446pp; English.

XX CC The invention relates to a novel method of predicting at least one toxic  
CC effect of a compound. The method comprises a gene expression profile of a  
CC tissue or cell sample exposed to the compound, and comparing the gene  
CC expression profile to a database comprising at least part of the data or  
CC information given in the specification. The methods are useful for  
CC predicting at least one toxic effect of a compound, predicting the  
CC progression of a toxic effect of a compound, predicting the renal  
CC toxicity of a compound, or identifying toxicity markers in tissues or  
CC cells exposed to known renal toxin. The genes are useful as toxicity  
CC markers in drug screening and toxicity assays, in monitoring disease or  
CC physiological states, or disease progression. This polynucleotide  
CC represents a rat DNA sequence relating to the toxic effect database  
CC described in the specification. NOTE: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the World Intellectual Property  
CC Organization

XX SQ Sequence 539 BP; 126 A; 123 C; 158 G; 132 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 176 Length: 539  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ABT41439 (1-539)

Qy 1 TrrpIleGlyHisAspAlaGlyHis 8

Db 274 TGGACAGGGCACCAGGCGAGTTCAT 297

RESULT 31

ACH73652

ID ACH73652 standard; DNA; 565 BP.

XX AC ACH73652;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon probe #6847.

XX KW Human; probe; ss; gene expression; single exon probe; microarray;  
KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX FN US2003194704-A1.

XX PD 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX PR 03-APR-2002; 2002US-00029386.

XX PA (PENN/) PENN S G.

XX PA (RANK/) RANK D R.

XX PA (HANZ/) HANZEL D K.

XX PI Penn SG, Rank DR, Hanzel DK;

XX DR WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probe for measuring human gene  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 PS Claim 15; SEQ ID NO 6847; 80pp; English.  
 XX  
 CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressable isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 XX  
 SQ Sequence 565 BP; 126 A; 135 C; 202 G; 102 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 186 Length: 565  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ACH73652 (1-565)

Oy 1 TrpIleGlyHisAspAlaGlyHis 8  
 |||||  
 Db 241 TGGATAGGCGCATTCATTGGCCAC 264  
 |||||

RESULT 32  
 ACH90983/c  
 ID ACH90983 standard; DNA; 571 BP.  
 XX  
 AC ACH90983;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 XX Human genome derived single exon probe #24178.  
 DE  
 XX Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX

OS Homo sapiens.  
 XX US2003194704-A1.  
 PN  
 XX 16-OCT-2003.  
 PD  
 XX  
 PF 03-APR-2002; 2002US-00029386.  
 XX  
 PR 03-APR-2002; 2002US-00029386.  
 XX  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 XX WPI; 2004-119264/12.  
 XX  
 PT New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 PS Claim 1; SEQ ID NO 24178; 80pp; English.  
 XX  
 CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressable isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 XX  
 SQ Sequence 571 BP; 105 A; 203 C; 137 G; 126 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 188 Length: 571  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ACH90983 (1-571)

OY 1 TrpIleGlyHisAspAlaGlyHis 8  
 DB 320 TGGATAGGCGATTCATTGGCCAC 297  
 RESULT 33  
 ACH68939 standard; DNA; 589 BP.  
 XX  
 AC ACH68939;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human genome derived single exon probe #2134.  
 XX  
 KW Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003194704-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 03-APR-2002; 2002US-00029386.  
 XX  
 PR 03-APR-2002; 2002US-00029386.  
 XX  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ) HANZEL D K.  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 XX  
 DR WPI; 2004-119264/12.  
 XX  
 PT New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 PS Claim 15; SEQ ID NO 2134; 80pp; English.  
 XX  
 CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC a method of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above). The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 XX  
 SQ Sequence 589 BP; 148 A; 139 C; 140 G; 162 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 194 Length: 589  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-029-756-6 (1-8) x ACH68939 (1-589)  
 OY 1 TrpIleGlyHisAspAlaGlyHis 8  
 DB 87 TGGATTGGCAGACATGGGCCAC 110  
 RESULT 34  
 AAS05580/c  
 ID AAS05580 standard; DNA; 650 BP.  
 XX  
 AC AAS05580;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Mammalian vestibular system geotactic behaviour modulator gene #180.  
 XX  
 KW Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo;  
 KW graviperceptive disorder; motion sickness; labyrinthitis; syphilis; ds;  
 KW Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy;  
 KW trauma; infection of the middle ear; ototoxic agent exposure.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200140519-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US032639.  
 XX  
 PR 02-DEC-1999; 99US-0168579P.  
 PR 26-SEP-2000; 2000US-00669751.  
 XX  
 PA (NEUR-) NEUROSCIENCES RES FOUND INC.  
 XX  
 PI Greenspan RJ;  
 XX  
 DR WPI; 2001-356159/37.  
 XX  
 PT New isolated nucleic acid having mammalian vestibular system-modulating  
 PT activity useful in the treatment of disorders such as motion sickness and  
 PT vertigo.  
 XX  
 PS Claim 59; Page 151; 179pp; English.  
 XX  
 CC The sequences shown in AAS05401-AAS05661 represent DNA with mammalian  
 CC vestibular system-modulating activity. The DNA sequences can be used in a  
 CC method whereby a first and second strain of an invertebrate is obtained,  
 CC and both are subjected to conditions in which the strains exhibit  
 CC different geotactic behaviour. Genes that are differentially expressed in  
 CC the first strain relative to the second strain are then identified.  
 CC Mammalian genes having substantially the same nucleic acid sequence as  
 CC these genes are used to decrease the symptoms of graviorceptive  
 CC disorders such as motion sickness, vertigo, labyrinthitis, Meniere's  
 CC disease, acoustic neuroma, multiple sclerosis, syphilis, trauma,  
 CC infection of the middle ear, exposure to ototoxic agents and epilepsy  
 XX  
 SQ Sequence 650 BP; 173 A; 162 C; 131 G; 184 T; 0 U; 0 Other;



Alignment Scores: 216 Length: 650  
Pred. No.: 42.00 Matches: 6  
Score: 75.00% Conservative: 0  
Percent Similarity: 75.00% Mismatches: 2  
Best Local Similarity: 75.00% Indels: 0  
Query Match: 79.25% Gaps: 0  
DB: 5

US-10-029-756-6 (1-8) x AAS05580 (1-650)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 415 TGGTGTGGGCATAGCGCAGGCAC 392

RESULT 35  
AAH05583/C  
ID AAH05583 standard; cDNA; 734 BP.  
XX  
AC AAH05583;  
XX  
XX 26-JUN-2001 (first entry)  
XX  
DE Human cDNA clone (5'-primer) SEQ ID NO:2418.  
XX  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
XX Homo sapiens.  
XX  
XX EPI074617-A2.  
XX  
XX 07-FEB-2001.  
XX  
XX 28-JUL-2000; 2000EP-00116126.  
XX  
XX 29-JUL-1999; 99JP-00248036.  
XX  
XX 27-AUG-1999; 99JP-00300253.  
XX  
XX 11-JAN-2000; 2000JP-00118776.  
XX  
XX 02-MAY-2000; 2000JP-00183767.  
XX  
XX 09-JUN-2000; 2000JP-00241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX  
XX WPI; 2001-318749/34.  
XX  
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 1; SEQ ID NO 2418; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX Sequence 734 BP; 211 A; 190 C; 153 G; 177 T; 0 U; 3 Other;

Alignment Scores: 246 Length: 734  
Pred. No.: 42.00 Matches: 6  
Score: 75.00% Conservative: 0  
Percent Similarity: 75.00% Mismatches: 2  
Best Local Similarity: 75.00% Indels: 0  
Query Match: 79.25% Gaps: 0  
DB: 4

US-10-029-756-6 (1-8) x AAH05583 (1-734)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 427 TGGATTGGGCACAGCATGGGCCAC 404

RESULT 36  
ABI99493  
ID ABI99493 standard; cDNA; 1514 BP.  
XX  
AC ABI99493;  
XX  
XX 07-MAR-2002 (first entry)  
XX  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:463.  
XX  
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
XX Mus musculus.  
XX  
XX WO200188188-A2.  
XX  
XX 22-NOV-2001.  
XX  
XX 18-MAY-2001; 2001WO-JP004192.  
XX  
XX 18-MAY-2000; 2000JP-00145977.  
XX  
XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX  
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX  
XX WPI; 2002-034733/04.  
XX  
XX P-PSDB; ABB57191.  
XX  
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

PS Claim 2; Page 1289-1290; 2690pp; English.

XX The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention

XX

SQ Sequence 1514 BP; 484 A; 267 C; 350 G; 413 T; 0 U; 0 Other;

Alignment Scores: 539 Length: 1514  
 Pred. No.: 42.00 Matches: 6  
 Score: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABI9493 (1-1514)

QY 1 TtpileGlyHisAspAlaGlyHis 8  
 |||||  
 DB 400 TGGATTGGCCACCGGGAGGGCAC 423

RESULT 37  
 AAQ20695  
 ID AAQ20695 standard; cDNA; 1542 BP.

AC AAQ20695;

XX 24-APR-1992 (first entry)

XX Mouse OSF.1.

XX MK; calvarial cell; probe; diagnosis; osteoblast; cranial nerve cell; ss.

XX Mus musculus.

XX Key Location/Qualifiers  
 XX CDS 229..735  
 FT /\*tag= a  
 FT /label= I-I

XX W09200324-A.

XX 09-JAN-1992.

XX 29-JUN-1990; 90JP-00169824.

XX 29-JUN-1990; 90JP-00169824.

XX 28-SEP-1990; 90JP-00256810.

XX (FARH ) HOECHST JAPAN LTD.

XX Hashimoto T, Tezuka K, Kumegawa S, Takagi C;

XX WPI; 1992-041516/05.

XX P-PSDB; AAR20238.  
 XX Protein from mouse calvarial cells - differentiates growth of  
 XX osteoblast(s) and cranial nerve cells, for treating and diagnosing  
 XX osteoporosis and dementia.

XX Disclosure; Fig 3 (1-5); 43pp; Japanese.

XX A cDNA library was constructed from mouse calvarial cell line MC3T3E1.  
 XX Differential screening in NIH3T3 cells (ATCC CRL-1658) and cloning, then  
 XX insertion into vector pUC118 gave plasmid pMC031 which contains the DNA  
 XX coding for mouse OSF-1 (AAQ20695). This plasmid was used as a probe to  
 XX clone by plaque hybridisation from a human cDNA library to give a phage  
 XX clone, HBRI. Insertion into vector pUC118 gave pHBRI which may be used  
 XX diagnostically or the OSF-1 cDNA (AAQ20696) incorporated (with poly-A  
 XX signal sequence and SV40 T-cell antigen promoter) into a vector (such as  
 XX pHSB-757) for expression (e.g. in CHO cells) of the protein. See also  
 XX AAQ20695-97

SQ Sequence 1542 BP; 488 A; 277 C; 360 G; 417 T; 0 U; 0 Other;

Alignment Scores: 549 Length: 1542  
 Pred. No.: 42.00 Matches: 6  
 Score:

Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAQ20695 (1-1542)

QY 1 TtpileGlyHisAspAlaGlyHis 8  
 |||||  
 DB 414 TGGATTGGCCACCGGGAGGGCAC 437

RESULT 38  
 AAZ44851  
 ID AAZ44851 standard; DNA; 1606 BP.

XX AAZ44851;

XX 27-APR-2000 (first entry)

XX Sphingolipid desaturase DNA.

XX Sphingolipid desaturase; sldi; sphingobase; ceramide; capnoid;  
 XX transgenic plant; crop plant; delta-8-unsaturated long-chain base;  
 XX tolerance; resistance; soil salinity; ion stress; toxicity; drought;  
 XX cold; frost; phytopathogenic microorganism; flowering time; cosmetic;  
 XX pharmaceutical; food; chemical raw material; ds.

XX Unidentified.

XX Key Location/Qualifiers  
 XX CDS 88..1464  
 FT /\*tag= a  
 FT /product= "Sphingolipid desaturase"

XX DE19828850-A1.

XX 30-DEC-1999.

XX 27-JUN-1998; 98DE-01028850.

XX 27-JUN-1998; 98DE-01028850.

XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

XX Heinz E, Zaehringer U, Schmidt H, Sperling P;

XX WPI; 2000-127549/12.

XX P-PSDB; AAY51348.

XX New sphingolipid desaturase that selectively introduces double bond into  
 XX sphingolipids and capnoids.

XX Disclosure; Fig 15; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively  
 XX introduces a double bond into the sphingobase of the ceramide residue of  
 XX sphingolipids and capnoids. A DNA sequence encoding the sphingolipid  
 XX desaturase, or a vector containing the DNA sequence, can be used to  
 XX produce transgenic plants, especially crop plants, with an increased or  
 XX decreased delta-8-unsaturated long-chain base content or an altered delta  
 XX -8-unsaturated long-chain base cis/trans ratio, especially to compensate  
 XX for a delta-8-unsaturated long-chain base deficiency, to exclude  
 XX production of delta-8-unsaturated bases, to increase tolerance or  
 XX resistance to soil salinity, ion stress or toxicity, drought, wet  
 XX conditions, cold or frost and/or phytopathogenic microorganisms, or to  
 XX alter size growth and flowering time. Cells, transgenic organisms or  
 XX plants containing the DNA sequence can be used to produce sphingolipids  
 XX and capnoids with unsaturated sphingobases. The sphingolipids or capnoids  
 XX can be used in cosmetics, pharmaceuticals and foods and as chemical raw  
 XX materials. This sequence encodes a sphingolipid desaturase protein  
 XX described in the method of the invention

XX Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 U; 0 Other;



CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
CC prokaryotic essential genes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1833 BP; 580 A; 292 C; 386 G; 575 T; 0 U; 0 Other;

Alignment Scores: 662 Length: 1833  
Pred. No.: 42.00 Matches: 6  
Score: 87.50% Conservative: 1  
Percent Similarity: 75.00% Mismatches: 1  
Best Local Similarity: 79.25% Indels: 0  
Query Match: 8 Gaps: 0  
DB:

US-10-029-756-6 (1-8) x ACA37407 (1-1833)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||...|||  
Db 801 TGGTATGTCATGATGCTGGTCAT 824

RESULT 41  
AAH15974/c  
ID AAH15974 standard; cDNA; 1866 BP.  
XX  
AC AAH15974;  
XX  
XX 26-JUN-2001 (first entry)  
XX  
XX Human cDNA sequence SEQ ID NO:14586.  
XX  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP1074617-A2.  
XX  
XX 07-FEB-2001.  
XX  
XX 28-JUL-2000; 2000EP-00116126.  
XX  
XX 29-JUL-1999; 99JP-00248036.  
XX  
XX 27-AUG-1999; 99JP-00300253.  
XX  
XX 11-JAN-2000; 2000JP-00118776.  
XX  
XX 02-MAY-2000; 2000JP-00183767.  
XX  
XX 09-JUN-2000; 2000JP-00241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX  
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-  
XX length cDNAs defined in the specification, and for the detection and/or  
XX diagnosis of the abnormality of the proteins encoded by the full-length  
XX cDNAs.  
XX  
XX Claim 8; SEQ ID NO 14586; 2537pp + Sequence Listing; English.  
XX  
XX The present invention describes primer sets for synthesising 5602 full-  
XX length cDNAs defined in the specification. Where a primer set comprises:  
XX (a) an oligo-dr primer and an oligonucleotide complementary to the  
XX complementary strand of a polynucleotide which comprises one of the 5602  
XX nucleotide sequences defined in the specification, where the  
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in the  
CC specification. The primer sets can be used in antisense therapy and in  
CC gene therapy. The primers are useful for synthesising polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893  
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent  
CC oligonucleotides, all of which are used in the exemplification of the  
CC present invention  
XX  
SQ Sequence 1866 BP; 512 A; 409 C; 390 G; 555 T; 0 U; 0 Other;

Alignment Scores: 675 Length: 1866  
Pred. No.: 42.00 Matches: 6  
Score: 75.00% Conservative: 0  
Percent Similarity: 75.00% Mismatches: 2  
Best Local Similarity: 79.25% Indels: 0  
Query Match: 4 Gaps: 0  
DB:

US-10-029-756-6 (1-8) x AAH15974 (1-1866)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||...|||  
Db 427 TGGATTGGCACAGCATGGGCCAC 404

RESULT 42  
ADO07820/c  
ID ADO07820 standard; cDNA; 1923 BP.  
XX  
AC ADO07820;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Human polynucleotide #43.  
XX  
XX Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
XX anorectic; antidiabetic.  
XX  
XX Homo sapiens.  
XX  
XX US2004071700-A1.  
XX  
XX 15-APR-2004.  
XX  
XX 09-OCT-2002; 2002US-00267502.  
XX  
XX 09-OCT-2002; 2002US-00267502.  
XX  
XX (LIFE-) LIFE SCI DEV CORP.  
XX  
XX Kim J, Galant R;  
XX  
XX WPI; 2004-328526/30.  
XX  
XX P-PSDB; ADO08037.  
XX  
XX Identifying compounds that influence fat cell number or size for treating  
XX or preventing obesity or diabetes by exposing the cell to the agent and  
XX identifying fat cell number or size relative to cells not exposed to the  
XX agent.  
XX  
XX Claim 1; SEQ ID NO 146; 275pp; English.  
XX  
XX The invention relates to a method of identifying compounds that influence  
XX fat cell number or size comprising providing a cell that expresses a gene  
XX and an agent, exposing the cell to the agent and identifying fat cell

CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC human cDNA used in the scope of the invention.

XX  
 SQ Sequence 1923 BP; 485 A; 552 C; 449 G; 437 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 697 Length: 1923  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ADO07820 (1-1923)

QY 1 TtpileglyHisAspAlaGlyHis 8  
 DB 1527 TGGATAGGCATTCCTATGGCCAC 1504

RESULT 43  
 AAS74417/C  
 ID AAS74417 standard; cDNA; 1996 BP.

AC AAS74417;  
 XX 13-FEB-2002 (first entry)

DT DNA encoding novel human diagnostic protein #10221.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

PF 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG10230.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX Claim 1; SEQ ID NO 10221; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 1996 BP; 762 A; 447 C; 350 G; 437 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 726 Length: 1996  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x AAS74417 (1-1996)

QY 1 TtpileglyHisAspAlaGlyHis 8  
 DB 1914 TGGATTGGGCACAGCATGGCCAC 1891

RESULT 44  
 AAZ42116/C  
 ID AAZ42116 standard; cDNA; 2238 BP.

AC AAZ42116;

XX 31-JAN-2000 (first entry)

DT Human endometrium tumour cDNA derived EST 136.

DE Endometrium; human; tumour; cancer; anticancer; cytostatic;  
 KW EST: treatment; uterine; gene therapy; expressed sequence tag; ss.

XX Homo sapiens.

OS DE19817948-A1.

PN 21-OCT-1999.

PD 17-APR-1998; 98DE-01017948.

PF 17-APR-1998; 98DE-01017948.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI; 1999-591957/51.

XX New nucleic acid sequences expressed in uterine cancer tissues, and  
 PT derived polypeptides, for treatment of uterine and endometrial cancer and  
 PT identification of therapeutic agents.

XX Claim 3; Page 269-270; 444pp; German.

XX This invention describes novel human nucleic acid (cDNA) sequences (A),  
CC that are highly expressed in uterine tumour tissue and which have  
CC anticancer and cytostatic activity. (A) are used (i) for recombinant  
CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)  
CC are used (i) to identify agents suitable for treatment of uterine or  
CC endometrial cancer; (ii) directly for treating these forms of cancer  
CC (including expression from gene therapy vectors) and (iii) for generation  
CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
CC sequence tags) from a particular tissue type before comparison of  
CC expression patterns. This allows a significantly longer fragment of the  
CC gene to be revealed, so should reduce the number of failures associated  
CC with the fact that ESTs from different libraries may represent different  
CC parts of the same unknown gene, distorting the estimated frequency of  
CC occurrence in a particular tissue. AA241981-AA242121 represent EST  
CC fragments derived from a human endometrium tumour cDNA library which  
CC encode the protein sequences represented in AA259941-Y60328  
XX

SQ Sequence 2238 BP; 602 A; 519 C; 463 G; 653 T; 0 U; 1 Other;

Alignment Scores:  
Pred. No.: 821 Length: 2238  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AA242116 (1-2238)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||  
Db 331 TGGATAGGCGATTCATTGGCCAC 308

RESULT 45

ID ABK83895/c  
ID ABK83895 standard; cDNA; 2307 BP.

XX AC ABK83895;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #466.

XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.

XX OS Homo sapiens.

XX PN WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;

XX DR WPI; 2002-435328/46.

XX PT Detecting granulocyte activation by detecting differential expression of  
PT genes associated with granulocyte activation, which serves as diagnostic  
PT markers that is useful for monitoring disease states and drug toxicity.

PS Claim 1; SEQ ID NO 466; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
CC DNA chip analysis as given in the specification, and comparing the  
CC expression level to an expression level in an unactivated GC, where  
CC differential expression of Gs is indicative of GCA. Also included are  
CC modulating (M2) GA by contacting GC with an agent that alters the  
CC expression of at least one gene in Gs; (2) screening (M3) for an agent  
CC capable of modulating GCA or an inflammation (especially chronic) in a  
CC tissue, an allergic response in a subject, exposure of a subject to a  
CC pathogen or sterile inflammatory disease using the gene expression  
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a  
CC tissue, an allergic response in a subject, exposure of a subject to a  
CC pathogen or sterile inflammatory disease, by detecting the level of  
CC expression in a sample of the tissue of gene(s) from Gs, where the level  
CC of expression of the gene is indicative of inflammation; (4) treating  
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic  
CC response in a subject, exposure of a subject to a pathogen or sterile  
CC inflammatory disease, by contacting a tissue having inflammation with an  
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1  
CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful  
CC for screening an agent capable of modulating GCA preferably in an  
CC inflammation in a tissue; M4 is useful for detecting an inflammation  
CC (especially chronic) in a tissue, an allergic response in a subject,  
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.  
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,  
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult  
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's  
CC disease, ulcerative colitis, periodontal disease; also bacterial  
CC infection, viral infection, parasitic infection, protozoal infection,  
CC fungal infection and M5 is useful for treating one of the above  
CC conditions. The present sequence represents a gene differentially  
CC expressed in granulocytes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 2307 BP; 626 A; 532 C; 488 G; 655 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 849 Length: 2307  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABK83895 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||  
Db 550 TGGATAGGCGATTCATTGGCCAC 527

RESULT 46

ADD12700/c

ID ADD12700 standard; cDNA; 2458 BP.

XX AC ADD12700;

XX DT 01-JAN-2004 (first entry)

XX DE Human cDNA expressed during adipocyte differentiation #46.

XX ss; gene; human; adipocyte differentiation; obesity; type II diabetes;  
KW lipodystrophy; hyperinsulinaemia.  
XX OS Homo sapiens.

XX PN US2003113720-A1.

XX PD 19-JUN-2003.

PF 30-JUL-2001; 2001US-00918624.  
 XX  
 PR 28-JUL-2000; 2000US-0222470P.  
 XX  
 PA (SCHE/) SCHEBYE X M.  
 PA (SORN/) SORNASSE T.  
 XX  
 PI Schebye XM, Sornasse T;  
 XX  
 XX WPI; 2003-810888/76.  
 XX  
 XX Novel isolated cDNAs expressed in adipocyte differentiation useful for  
 PT treating subject with disorder such as obesity, type II diabetes,  
 PT lipodystrophy or hyperinsulinemia.  
 XX  
 XX Claim 1; SEQ ID NO 46; 105pp; English.  
 XX  
 CC The invention relates to an isolated cDNA expressed during adipocyte  
 CC differentiation. The cDNA is useful for treating a subject with a  
 CC disorder such as obesity, type II diabetes, lipodystrophy or  
 CC hyperinsulinemia. The nucleic acid is useful for a high throughput  
 CC method of using a cDNA to screen several molecules or compounds to  
 CC identify a ligand which specifically binds the cDNA which involves  
 CC combining the nucleic acid with several molecules or compounds under  
 CC conditions to allow specific binding, and detecting specific binding  
 CC between each cDNA and at least one molecule or compound, thus identifying  
 CC a ligand that specifically binds to each cDNA. The several molecules or  
 CC compounds are chosen from DNA molecules, RNA molecules, peptide nucleic  
 CC acid molecules, mimetics, peptides, transcription factors, repressors and  
 CC regulatory proteins. The present sequence represents a human cDNA  
 CC expressed during adipocyte differentiation.  
 XX  
 SQ Sequence 2458 BP; 679 A; 543 C; 537 G; 699 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 909 Length: 2458  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 10 Gaps: 0  
 US-10-029-756-6 (1-8) x ADD12700 (1-2458)  
 Qy 1 TptleGlyHisAspAlaGlyHis 8  
 Db 991 TGGATTGGGCACAGCATGGCCAC 968  
 RESULT 47  
 ADB63204/c  
 ID ADB63204 standard; cDNA; 2486 BP.  
 XX  
 AC ADB63204;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Human cDNA encoding clone SPLEN20138600.  
 XX  
 KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;  
 KW tissue regeneration; cell regeneration; membrane protein;  
 KW signal transduction-related protein; transcription-related protein;  
 KW osteoporosis; neurological disease; cancer; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1166..1582  
 FT /\*tag= a  
 FT /product= "Clone SPLEN20138600 protein"  
 XX  
 PN EPI308459-A2.  
 XX  
 PD 07-MAY-2003.  
 XX  
 XX 28-MAR-2002; 2002EP-00007401.  
 XX  
 PR 05-NOV-2001; 2001JP-00379298.  
 PR 25-JAN-2002; 2002US-00350978.  
 XX  
 XX (HELL-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX  
 DR WPI; 2003-450961/43.  
 DR P-PSDB; ADB65174.  
 XX  
 PT New polynucleotides and polypeptides, useful for developing a diagnostic  
 PT marker or medicines for regulation of their expression and activity, or  
 PT as targets of gene therapy.  
 XX  
 PS Claim 1; Page; 222pp; English.  
 XX  
 CC The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or  
 CC peptide of the polynucleotide by contacting the polypeptide or peptide  
 CC with the antibody of the encoded protein, and observing the binding  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesising the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related  
 CC genes may be included in them, for developing a diagnostic marker or  
 CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related proteins,  
 CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence  
 CC data for this patent is not represented in the printed specification, but  
 CC is based on sequence information supplied by the European Patent Office.  
 XX  
 SQ Sequence 2486 BP; 679 A; 594 C; 532 G; 681 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 920 Length: 2486  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 10 Gaps: 0  
 US-10-029-756-6 (1-8) x ADB63204 (1-2486)  
 Qy 1 TptleGlyHisAspAlaGlyHis 8  
 Db 1272 TGGATAGGGCATTCATTGGCCAC 1249  
 RESULT 48  
 ABV25875/c  
 ID ABV25875 standard; cDNA; 2702 BP.  
 XX  
 AC ABV25875;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker CDNA 25866.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

```
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 5224; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX SQ Sequence 2702 BP; 714 A; 615 C; 568 G; 788 T; 0 U; 17 Other;

Alignment Scores:
Pred. No.: 1.01e+03 Length: 2702
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x ABV25875 (1-2702)
Qy 1 TtpIleGlyHisAspAlaGlyHis 8
Db 710 TGGATAGGCGCATTCATTGGCCAC 687

RESULT 49
ABL22487/c
ID ABL22487 standard; DNA; 2741 BP.
XX ABL22487;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 18934.
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 18934.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX Drosophila melanogaster.
XX

pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 11-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX Claim 1; SEQ ID NO 18934; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 2741 BP; 643 A; 763 C; 777 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.02e+03 Length: 2741
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL22487 (1-2741)
Qy 1 TtpIleGlyHisAspAlaGlyHis 8
Db 93 TGGTGTGGCATAGCGCGGCAC 70

RESULT 50
AAC77708/c
ID AAC77708 standard; cDNA; 2804 BP.
XX AAC77708;
XX 08-FEB-2001 (first entry)
XX Human cancer associated gene sequence SEQ ID NO:102.
XX Human; cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; cancer; immunomodulator;
XX antidiabetic; antisthmatic; antirheumatic; antiarthritic; antiviral;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
XX dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
XX vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening; ss.
XX Homo sapiens.
XX WO20005350-A1.
XX
```



PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005882.  
XX  
XX 12-MAR-1999; 99US-0124270P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
FA  
XX Rosen CA, Ruben SM;  
XX  
XX WPI: 2000-587533/55.  
XX  
XX P-PSDB; AAB43499.  
XX  
XX  
XX Novel isolated nucleic acids comprising sequences encoding peptides  
XX useful for treating or diagnosing e.g. cancer.  
XX  
XX Claim 1; Page 692-693; 2352pp; English.  
XX  
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
XX AAB43398 to AAB44239. The proteins can have activities based on the  
XX tissues and cells the genes are expressed in. Example of activities  
XX include: cytostatic; proliferative; vulnerary; immunomodulator;  
XX antidiabetic; antiaesthetic; antirheumatic; antiarthritic;  
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
XX dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
XX nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
XX polynucleotides and polypeptides can be used for preventing, treating or  
XX ameliorating medical conditions and diagnosing pathological conditions.  
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
XX the present invention may be used to treat immune disorders by activating  
XX or inhibiting the proliferation, differentiation or mobilisation of  
XX immune cells, to treat disorders of haematopoietic cells, autoimmune  
XX disorders, allergic reactions, graft versus host disease and organ  
XX rejection, modulate haemostatic or thrombolytic activity, modulate  
XX inflammation, cancers, cardiovascular disorders, neurological disease and  
XX bacterial or viral infections. The peptides, nucleotides, antibodies,  
XX agonists and antagonists may be also used in drug screens. AAC78449 to  
XX AAC78457 and AAB44240 represent sequences used in the exemplification of  
XX the present invention  
XX  
SQ Sequence 2804 BP; 764 A; 682 C; 596 G; 758 T; 0 U; 4 Other;

Alignment Scores:  
Pred. No.: 1.05e+03 Length: 2804  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAC77708 (1-2804)

Qy 1 TptlleglyHisAepAlaGlyHis 8  
|||  
Db 979 TGGATAGGGCATTCCATTGGCCAC 956  
|||  
RESULT 51  
AAS61862/c  
ID AAS61862 standard; cDNA; 2846 BP.  
XX  
XX AAS61862;  
XX  
XX 29-JAN-2002 (first entry)  
XX  
XX Lung small cell carcinoma antigen, cDNA #403.  
XX  
XX Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;  
XX lung cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200177168-A2.  
XX  
XX

PD 18-OCT-2001.  
XX  
PF 11-APR-2001; 2001WO-US011859.  
XX  
XX 11-APR-2000; 2000US-0196780P.  
XX  
XX 21-JUN-2000; 2000US-0213361P.  
XX  
XX 01-SEP-2000; 2000US-0229783P.  
XX  
XX 05-SEP-2000; 2000US-0230629P.  
XX  
XX 14-SEP-2000; 2000US-0232565P.  
XX  
XX 19-DEC-2000; 2000US-0257037P.  
XX  
XX 08-JAN-2001; 2001US-0260796P.  
XX  
XX (CORI-) CORIXA CORP.  
FA  
XX Lodes MJ, Wang T, Mohamath R, Indirias CY;  
XX  
XX WPI: 2002-010896/01.  
XX  
XX P-PSDB; RAU69422.  
XX  
XX Lung tumor polynucleotide and polypeptides useful in therapy and  
XX diagnosis of cancer especially lung cancer.  
XX  
XX Claim 1; Page 273-274; 295pp; English.  
XX  
XX The invention relates to novel isolated lung small cell cancer antigen  
XX polynucleotides (I) and polypeptides (II) used in a method of detecting  
XX cancer in a patient. The method is optionally performed by utilising  
XX oligonucleotides (III), where the biological sample from the patient is  
XX contacted with (III), detecting the amount of polynucleotide hybridised  
XX to (III) in the sample and comparing the amount of polynucleotide to a  
XX predetermined cut-off value and thereby determining cancer in a patient.  
XX (I), (II) or antigen-presenting cells expressing (II) is useful for  
XX stimulating and/or expanding T cells specific for a tumour protein. The  
XX method comprises contacting T cells with one of the components under  
XX conditions to permit the stimulation and/or expansion of the cells. A  
XX composition comprising (I) is useful for stimulating an immune response  
XX in a patient and for inhibiting the development of a cancer especially  
XX lung cancer in a patient. An isolated T cell population is useful for  
XX removing tumour cells from the biological sample and for inhibiting the  
XX development of cancer in a patient. AAS61460-AAS61874 represent novel  
XX human lung small cell cancer antigen coding sequences of the invention  
XX  
SQ Sequence 2846 BP; 818 A; 614 C; 633 G; 781 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 2846  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AAS61862 (1-2846)

Qy 1 TptlleglyHisAepAlaGlyHis 8  
|||  
Db 1351 TGGATTGGGCACAGCATGGGCCAC 1328  
|||  
RESULT 52  
ADE56172/c  
ID ADE56172 standard; DNA; 2893 BP.  
XX  
XX ADE56172;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Rat gene D38492, SEQ ID NO 2021.  
XX  
XX Rat; ds; gene; pain; neuronal tissue; gene therapy;  
XX spinal segmental nerve injury; chronic constriction injury;CCI;  
XX spared nerve injury; SNI; Chung.  
XX  
XX Rattus norvegicus.  
XX  
XX

XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 XX 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-0333347P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX (FARB ) BAYER AG.  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 XX GENBANK; D38492.  
 XX New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.  
 XX Claim 1; Page: 101pp; English.  
 XX The invention discloses a composition comprising two or more isolated rat  
 XX or human polynucleotides or a polynucleotide which represents a fragment,  
 XX derived or allelic variation of the nucleic acid sequence. Also  
 XX claimed are a vector comprising the novel polynucleotide, a host cell  
 XX comprising the vector, a method for identifying a nucleotide sequence  
 XX which is differentially regulated in an animal subjected to pain and a  
 XX kit to perform the method, an array, a method for identifying an agent  
 XX that increases or decreases the expression of the polynucleotide sequence  
 XX that is differentially expressed in neuronal tissue of a first animal  
 XX subjected to pain, a method for identifying a compound which differentially  
 XX the expression of a polynucleotide sequence which is differentially  
 XX expressed in an animal subjected to pain, a method for identifying a  
 XX compound that regulates the activity of one or more of the  
 XX polynucleotides, a method for producing a pharmaceutical composition, a  
 XX method for identifying a compound or small molecule that regulates the  
 XX activity in an animal of one or more of the polypeptides given in the  
 XX specification, a method for identifying a compound useful in treating  
 XX pain and a pharmaceutical composition comprising the one or more  
 XX polypeptides or their antibodies. The polynucleotide or the compound that  
 XX modulates its activity is useful for preparing a medicament for treating  
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 XX therapy). The sequence presented is a rat DNA (shown in Table 2 of the  
 XX specification) which encodes one of the polypeptides of the invention  
 XX which is differentially expressed during pain. Note: The sequence data  
 XX for this patent did not form part of the printed specification, but was  
 XX obtained in electronic form directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2893 BP; 824 A; 726 C; 702 G; 641 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.08e+03 Length: 2893  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADE56172 (1-2893)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
 |||||  
 Db 2644 TGGATAGCCACGACAGTCCAC 2621  
 |||||

RESULT 53  
 ABQ54696/c  
 ID ABQ54696 standard; cDNA; 2984 BP.  
 XX

AC ABQ54696;  
 XX 22-AUG-2002 (first entry)  
 XX Human ovarian antigen HLYDC86 cDNA, SEQ ID NO:576.  
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 XX inflammatory condition; immune disorder; blood disorder;  
 XX cardiovascular disorder; respiratory disorder; neurological disorder;  
 XX gastrointestinal disorder; urinary system disorder; drug screening;  
 XX gene therapy; chromosome mapping; forensic analysis;  
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 XX antiinflammatory; gynaecological; reproductive; chromosome 14q24.3; gene;  
 XX ss.  
 XX Homo sapiens.  
 XX OS  
 XX WO200200677-A1.  
 XX PN  
 XX 03-JAN-2002.  
 XX PD  
 XX 07-JUN-2001; 2001WO-US018569.  
 XX PF  
 XX 07-JUN-2000; 2000US-0209467P.  
 XX PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PA  
 XX Birse CE, Rosen CA;  
 XX PI  
 XX WPI; 2002-147878/19.  
 XX DR  
 XX P-FSDB; ABP41619.  
 XX DR  
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 XX cancer), immune disorders, cardiovascular disorders and neurological  
 XX diseases.  
 XX PT  
 XX Claim 1; SEQ ID NO 576; 2922pp; English.  
 XX PS  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 XX encompasses polypeptides 90% identical and polynucleotides 95% identical  
 XX to the sequences of the invention. The invention additionally relates to  
 XX recombinant vectors and host cells comprising human ovarian antigen  
 XX polynucleotides, antibodies against human ovarian antigens, and the use  
 XX of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 XX treating, prognosing or preventing various ovary and/or breast-related  
 XX disorders. Such conditions include ovarian cancer and breast cancer, and  
 XX metastatic tumours of ovarian or breast origin, reproductive system  
 XX disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 XX vaginitis), immune disorders (e.g., congenital and acquired  
 XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 XX blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 XX respiratory disorders, neurological disorders, gastrointestinal disorders  
 XX and urinary system disorders. Ovarian antigen polypeptides and  
 XX polynucleotides may also be used in screening for compounds which  
 XX modulate ovarian antigen expression or activity. The polynucleotides may  
 XX further be used for gene therapy, chromosome mapping, in the  
 XX identification of individuals and in forensic analysis, and the  
 XX polypeptides may be used as food additives or to prepare antibodies  
 XX useful in disease diagnosis, drug targeting and phenotyping. The present  
 XX sequence represents cDNA encoding a human ovarian antigen of the  
 XX invention. Note: The sequence data for this patent did not form part of  
 XX the printed specification, but was obtained in electronic format directly  
 XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 2984 BP; 821 A; 720 C; 646 G; 792 T; 0 U; 5 Other;

Alignment Scores:  
Pred. No.: 1.12e+03 Length: 2984  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: Gaps: 0

US-10-029-756-6 (1-8) x ABQ54696 (1-2984)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||  
Db 1177 TGGATAGGCATTCATTGGCCAC 1154

RESULT 54  
AAV70355/c  
ID AAV70355 standard; cDNA; 2995 BP.

XX AAV70355;

DT 08-FEB-1999 (first entry)

DE Human h-NUMB encoding cDNA.

XX Human; cytoplasmic protein; EH-containing protein; epa15; epa15R;  
KW epa15 homology; intracellular interaction; EH domain binding specificity;  
KW signal transducer; NPF motif; h-NUMB; h-RAB; h-RAB-R; ehb3;  
KW ehb10; ehb21; cell proliferation; diagnosis; detection; ss.

XX Homo sapiens.

Key Location/Qualifiers  
FH 279. .2090  
FT CDS  
ET /\*tag= a

XX WO9846744-A1.

XX 22-OCT-1998.

XX 06-APR-1998; 98WO-IT000077.

XX 15-APR-1997; 97IT-MI000868.

XX (EUON-) IST EURO DI ONCOLOGIA SRL.

PI Salcini AE, Doria M, Pellicci PG, Di Fiore PP;

XX WPI; 1998-594574/50.

DR P-PSDB; AAW83214.

XX New isolated EH domain binding proteins and peptide(s) - obtained using  
PT signal transducers epa15 and epa15R containing EH domains by detecting  
ET specific binding activity.

XX Claim 3; Page 45-47; 90pp; English.

XX The present invention describes a new intracellular interactor and novel  
CC protein:protein interaction (EH) domain binding protein having (parts of)  
CC one of the following human derived sequences designated: (I) h-NUMB; (II)  
CC h-NUMB-R; (III) h-RAB-R; (IV) ehb3; (V) ehb10; or (VI) ehb21. The present  
CC invention also describes peptides containing at least one NPF (Asp-Pro-  
CC Phe) motif, able to bind to a protein with at least one EH domain. The  
CC proteins with a NPF-containing peptide or the peptides themselves can be  
CC used to identify and purify EH containing proteins. Antisense RNA,  
CC complementary to mRNA encoding h-NUMB, h-NUMB-R, ehb3, ehb10, or  
CC ehb21, can be used for diagnostic and therapeutic uses. Products from the  
CC present invention can also be used to develop agents for use in control  
CC of cell proliferation. The present sequence encodes human h-NUMB

XX Sequence 2995 BP; 837 A; 733 C; 696 G; 729 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.13e+03 Length: 2995  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: Gaps: 0

US-10-029-756-6 (1-8) x AAV70355 (1-2995)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||  
Db 1694 TGGATAGGCATTCATTGGCCAC 1671

RESULT 55  
ADR25565/c  
ID ADR25565 standard; DNA; 3050 BP.

XX ADR25565;

DT 21-OCT-2004 (first entry)

DE Breast cancer prognosis marker #1426.

KW ds; breast cancer; prognosis; gene expression; diagnosis.

XX Homo sapiens.

XX WO2004065545-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.

XX 15-JAN-2003; 2003US-00342887.

XX (ROSE-) ROSETTA INPHARMATICS LLC.  
XX (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

XX WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises  
PT determining the similarity between the level of expression of each of  
PT five genes in a cell sample taken from patient, to control levels.

XX Disclosure; SEQ ID NO 1426; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient  
CC according to prognosis by determining the similarity between the level of  
CC expression of each of five genes for which markers are listed in the  
CC specification, in a cell sample taken from the breast cancer patient, to  
CC control levels of expression for each respective five genes to obtain a  
CC patient similarity value. The methods are useful for classifying a breast  
CC cancer patient according to prognosis. Kits and computer program products  
CC are useful for data analysis using the diagnostic, prognostic and  
CC statistical methods of the invention. This sequence corresponds to a  
CC marker used in the method of the invention.

XX Sequence 3050 BP; 850 A; 651 C; 713 G; 836 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.15e+03 Length: 3050  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: Gaps: 0

US-10-029-756-6 (1-8) x ADR25565 (1-3050)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||

Db 1606 TGGATTGGGCACGATGGGCCAC 1583

RESULT 56

AA561859/c

ID AA561859 standard; cDNA; 3079 BP.

XX AC AA561859;

XX DT 29-JAN-2002 (first entry)

XX DE Lung small cell carcinoma antigen, cDNA #400.

XX KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;

XX KW lung cancer; ss.

XX OS Homo sapiens.

XX FN WO200177168-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-US011859.

XX PR 11-APR-2000; 2000US-0196780P.

XX PR 21-JUN-2000; 2000US-0213361P.

XX PR 01-SEP-2000; 2000US-0229763P.

XX PR 05-SEP-2000; 2000US-0230629P.

XX PR 14-SEP-2000; 2000US-0232565P.

XX PR 19-DEC-2000; 2000US-0257037P.

XX PR 08-JAN-2001; 2001US-0260796P.

XX PA (CORI-) CORIXA CORP.

XX PI Lodes MJ, Wang T, Mohamath R, Indirias CY;

XX DR WPI; 2002-010896/01.

XX DR P-PSDB; RAU69419.

XX PT Lung tumor polynucleotide and polypeptides useful in therapy and diagnosis of cancer especially lung cancer.

XX PS Claim 1; Page 269-270; 295pp; English.

XX CC The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. AA561460-AA561874 represent novel human lung small cell cancer antigen coding sequences of the invention

SQ Sequence 3079 BP; 865 A; 652 C; 719 G; 843 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.16e+03 Length: 3079

Score: 42.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2

Query Match: 79.25% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AA561859 (1-3079)

QY 1 TripileGlyHisAspAlaGlyHis 8

Db 1613 TGGATTGGGCACGATGGGCCAC 1590

RESULT 57

AAI59203/c

ID AAI59203 standard; cDNA; 3144 BP.

XX AC AAI59203;

XX DT 22-OCT-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 1406.

XX KW Human; nototropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.

XX OS Homo sapiens.

XX FN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR P-PSDB; AAM40047.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

XX PS Claim 1; SEQ ID NO 1406; 10078pp; English.

XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nototropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC C.N.S disorders. Note: The sequence data for this patent did not form CC part of the printed specification

XX SQ Sequence 3144 BP; 879 A; 671 C; 742 G; 852 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.19e+03 Length: 3144

Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAI59203 (1-3144)

QY 1 TptileGlyHisAspAlaGlyHis 8  
DB 1664 TGGATTGGGCACAGCATGGCCAC 1641

RESULT 58

ID ADO99427/c  
ADQ99427 standard; cDNA; 3144 BP.

XX

XX

XX

AC ADO99427;

DT 23-SEP-2004 (first entry)

DE DNA encoding human GPCR-like protein segid 1097.

KW ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic;

KW antidiabetic; GPCR-like protein; ophthalmic disorder;

KW neurological disorder; immunological disorder; nephritic disorder;

KW hormonal dysfunction; cancer; atherosclerosis; diabetes;

KW molecular weight marker; food supplement; human; ss.

XX Homo sapiens.

XX US6569662-B1.

XX 27-MAY-2003.

XX 19-JUL-2000; 2000US-00620312.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Drmanac RT;

XX WPI; 2001-442255/47.

XX New G-protein-coupled receptor-like polypeptides and polynucleotides,

XX useful for treating diseases of ophthalmic, neurological, immunological

XX and nephritic systems and hormonal dysfunction, cancer, atherosclerosis

XX and diabetes.

XX Example 2; SEQ ID NO 1097; 92pp; English.

XX The invention describes an isolated polynucleotide (I) comprising a fully

XX defined (31) of 749, 3188, 2484, 1165, 2936, 1467, 5773, 5714, 4041,

XX 1372, 3996, 3945, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as

XX given in the specification, its translated or protein coding portion, its

XX extracellular portion or its active domain. The GPCR-like polypeptides

XX and polynucleotides are useful for the treatment of diseases of

XX ophthalmic, neurological, immunological and nephritic systems. They may

XX also be used to treat hormonal dysfunction, cancer, atherosclerosis and

XX diabetes. The antibodies are useful for detecting or quantitating the

XX polypeptide in tissue. The polypeptides can also be used as molecular

XX weight markers and as a food supplement. This sequence represents a human

XX polynucleotide of the invention.

XX Sequence 3144 BP; 879 A; 671 C; 742 G; 852 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 1.19e+03 Length: 3144

Score: 42.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2

Query Match: 79.25% Indels: 0

DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x ADO99427 (1-3144)

QY 1 TptileGlyHisAspAlaGlyHis 8  
DB 1664 TGGATTGGGCACAGCATGGCCAC 1641

RESULT 59

ID ADB49187/c  
ADB49187 standard; cDNA; 3144 BP.

XX

XX

XX

AC ADB49187;

DT 04-DEC-2003 (first entry)

DE Novel human cDNA SEQ ID NO 1097.

XX ss; cancer; neurodegenerative disease; human.

XX Homo sapiens.

XX OS

XX US2003104529-A1.

XX 05-JUN-2003.

XX 04-JAN-2002; 2002US-00037270.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 19-JUL-2000; 2000US-00620312.

XX (ZHOU/) ZHOU P.

XX (TANG/) TANG Y T.

XX (LIUC/) LIU C.

XX (ASUN/) ASUNDI V.

XX (DRMA/) DRMANAC R T.

XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;

XX WPI; 2003-678194/64.

XX New polynucleotide, useful for treating diseases e.g., cancer or

XX neurodegenerative diseases.

XX Claim 1; SEQ ID NO 1097; 99pp; English.

XX The invention relates to a polynucleotide comprising a sequence given in

XX the specification, or its mature protein-coding portion, or its

XX complement. The polynucleotide is useful for treating diseases e.g.,

XX cancer or neurodegenerative diseases and many others listed in the

XX specification. The present sequence represents a novel human cDNA. Note:

XX The sequence data for this patent did not form part of the printed

XX specification but was obtained in electronic format directly from USPTO

XX at seqdata.uspto.gov/sequence.html?docID=20030104529.

XX Sequence 3144 BP; 879 A; 671 C; 742 G; 852 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 1.19e+03 Length: 3144

Score: 42.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2

Query Match: 79.25% Indels: 0

DB: 9 Gaps: 0

US-10-029-756-6 (1-8) x ADB49187 (1-3144)

QY 1 TptileGlyHisAspAlaGlyHis 8  
DB 1664 TGGATTGGGCACAGCATGGCCAC 1641

RESULT 60

```

ABL13718/c
ID ABL13718 standard; cDNA; 3155 BP.
AC ABL13718;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 35636.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-658660/75.
DR
XX P-PSDB; ABB69615.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Claim 1; SEQ ID NO 35636; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 3155 BP; 868 A; 759 C; 728 G; 800 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.19e+03 Length: 3155
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x ABL13718 (1-3155)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 2611 TGGTGTGGCATAGCGAGGGGCAC 2588
RESULT 61
ABX71357/c
ID ABX71357 standard; cDNA; 3237 BP.
XX
XX AC ABX71357;
XX
XX 14-APR-2003 (first entry)
XX
XX Human signal transduction-associated cDNA from clone DKFZphtes3_lcl.
XX
Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
Homo sapiens.
WO200112659-A2.
22-FEB-2001.
18-AUG-2000; 2000WO-IB001496.
18-AUG-1999; 99US-0149499P.
28-SEP-1999; 99US-0156503P.
(GEHU-) GERMAN HUMAN GENOME PROJECT.
Wiemann S;
WPI; 2001-327840/34.
P-PSDB; ABUS3065.
Nucleic acids having the sequences of clones isolated from libraries of
different human tissues, useful in recombinant DNA methodologies.
Claim 1; Page 658-659; 1095pp; English.
This invention describes novel polynucleotides and polypeptides isolated
from human cDNA libraries which can be used for gene therapy or in
vaccines. The polynucleotides of the invention and antibodies encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate polypeptide expression. The products of the
invention may also be used to identify modulators of expression and
activity and to down regulate expression and activity. The antibodies of
the invention may also be used as diagnostic agents for detecting the
presence of polypeptides in samples. This sequence encodes a polypeptide
described in the disclosure of the invention
XX
XX Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.22e+03 Length: 3237
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 5 Gaps: 0
US-10-029-756-6 (1-8) x ABX71357 (1-3237)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1760 TGGATTGGGCACAGCATGGGCCAC 1737
RESULT 62
ADP64967/c
ID ADP64967 standard; DNA; 3237 BP.
XX
XX AC ADP64967;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human Rac GTPase activating protein 1 (RACGAP1) DNA sequence.
XX
XX autoimmune disease; arthritis; gene expression analysis;
XX rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; ds; human.
XX
XX Homo sapiens.
XX
XX WO2003072827-A1.
XX

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PD 04-SEP-2003.  
 XX 31-OCT-2002; 2002WO-US035433.  
 XX 31-OCT-2001; 2001US-0336220P.  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX Hirsch R, Thorton SL;  
 FI WPI; 2003-712740/67.  
 DR GENBANK; NM\_013277.  
 DR  
 XX  
 XX Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.  
 XX  
 XX Disclosure; Page; 56pp; English.  
 XX  
 XX The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This polynucleotide  
 CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.  
 XX  
 XX Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.22e+03 Length: 3237  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 11 Gaps: 0  
 US-10-029-756-6 (1-8) x ADP64967 (1-3237)  
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
 Db 1760 TGGATTGGGCACAGCATGGGCCAC 1737  
 RESULT 63  
 ADP65420/C  
 ID ADP65420 standard; DNA; 3237 BP.  
 XX  
 XX AC ADP65420;  
 XX  
 XX 12-AUG-2004 (first entry)  
 XX  
 XX Human mRNA, cDNA DKFPz34C011 (from clone DKFPz34C011), DNA.  
 DE  
 XX

KW autoimmune disease; arthritis; gene expression analysis;  
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KW immune; ds; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003072827-A1.  
 PN  
 XX 04-SEP-2003.  
 PD  
 XX 31-OCT-2002; 2002WO-US035433.  
 PF  
 XX 31-OCT-2001; 2001US-0336220P.  
 PR  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PA  
 XX Hirsch R, Thorton SL;  
 FI WPI; 2003-712740/67.  
 DR GENBANK; AL136794.  
 DR  
 XX Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.  
 XX  
 XX Disclosure; Page; 56pp; English.  
 XX  
 XX The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This polynucleotide  
 CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.  
 XX  
 XX Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.22e+03 Length: 3237  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 11 Gaps: 0  
 US-10-029-756-6 (1-8) x ADP65420 (1-3237)  
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
 Db 1760 TGGATTGGGCACAGCATGGGCCAC 1737  
 RESULT 63  
 ADP65420/C  
 ID ADP65420 standard; DNA; 3237 BP.  
 XX  
 XX AC ADP65420;  
 XX  
 XX 12-AUG-2004 (first entry)  
 XX  
 XX Human mRNA, cDNA DKFPz34C011 (from clone DKFPz34C011), DNA.  
 DE  
 XX

```
RESULT 64
ADO20213/c
ID ADO20213 standard; cDNA; 3237 BP.
XX AC
XX AC ADO20213;
XX DT
XX DE
XX DE Human PRO polynucleotide #559.
XX KW
XX KW Human; PRO; gene; ss; immune related disorder;
XX KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
XX KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
XX KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
XX KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
XX KW renal disease; demyelinating disease; central nervous system;
XX KW peripheral nervous system; demyelinating polyneuropathy;
XX KW Guillain-Barre syndrome;
XX KW chronic inflammatory demyelinating polyneuropathy.
XX OS
XX OS Homo sapiens.
XX FN
XX FN WO2004043361-A2.
XX PD
XX PD 27-MAY-2004.
XX PF
XX PF 06-NOV-2003; 2003WO-US035268.
XX PR
XX PR 08-NOV-2002; 2002US-0425235P.
XX PA
XX PA (GETH ) GENENTECH INC.
XX PI
XX PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
XX PI Wood WI, Wu TD;
XX DR
XX DR WPI; 2004-420067/39.
XX DR P-PSDB; ADO20214.
XX PT
XX PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
XX PT treating an immune related disorder such as systemic lupus erythematosus,
XX PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX PT spondyloarthropathy.
XX PS
XX PS Claim 1; SEQ ID NO 1182; 1731pp; English.
XX CC
XX CC The invention relates to human PRO polypeptides and the polynucleotides
XX CC encoding them. The polypeptides and polynucleotides are useful for
XX CC treating and diagnosing immune related disorders in mammals. The immune
XX CC related disorders include systemic lupus erythematosus, rheumatoid
XX CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
XX CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
XX CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
XX CC mellitus, immune-mediated renal disease, demyelinating diseases of the
XX CC central or peripheral nervous system, demyelinating polyneuropathy,
XX CC Guillain-Barre syndrome and chronic inflammatory demyelinating
XX CC polyneuropathy. This sequence represents a human PRO polynucleotide of
XX CC the invention.
SQ Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.22e+03 Length: 3237
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
Gaps: 0
DB: 12

US-10-029-756-6 (1-8) x ADO20213 (1-3237)
QY 1 TrpIleGlyHisAspAlaGlyHis 8
|||||
```

```
Db 1760 TGGATTGGCACAGCATGGGCCAC 1737
RESULT 65
ACN39430/c
ID ACN39430 standard; cDNA; 3237 BP.
XX AC
XX AC ACN39430;
XX DT
XX DE
XX DE Tumour-associated antigenic target (TAT) cDNA DNA325648, SEQ ID NO:3566.
XX KW
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX KW tumour; diagnosis; cell proliferative disorder; breast cancer;
XX KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX KW central nervous system cancer; bladder cancer; pancreatic cancer;
XX KW cervical cancer; melanoma; leukaemia; hybridisation probe;
XX KW chromosome identification; chromosome mapping; gene mapping;
XX KW gene therapy; cytostatic; gene; ss.
XX OS
XX OS Homo sapiens.
XX FN
XX FN WO2004030615-A2.
XX PD
XX PD 15-APR-2004.
XX PF
XX PF 29-SEP-2003; 2003WO-US028547.
XX PR
XX PR 02-OCT-2002; 2002US-0414971P.
XX PA
XX PA (GETH ) GENENTECH INC.
XX PI
XX PI Wu TD, Zhang Z, Zhou Y;
XX DR
XX DR WPI; 2004-347921/32.
XX DR P-PSDB; ABM81380.
XX PT
XX PT New tumor-associated antigenic target polypeptides and nucleic acids,
XX PT useful in preparing a medicament for treating or detecting a
XX PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX PT prostate cancer or tumor.
XX PS
XX PS Claim 1; SEQ ID NO 3566; 7273pp; English.
XX CC
XX CC The invention relates to human tumour-associated antigenic target (TAT)
XX CC polypeptides, and their related nucleic acids. The TAT polypeptides are
XX CC overexpressed in cancer tissues compared to normal tissues, and may thus
XX CC serve as effective targets for the diagnosis and treatment of cancer in
XX CC mammals. The invention also relates to nucleic acid and polypeptide
XX CC sequences at least 80% identical to the TAT nucleic acids and
XX CC polypeptides; expression vectors and host cells comprising a TAT nucleic
XX CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX CC TAT polypeptide; and methods and compositions for the treatment or
XX CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX CC antibodies, antagonists, binding molecules and compositions are useful
XX CC for diagnosing or treating a cell proliferative disorder associated with
XX CC increased TAT expression, particularly cancers such as breast cancer,
XX CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX CC cancer, pancreatic cancer, cervical cancer, cancers of the central
XX CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX CC used as hybridisation probes, in chromosome and gene mapping, in
XX CC chromosome identification and in gene therapy. The present sequence
XX CC represents a TAT nucleic acid of the invention
SQ Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.22e+03 Length: 3237
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
```



DB: 13 Gaps: 0

US-10-029-756-6 (1-8) x ACN39430 (1-3237)

QY 1 TtpileGlyHisAspAlaGlyHis 8  
1760 TGGATTGGGCACAGCATGGCCAC 1737

DB RESULT 66  
ID AAS84091/c  
AC AAS84091;  
XX AAS84091;  
XX AAS84091;  
DT 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #19895.  
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR P-PSDB; ABG19904.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 1; SEQ ID NO 19895; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 3259 BP; 1296 A; 701 C; 604 G; 658 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.23e+03 Length: 3259  
Score: 42.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x AAS84091 (1-3259)

QY 1 TtpileGlyHisAspAlaGlyHis 8  
3177 TGGATTGGGCACAGCATGGCCAC 3154

DB RESULT 67  
ID ABL11165/c  
AC ABL11165;  
XX ABL11165;  
DT 26-MAR-2002 (first entry)  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 27977.  
DE Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX Drosophila melanogaster.  
XX WO200171042-A2.  
XX 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-US009231.  
PF 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX (PEKE) PE CORP NY.  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
DR P-PSDB; ABB67062.  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX Claim 1; SEQ ID NO 27977; 21pp + Sequence Listing; English.  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 3336 BP; 887 A; 919 C; 823 G; 707 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.26e+03 Length: 3336  
Score: 42.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL11165 (1-3336)

QY 2 IleGlyHisAspAlaGlyHis 8  
|||||

Db 1197 ATAGTTCACGATCTGGACAT 1177

RESULT 68  
ABK35882/c

ID ABK35882 standard; cDNA; 3355 BP.

XX  
XX ABK35882;

XX  
XX 08-MAY-2002 (first entry)

XX  
XX cDNA sequence #273 encoding novel human secreted protein.

DE  
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KW immune deficiency disorder; blood disorder; inflammatory disorder;  
KW infectious disorder; allergic condition; neurodegenerative disorder;  
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;  
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200177289-A2.  
FN  
XX 18-OCT-2001.  
PD  
XX 29-MAR-2001; 2001WO-US010232.  
XX  
XX 06-APR-2000; 2000US-0195605P.  
PR  
XX (GEMY ) GENETICS INST INC.  
PA  
XX Jacobs K, McCooy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;  
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;  
XX WPI; 2002-179322/23.  
DR  
XX Six hundred and twenty three polynucleotides derived from a variety of  
PT human tissue sources which encode secreted proteins, useful for treating  
PT immune deficiencies and disorders such as autoimmune disorders.  
XX  
XX Claim 1; Page 240-241; 33pp; English.  
PS  
XX The present invention relates to the isolation of novel cDNA sequences  
CC which encode human secreted proteins. The cDNA sequences have been  
CC derived from a variety of human tissues. The invention also provides a  
CC method for producing proteins from these polynucleotide sequences. The  
CC proteins are useful for identifying compounds that modulate their  
CC activity and production. The sequences of the invention are useful for  
CC treating diseases such as hyperproliferative disorders (e.g. cancer),  
CC immune deficiency disorders (e.g. severe combined immunodeficiency  
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders  
CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis),  
CC infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis,  
CC coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide  
CC sequences of the invention are also useful in gene therapy. ABK35610-  
CC ABK36232 represent the cDNA sequences of the invention that encode for  
CC novel human secreted proteins  
XX  
SQ Sequence 3355 BP; 828 A; 711 C; 712 G; 1103 T; 0 U; 1 Other;

Alignment Scores:  
Pred. No.: 1.27e+03 Length: 3355  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABK35882 (1-3355)

Qy 1 TtpileGlyHisAspAlaGlyHis 8  
|||||  
|||

Db 1598 TGGATAGGCGCATTCATTGGCCAC 1575

RESULT 70  
AAS78145/c

ID AAS78145 standard; cDNA; 3419 BP.

XX  
XX AAS78145;

Db 2940 TGGATTGGGCACGACATGGGCCAC 2917

RESULT 69  
AAS94909/c

ID AAS94909 standard; DNA; 3370 BP.

XX  
XX AAS94909;

XX  
XX 14-FEB-2002 (first entry)

XX  
XX Human DNA sequence #164 expressed during foam cell differentiation.

DE  
XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;  
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200177389-A2.  
FN  
XX 18-OCT-2001.  
PD  
XX 04-APR-2001; 2001WO-US011128.  
XX  
XX 05-APR-2000; 2000US-0195106P.  
PR  
XX (INCY-) INCYTE GENOMICS INC.  
PA  
XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;  
PI Tai J;  
XX WPI; 2002-010925/01.  
DR  
XX Composition useful for diagnosis of conditions, disorders or diseases  
PT associated with atherosclerosis, comprises several polynucleotides that  
PT are differentially expressed in foam cell development.  
XX  
XX Claim 1; Page 219-220; 315pp; English.  
PS  
XX The present invention relates to the isolation of human polynucleotide  
CC sequences that are differentially expressed during foam cell  
CC differentiation. The polynucleotide sequences of the invention or a  
CC composition comprising these polynucleotides are useful as a high  
CC throughput method for detecting altered expression of one or more  
CC polynucleotides in a sample. The polynucleotides can be used in the  
CC diagnosis of disorders associated with foam cell development such as  
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as  
CC coronary artery disease. The polynucleotide sequences can also be used as  
CC PCR primers and probes. The polynucleotides of the invention are also  
CC useful in gene therapy. AAS94746-AAS95021 represent the human  
CC polynucleotide sequences of the invention which are differentially  
CC expressed during foam cell differentiation  
XX  
SQ Sequence 3370 BP; 936 A; 791 C; 762 G; 881 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 3370  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AAS94909 (1-3370)

Qy 1 TtpileGlyHisAspAlaGlyHis 8  
|||||  
|||

Db 1598 TGGATAGGCGCATTCATTGGCCAC 1575

RESULT 70  
AAS78145/c

ID AAS78145 standard; cDNA; 3419 BP.

XX  
XX AAS78145;

XX 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #13949.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX PD 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX P-PSDB; ABG13958.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
XX Claim 1; SEQ ID NO 13949; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX sequences. (I) is useful as hybridisation probes, polymerase chain  
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX and in recombinant production of (II). The polynucleotides are also used  
XX in diagnostics as expressed sequence tags for identifying expressed  
XX genes. (I) is useful in gene therapy techniques to restore normal  
XX activity of (II) or to treat disease states involving (II). (II) is  
XX useful for generating antibodies against it, detecting or quantitating a  
XX polypeptide in tissue, as molecular weight markers and as a food  
XX supplement. (III) and its binding partners are useful in medical imaging  
XX of sites expressing (II). (I) and (II) are useful for treating disorders  
XX involving aberrant protein expression or biological activity. The  
XX polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
XX coding sequences of the invention. Note: The sequence data for this  
XX patent did not appear in the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 3419 BP; 1383 A; 751 C; 593 G; 692 T; 0 U; 0 Other;

Alignment Scores:  
Pred No.: 1.3e+03 Length: 3419  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x AAS78145 (1-3419)  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 3337 TGGATTGGGCACGACGATGGCCAC 3314  
RESULT 71  
ACC46735/c

ID ACC46735 standard; cDNA; 3470 BP.  
XX ACC46735;  
XX 02-JUN-2003 (first entry)  
XX Human dithp growth/development-associated protein-encoding cDNA.  
XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
XX cancer; cell proliferative disorder; autoimmune disorder;  
XX inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
XX neurological disorder; gastrointestinal disorder; transport disorder;  
XX connective tissue disorder; drug screening; proteome analysis;  
XX gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
XX disease model; toxicological testing; transcript imaging; growth;  
XX development; gene; ss.  
XX Homo sapiens.  
XX WO200297031-A2.  
XX 05-DEC-2002.  
XX 27-MAR-2002; 2002WO-US010056.  
XX 28-MAR-2001; 2001US-0279619P.  
XX 29-MAR-2001; 2001US-0280067P.  
XX 29-MAR-2001; 2001US-0280068P.  
XX 16-MAY-2001; 2001US-0291280P.  
XX 17-MAY-2001; 2001US-0291829P.  
XX 17-MAY-2001; 2001US-0291849P.  
XX 19-JUN-2001; 2001US-0299428P.  
XX 20-JUN-2001; 2001US-0299776P.  
XX 20-JUN-2001; 2001US-0300001P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Dafo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;  
XX Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX WPI; 2003-129518/12.  
XX P-PSDB; ABR41798.  
XX Novel human diagnostic and therapeutic polypeptide useful for identifying  
XX test compound which specifically binds to a polypeptide encoded by human  
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.  
XX Claim 2; SEQ ID NO 656; 591pp; English.  
XX The invention relates to novel human diagnostic and therapeutic  
XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
XX proteins (Dithp; ABR41136-ABR41812). The invention also relates to  
XX polynucleotide sequences at least 90% identical to the dithp cDNA  
XX sequences of the invention; recombinant vectors, host cells and  
XX transgenic organisms comprising a dithp nucleic acid sequence; the  
XX recombinant production of Dithp proteins; antibodies specific for Dithp  
XX proteins; microarrays comprising dithp nucleic acid sequences; methods of  
XX detecting dithp nucleotide and protein sequences; methods of screening  
XX for compounds which specifically bind a Dithp protein; and methods of  
XX assessing the toxicity of test compounds using a dithp hybridisation  
XX probe. Dithp nucleic acid sequences and Dithp proteins may be used in the  
XX diagnosis of a wide variety of conditions including cancer and other cell  
XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
XX viral, fungal or parasitic infections; hormonal disorders; metabolic  
XX disorders; neurological disorders; gastrointestinal disorders; transport  
XX disorders; and connective tissue disorders. They may also be used to  
XX screen for modulators of protein activity or gene expression. Dithp  
XX proteins can additionally be used in analysis of the proteome of a tissue  
XX or cell type and to induce antibodies. The dithp nucleic acids are  
XX additionally useful in somatic or germline gene therapy of the disorders

CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a dithp cDNA encoding a DITHP protein  
 CC which is associated with growth and development. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 3470 BP; 965 A; 812 C; 791 G; 902 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.32e+03 Length: 3470  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x ACC46735 (1-3470)

Qy 1 TptileGlyHisAspAlaGlyHis 8  
 |||||  
 Db 1720 TGGATAGGCATTCCTGGCCAC 1697

RESULT 72

ADE31423/c  
 ID ADE31423 standard; DNA; 4023 BP.

XX ADE31423;

DT 29-JAN-2004 (first entry)

DE Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 178.  
 KW diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic;  
 KW antiinflammatory; cerebroprotective; antilipemic; antidiabetic;  
 KW immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilizer;  
 KW osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic;  
 KW virucide; haemostatic; anti-HIV; antithyroid; thyromimetic;  
 KW dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant;  
 KW thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer;  
 KW gene therapy; protein replacement therapy; human; gene; ds.

XX Homo sapiens.

OS WO2003062376-A2.

PN 31-JUL-2003.

PD 13-JAN-2003; 2003WO-US001096.

PF 16-JAN-2002; 2002US-0349384P.

PR 17-JAN-2002; 2002US-0349413P.

PP 17-JAN-2002; 2002US-0349946P.

XX (INCY-) INCYTE GENOMICS INC.

XX Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GE, Jackson JL;  
 PI Yu JY, Tuason O, Yap PE, Anshey SR, Dam TC, Liu TF, Gerstein EH;  
 PI Peralta CH, Lewis SA, Chen A, Marwaha R, Lan RY, Urashka ME;  
 PI Krishnam SR, Kolluru V, Panesar IS;

XX WPI; 2003-636732/60.

DR P-PSDB; ADE31234.

XX New human diagnostic and therapeutic polynucleotides and polypeptides,  
 PT useful for diagnosing, treating or preventing e.g. leukemia, brain  
 PT cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke  
 PT or Alzheimer's.

XX Claim 1; SEQ ID NO 178; 634pp; English.

XX The invention relates to a novel isolated human diagnostic and  
 CC therapeutic polynucleotide (designated dithp). The novel dithp  
 CC polynucleotide comprises: any of 188 DNA sequences consisting of 195-7798  
 CC base pairs fully defined in the specification; a polynucleotide  
 CC comprising a naturally occurring polynucleotide sequence at least 90%  
 CC identical to the dithp polynucleotide; a polynucleotide complementary to  
 CC the dithp polynucleotide or its polynucleotide which is at least 90%  
 CC identical; or an RNA equivalent of any of the polynucleotides mentioned  
 CC above. The dithp polynucleotides have the following activities:  
 CC antiarteriosclerotic, antiinflammatory, cerebroprotective, antilipemic,  
 CC antidiabetic, immunosuppressive, neuroprotective, nootropic, neuroleptic,  
 CC tranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic,  
 CC hepatotropic, virucide, haemostatic, anti-HIV, antithyroid, thyromimetic,  
 CC dermatological, antibacterial, fungicide, vasotropic, anticonvulsant,  
 CC thrombolytic, anticoagulant, anorectic, cytostatic, antiulcer. The  
 CC novel DITHP polynucleotides polypeptide can be used in gene therapy and  
 CC protein replacement therapy. The dithp polynucleotides or DITHP  
 CC polypeptides are useful for diagnosing, preventing or treating diseases  
 CC associated with the expression of human molecules. In particular, these  
 CC diseases include cancers (e.g. adenocarcinoma, leukaemia, melanoma, brain  
 CC cancer, breast cancer, cervix cancer, bone cancer, liver cancer, lung  
 CC cancer) or other cell proliferative disorders (e.g. arteriosclerosis,  
 CC atherosclerosis, cirrhosis, hepatitis, polycythemia vera, primary  
 CC thrombocytopenia), autoimmune/inflammatory disorders (e.g. AIDS,  
 CC Addison's disease, thyroiditis, Crohn's disease, Graves' disease,  
 CC Hashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid  
 CC arthritis, scleroderma, systemic lupus erythematosus), infections (e.g.  
 CC viral, bacterial, fungal or parasitic infection), developmental disorders  
 CC (e.g. Cushing's syndrome or epilepsy), endocrine disorders (e.g.  
 CC thrombosis, hypopituitarism, hypogonadism, gigantism, goiter) metabolic  
 CC disorders (e.g. hypercholesterolaemia, hypoglycaemia, diabetes,  
 CC hyperlipidaemia, obesity), neurological disorders (e.g. ischaemic  
 CC cerebrovascular disease, stroke, Alzheimer's disease, Pick's disease,  
 CC Huntington's disease, Parkinson's disease, Creutzfeldt-Jakob disease,  
 CC anxiety, schizophrenia), gastrointestinal disorders (e.g. ulcers),  
 CC transport disorders (e.g. akinesia or multidrug resistance), or  
 CC connective tissue disorders (e.g. Paget's disease or rickets). This  
 CC polynucleotide sequence represents one of the human dithp DNA sequences  
 CC of the invention.

XX Sequence 4023 BP; 1082 A; 923 C; 833 G; 1185 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.55e+03 Length: 4023  
 Score: 42.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 79.25% Indels: 0  
 DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADE31423 (1-4023)

Qy 1 TptileGlyHisAspAlaGlyHis 8  
 |||||  
 Db 612 TGGATAGGCATTCCTGGCCAC 589

RESULT 73

ABL22486/c

ID ABL22486 standard; DNA; 4741 BP.

XX ABL22486;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 18931.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.

XX Drosophila melanogaster.

PN WO200171042-A2.

XX PD 27-SEP-2001.  
XX PF 23-MAR-2001; 2001WO-US009231.  
XX PR 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX DR WPI; 2001-656860/75.  
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.  
XX PT Claim 1; SEQ ID NO 10931; 21pp + Sequence Listing; English.  
XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 4741 BP; 1269 A; 1141 C; 1132 G; 1199 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.85e+03 Length: 4741  
Score: 42.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x ABL22486 (1-4741)  
QY 1 TrpIleGlyHisAspAlaGlyHis 8  
ID ABL11164 standard; cDNA; 6005 BP.  
XX AC ABL11164;  
XX DT 26-MAR-2002 (first entry)  
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27974.  
XX KW Drosophila; developmental biology; cell signalling; insecticide;  
XX KW pharmaceutical; gene; ss.  
XX OS Drosophila melanogaster.  
XX PN WO200171042-A2.  
XX PD 27-SEP-2001.  
XX PF 23-MAR-2001; 2001WO-US009231.  
XX PR 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PA (PEKE ) PE CORP NY.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

PI Venter JC, Adams M, Li PWD, Myers EW;  
XX DR WPI; 2001-656860/75.  
XX DR P-PSDB; ABB67061.  
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.  
XX PT Claim 1; SEQ ID NO 27974; 21pp + Sequence Listing; English.  
XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 6005 BP; 1693 A; 1451 C; 1343 G; 1518 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 2.39e+03 Length: 6005  
Score: 42.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 79.25% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x ABL11164 (1-6005)  
QY 2 IleGlyHisAspAlaGlyHis 8  
ID AAS78974/c  
DB 2315 ATAGGTACGATGCTGGACAT 2295  
RESULT 75  
AAS78974/c  
ID AAS78974 standard; cDNA; 8335 BP.  
XX AC AAS78974;  
XX DT 13-FEB-2002 (first entry)  
XX DE DNA encoding novel human diagnostic protein #14778.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI; 2001-639362/73.  
XX DR P-PSDB; ABG14787.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.



PF 30-JUL-2001; 2001US-00918995.  
XX  
PR 30-JUL-2001; 2001US-00918995.  
XX  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
XX  
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX  
DR WPI; 2003-615964/58.  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.  
XX  
PS Claim 1; SEQ ID NO 7604; 44pp; English.  
XX  
XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
XX  
SQ Sequence 418 BP; 109 A; 124 C; 101 G; 84 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 204 Length: 418  
Score: 41.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 71.43% Mismatches: 0  
Query Match: 77.36% Indels: 0  
DB: Gaps: 0  
  
US-10-029-756-6 (1-8) x ACH20392 (1-418)  
  
Qy 1 TrpIleGlyHisAspAlaGly 7  
Db 310 TGGGTGGGTCATGATTCGGG 290  
  
RESULT 78  
ABL93274  
ID ABL93274 standard; cDNA; 476 BP.  
XX  
AC ABL93274;  
XX  
XX 10-JUN-2002 (first entry)  
XX  
DE Arabidopsis thaliana nucleic acid sequence Ref:2027039 SEQ ID NO:39.  
XX  
KW Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;  
KW Genetic modification; gene; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
FN US2002023280-A1.  
XX  
PD 21-FEB-2002.  
  
XX 26-JAN-2001; 2001US-00770444.  
XX  
PR 27-JAN-2000; 2000US-0178502P.  
XX  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUYV/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
XX  
GORlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
PI Hurban P;  
XX  
WPI; 2002-267486/31.  
XX  
XX New Arabidopsis thaliana nucleic acid, for identifying homologous genes,  
PT producing compositions that modulate the expression or function of its  
PT encoded protein, and mapping functional regions of a protein.  
XX  
PS Claim 1; SEQ ID NO 39; 44pp; English.  
XX  
XX The present invention describes an Arabidopsis thaliana nucleic acid (1)  
CC comprising a sequence capable of hybridising under stringent conditions  
CC to a sequence (S1) selected from any one of the 999 sequences given in  
CC ABL93236 to ABL94234. (1) have insecticide and fungicide activities, and  
CC they can be used as protein expression modulators. (1) can be used in  
CC identifying homologous or related genes, in producing compositions that  
CC modulate the expression or function of their encoded proteins, mapping  
CC functional regions of the proteins, and in studying associated  
CC physiological pathways. (1) can also be used: (1) for the genetic  
CC manipulation of cells, particularly plant cells; (2) in screening assays  
CC of various plant strains to determine the strains that are best capable  
CC of withstanding a particular disease or environmental stress; (3) for  
CC enhancing or inhibiting production of a biosynthetic product in a plant;  
CC (4) as probes in mapping and in diagnosis, in genetic modification and  
CC for screening purposes, to generate additional copies of the nucleic  
CC acids, to generate ribozymes or antisense oligonucleotides, and as single  
CC -stranded DNA probes or as triple-stand forming oligonucleotides; and (5)  
CC for generating genetically modified transgenic organisms. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site  
XX  
SQ Sequence 476 BP; 98 A; 145 C; 95 G; 136 T; 0 U; 2 Other;  
  
Alignment Scores:  
Pred. No.: 234 Length: 476  
Score: 41.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 77.36% Indels: 0  
DB: Gaps: 0  
  
US-10-029-756-6 (1-8) x ABL93274 (1-476)  
  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8

::|||||:::|||||  
 TACATAGGTCACGATTCTGGTCAT 359

CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC [sedata.uspto.gov/sequence.html?DocID=20030194704](http://sedata.uspto.gov/sequence.html?DocID=20030194704)

Sequence 514 BP: 115 A; 157 C; 156 G; 86 T; 0 U; 0 Other;

ACH78188:

DT 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #11383.

KW Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

OS Homo sapiens.

US2003194704-A1.

PD 16-OCT-2003.

03-APR-2002; 2002US-00029386.

PR 03-APR-2002; 2002US-00029386.

PA (PENN/) PENN S G.

PA (HANZ/) HANZEL D K.

Penn SG, Rank DR,

DR WPI: 2004-119264/12.

PT New human genome-derived

PT splicing events, for assessing genomic alterations or as tools for PT surveying tissues.

PS Claim 15; SEQ ID NO 11383; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subcription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this



CC variations as indicated in (S1, SEQ ID NO:1 to 168) of the PA gene locus  
 CC of the subject and where the single nucleotide polymorphism (SNP) class  
 CC of the SNP is a cardiovascular disease (CVD) as described in PA SNPs, SNP  
 CC classes and putative PA genes listing table given in the specification,  
 CC where a risk genotype has a risk ratio of greater than 1 as described in  
 CC the correlation table of genotypes of PA SNPs to relative risk as given  
 CC in the specification; (11) determining (M4) a patient's individual  
 CC response to statin therapy, including drug efficacy and adverse drug  
 CC reactions, involves determining the identity of nucleotide variation in  
 CC sequences of (S1) of the PA gene locus of the subject and where the SNP  
 CC class of the SNP is adverse drug response (ADR), drug efficacy (EPF), or  
 CC both as described in PA SNPs, SNP classes and putative PA genes listing  
 CC table given in the specification, where the probability for such response  
 CC can as described in the correlation table of genotypes of PA SNPs to  
 CC relative risk as given in the specification; (12) use of (M4) for  
 CC preparation of medicament tailored to suit a patient's response to statin  
 CC therapy; and (13) a kit (V1) for assessing cardiovascular status or  
 CC statin response. (M2) is useful for screening for agents which regulate  
 CC the activity of PA gene. (M3) is useful for determining whether a human  
 CC subject has, or is at the risk of developing a cardiovascular disease.  
 CC (M4) is useful for determining a patient's individual response to statin  
 CC therapy. (M4) is useful for preparation of medicament tailored to suit a  
 CC patient's response to statin therapy.

SQ Sequence 544 BP; 137 A; 143 C; 150 G; 113 T; 0 U; 1 Other;

# Alignment Scores:

Pred. No.: 271 Length: 544  
 Score: 41.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 2  
 Best Local Similarity: 71.43% Mismatches: 0  
 Query Match: 77.36% Indels: 0  
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ADJ84393 (1-544)

Qy 1 TrpIeglyHisAspAlaGly 7

Db 485 TGGGTGGTCATGATTCGGG 505

RESULT 81

AAK63843/C

ID AAK63843 standard; cDNA; 564 BP.

AC AAK63843;

DT 06-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8903.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 XX cytostatic; gene therapy; vaccine; metastasis; ss.

OS Homo sapiens.

FN WO200157182-A2.

XX 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214866P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225575P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226686P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 05-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241878P.  
 PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249254P.  
PR 17-NOV-2000; 2000US-0249256P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483426/52.  
XX P-ESDB; AAM91062.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
XX Claim 1; SEQ ID NO 8903; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
XX activity, and can be used in gene therapy and vaccine production. (I)  
XX proteins and polynucleotides may be used in the prevention, diagnosis and  
XX treatment of diseases associated with inappropriate (I) expression. For  
XX example, they may be used to treat disorders associated with decreased  
XX expression by rectifying mutations or deletions in a patient's genome  
XX that affect the activity of (I) by expressing inactive proteins or to  
XX supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
CC represent sequences used in the exemplification of the present invention  
XX  
XX Sequence 564 BP; 76 A; 165 C; 121 G; 198 T; 0 U; 4 Other;  
SQ  
Alignment Scores:  
Pred. No.: 281 Length: 564  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x AAK63843 (1-564)  
Oy 1 TrpIleGlyHisaspAlaGlyHis 8  
Db 223 TGGATTGGACATCGAGGAGGTAC 200  
RESULT 82  
ADS60395/c  
ID ADS60395 standard; cDNA; 656 BP.  
XX AC ADS60395;  
XX 02-DEC-2004 (first entry)  
XX Bacterial polynucleotide #12382.  
XX Recombinant DNA construct; transformed plant; improved plant property;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
XX pathogen tolerance; pest tolerance; plant disease resistance;  
XX cell cycle pathway modification; plant growth regulator;  
XX homologous recombination; seed oil yield; protein yield; carbohydrate;  
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
XX bacterial polynucleotide; gene; ss.  
XX OS Bacteria.  
XX US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 36069; 122pp; English.  
XX The invention relates to a recombinant DNA construct comprising a  
XX promoter functional in a plant cell, where the promoter is positioned to  
XX provide for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source. The invention also relates to a transformed plant





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XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX PR New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 30806; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polynucleotide used in
XX CC the scope of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 780 BP; 125 A; 238 C; 264 G; 153 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 399 Length: 780
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 13 Gaps: 0

US-10-029-756-6 (1-8) x ADS55132 (1-780)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 691 TGGCGAGGTCCAGCATCGCCAC 658

RESULT 87
AAF82258
ID AAF82258 standard; DNA; 816 BP.
XX AC AAF82258;
XX DT 21-JUN-2001 (first entry)
XX DE Bacillus subtilis IFO 3336 DNA sequence.
XX KW Bacterial; poly-gamma-L-glutamic acid; L-PGA;
XX KW poly-gamma-D,L-glutamic acid; PGA; glutamate racemase; ds.
XX OS Bacillus subtilis.
XX FH Key Location/Qualifiers
XX FT CDS 1..816
XX FT /*tag= a
XX FT /transl_except= (pos:1..3,aa:Met)
XX PN JP2001017182-A.
```

```
XX 23-JAN-2001.
XX PF 09-JUL-1999; 99JP-00196335.
XX PR 09-JUL-1999; 99JP-00196335.
XX PA (NAGS ) NAGASE SANGYO KK.
XX DR WPI; 2001-285408/30.
XX DR P-PSDB; AAB74027.
XX PT New nucleic acid encoding a glutamate racemase enzyme useful for the
XX PT preparation of poly-gamma-glutamic acid.
XX PS Disclosure; Page 15-16; 17pp; Japanese.
XX CC The present sequence is one of four open reading frames of a region of
XX CC DNA from Bacillus subtilis that encodes an enzyme which is useful in the
XX CC production of poly-gamma-L-glutamic acid (L-PGA) or poly-gamma-D,L-
XX CC glutamic acid (PGA). A plasmid comprising DNA encoding the enzyme may be
XX CC used to transform Escherichia coli. The transformants express the enzyme
XX CC and PGA is produced in the culture
XX SQ Sequence 816 BP; 240 A; 180 C; 203 G; 193 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 419 Length: 816
Score: 41.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAF82258 (1-816)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 754 TGGTTGGCCATGAAGTCGGCAT 777

RESULT 88
ADE81200
ID ADE81200 standard; DNA; 921 BP.
XX AC ADE81200;
XX DT 29-JAN-2004 (first entry)
XX DE Orf14 coding sequence, SEQ ID 28.
XX KW ML-236B; HMG-CoA reducing enzyme; ds; Orf14.
XX OS Penicillium citrinum.
XX FH Key Location/Qualifiers
XX FT CDS 1..921
XX FT /*tag= a
XX FT /product= "Orf14"
XX PN JP2003116567-A.
XX DT 22-APR-2003.
XX PF 15-OCT-2001; 2001JP-00316578.
XX PR 15-OCT-2001; 2001JP-00316578.
XX PA (SANYO ) SANKYO CO LTD.
XX DR WPI; 2003-817677/77.
XX DR P-PSDB; ADE81201.
XX PT Novel DNA associated with synthesis of ML-236B, useful for improving ML-
```

PT 236B production in ML-236B producing microbe.  
XX Example 8; SEQ ID NO 28; 142pp; Japanese.  
XX The present invention relates to a DNA sequence (I, ADE81173), which is  
CC associated with ML-236B synthesis. (I) is useful for improving ML-236B  
CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing  
CC microbe. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 921 BP; 232 A; 237 C; 246 G; 206 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 478 Length: 921  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservatives: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 10 Gaps: 0  
  
US-10-029-756-6 (1-8) x ADE81200 (1-921)  
  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 744 TGGCAAGGACACGACAGAGGTTCAT 767  
  
RESULT 89  
AAAF71706  
ID AAF71706 standard; DNA; 955 BP.  
AC AAF71706;  
XX  
XX 30-APR-2001 (first entry)  
DT  
XX  
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:693.  
XX  
XX Corynebacterium glutamicum; carbon metabolism and energy production;  
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;  
KW fine chemical production; organic acid; proteinogenic amino acid;  
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.  
XX  
XX Corynebacterium glutamicum.  
OS  
XX  
XX WO200100844-A2.  
XX  
XX 04-JAN-2001.  
XX  
XX 23-JUN-2000; 2000WO-IB000943.  
XX  
XX 25-JUN-1999; 99US-0141031P.  
XX 08-JUL-1999; 99DE-01031412.  
XX 08-JUL-1999; 99DE-01031413.  
XX 08-JUL-1999; 99DE-01031419.  
XX 08-JUL-1999; 99DE-01031420.  
XX 08-JUL-1999; 99DE-01031424.  
XX 08-JUL-1999; 99DE-01031428.  
XX 08-JUL-1999; 99DE-01031431.  
XX 08-JUL-1999; 99DE-01031433.  
XX 08-JUL-1999; 99DE-01031434.  
XX 08-JUL-1999; 99DE-01031510.  
XX 08-JUL-1999; 99DE-01031562.  
XX 08-JUL-1999; 99DE-01031634.  
XX 09-JUL-1999; 99DE-01032180.  
XX 09-JUL-1999; 99DE-01032227.  
XX 09-JUL-1999; 99DE-01032230.  
XX 09-JUL-1999; 99US-0143208P.  
XX 14-JUL-1999; 99DE-01032924.  
XX 14-JUL-1999; 99DE-01032973.  
XX 14-JUL-1999; 99DE-01033005.  
XX 27-AUG-1999; 99DE-01040765.  
XX 31-AUG-1999; 99US-0151572P.  
  
105 03-SEP-1999; 99DE-01042076.  
106 03-SEP-1999; 99DE-01042079.  
107 03-SEP-1999; 99DE-01042086.  
108 03-SEP-1999; 99DE-01042087.  
109 03-SEP-1999; 99DE-01042088.  
110 03-SEP-1999; 99DE-01042095.  
111 03-SEP-1999; 99DE-01042123.  
112 03-SEP-1999; 99DE-01042125.  
113  
114 (BADI ) BASF AG.  
115  
116 Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
117 WPI; 2001-061975/07.  
118 P-PSDB; AAB79589.  
119  
120 New isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
121 metabolism and oxidative phosphorylation protein for production or  
122 modulation of production of fine chemicals e.g. amino acids,  
123 carbohydrates or enzymes.  
124  
125 Claim 3; Page 1128-1129; 1246pp; English.  
126  
127 AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
128 metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243  
129 to AAB 79633 which are involved in carbon metabolism and energy  
130 production. The C. glutamicum SMP gene can be used in vectors (II) for  
131 expression in host cells and production or modulation of production of  
132 fine chemicals, such as, an organic acid, a proteinogenic or  
133 nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a  
134 nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,  
135 a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a  
136 polyketide, or an enzyme. The presence of (I) or SMP proteins (III)  
137 encoded by them are used for diagnosing the presence or activity of  
138 Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells  
139 containing them are used to map genomes of organisms related to C.  
140 glutamicum, identify and localise C. glutamicum sequences of interest, in  
141 evolutionary studies, in determining SMP protein regions required for  
142 function, in modulating SMP protein activity, in modulating the  
143 metabolism of sugars, and in modulating high-energy molecule production  
144 in a cell (i.e. ATP, NADPH)  
145  
146 SQ Sequence 955 BP; 151 A; 272 C; 256 G; 276 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 497 Length: 955  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservatives: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-029-756-6 (1-8) x AAF71706 (1-955)  
  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 613 TGGATTGGCCATGCTGCTGGGCAT 636  
  
RESULT 90  
ADA69970/c  
ID ADA69970 standard; DNA; 1143 BP.  
XX  
XX ADA69970;  
AC  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX  
XX Rice gene, SEQ ID 3293.  
XX  
XX Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
XX Oryza sativa.  
OS  
XX

PN WO2003000898-A1.  
XX 03-JAN-2003.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX Identifying at least one gene involved in plant resistance or response to  
XX pathogenic infection for conferring resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection by determining or detecting plant  
XX gene expression.  
XX Claim 6; SEQ ID NO 3293; 899pp; English.  
XX The present invention relates to a method (M1) for identifying genes  
XX involved in plant resistance or response to pathogenic infection. M1  
XX comprises identifying a gene whose expression is significantly altered in  
XX the incompatible interaction of plant gene expression relative to  
XX expression of the gene in an uninfected plant, in a mutant plant that  
XX does not express a gene associated with response to pathogenic infection,  
XX or in a corresponding incompatible or compatible interaction. (M1) is  
XX useful for conferring resistance to resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection. The present sequence was used to  
XX illustrate the invention.  
XX SQ Sequence 1143 BP; 229 A; 305 C; 315 G; 294 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. NO.: 604 Length: 1143  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-029-756-6 (1-8) x ADA69970 (1-1143)  
  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
|||||  
Db 430 TGGATAGGCGATGGACGTGTCAC 407  
  
RESULT 91  
ID AAK86046/c  
XX AAK86046 standard; DNA; 1161 BP.  
XX AAK86046;  
XX  
XX 07-NOV-2001 (first entry)  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40858.  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
XX cytostatic; gene therapy; vaccine; metastasis; ds.  
XX Homo sapiens.  
XX  
XX WO200157182-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001354.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 18-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226888P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 01-SEP-2000; 2000US-0228924P.  
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PR 01-SEP-2000; 2000US-0229344P.  
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PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 08-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
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PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
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PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 27-SEP-2000; 2000US-0235834P.  
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PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
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PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249272P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250161P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251088P.  
PR 05-DEC-2000; 2000US-0251719P.  
PR 06-DEC-2000; 2000US-0251799P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-483426/52.  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX Disclosure; SEQ ID NO 40858; 3071pp + Sequence Listing; English.  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)

CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
CC represent sequences used in the exemplification of the present invention  
XX  
XX Sequence 1161 BP; 234 A; 330 C; 268 G; 328 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 614 Length: 1161  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-6 (1-8) x AAK86046 (1-1161)  
Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
Db 816 TGGATTGGACATCGAGGAGGTAC 793  
RESULT 92  
AAZ96369  
ID AAZ96369 standard; DNA; 1311 BP.  
XX AAZ96369;  
XX 10-APR-2000 (first entry)  
XX S. pneumoniae derived DNA from ORF #197.  
XX Treatment; prevention; disease; diagnosis; gene therapy; screening;  
XX bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.  
XX Streptococcus pneumoniae.  
XX WO9806734-A1.  
XX 19-FEB-1998.  
XX 15-AUG-1997; 97WO-US014436.  
XX 16-AUG-1996; 96US-0024022P.  
XX (SWIK ) SMITHKLINE BEECHAM CORP.  
XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;  
XX Stodola RK;  
XX WPI; 1998-159452/14.  
XX P-PSDB; AAY86038.  
XX Streptococcus pneumoniae proteins and related DNA - useful for screening  
XX compounds for antibacterial activity.  
XX Claim 4; Page 228-229; 640pp; English.  
XX This invention describes novel isolated Streptococcus pneumoniae  
XX polynucleotides (see AAZ96173-296494) and their encoded proteins (see  
XX AAY8792-Y86182). The DNA, vectors and host cells described in the method  
XX of the invention are useful for the recombinant expression of the



CC polypeptides. The polypeptides are useful for treatment or prevention of  
CC disease, or diagnosis of disease related to expression or activity of  
CC such a polypeptide. They can also be used to screen for compounds which  
CC interact with and inhibit or activate such a polypeptide. The  
CC polypeptides (or DNA encoding them, via gene therapy) are also useful for  
CC inducing an immunological response in a mammal. The antagonists are  
CC useful to inhibit such bacterial polypeptides. The polypeptides are  
CC particularly useful to identify antimicrobial compounds and antibiotics.  
CC They are also useful to determine their role in pathogenesis of  
CC infection, dysfunction and disease

XX SQ Sequence 1311 BP; 363 A; 249 C; 296 G; 403 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 700 Length: 1311  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAZ96369 (1-1311)

Qy 1 TptileGlyHisAspAlaGlyHis 8  
Db 365 TGGATTGGCGATGATGATATCAT 388

#### RESULT 93

ABZ12753  
ID ABZ12753 standard; DNA; 1350 BP.

XX AC ABZ12753;

XX DT 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.

XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX OS Arabidopsis thaliana.

XX PN WO200216655-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US026685.

XX PR 24-AUG-2000; 2000US-0227866P.

XX PR 26-JAN-2001; 2001US-0264647P.

XX PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI ) SCRIPPS RES INST.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and

XX producing plants with increased tolerance to these abiotic stresses.

XX Claim 6; SEQ ID NO 558; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant  
XX cell has been exposed, comprising: (a) contacting nucleic acid  
XX representative of expressed polynucleotides in the plant cell with an  
XX array or probes representative of the plant cell genome; and (b)  
XX detecting a profile of expressed polynucleotides in the plant cell  
XX characteristic of a stress response. The method is useful in the  
XX production of transgenic plants, cells and seeds and in producing plants  
XX with increased tolerance to abiotic stress. The present sequence is that  
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
XX in methods of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX SQ Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 722 Length: 1350  
Score: 41.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 77.36% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABZ12753 (1-1350)

Qy 1 TptileGlyHisAspAlaGlyHis 8  
Db 469 TACATAGTCACGATTCGTGCAT 492

#### RESULT 94

ABA01201/c  
ID ABA01201 standard; DNA; 1461 BP.

XX AC ABA01201;

XX DT 25-JAN-2002 (first entry)

XX DE Aldehyde-dehydrogenase coding sequence.

XX KW Aldehyde-dehydrogenase; enzyme; phenanthrene; anthracene; ds.

XX OS Nocardioides sp. KP7.

XX FH Key Location/Qualifiers

XX CDS 1..1461

XX FT /\*tag= a

XX FT /product= "Aldehyde-dehydrogenase"

XX PN JP2001245662-A.

XX PD 11-SEP-2001.

XX PF 03-MAR-2000; 2000JP-00059523.

XX PR 03-MAR-2000; 2000JP-00059523.

XX PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.

XX WPI; 2002-002935/01.

XX DR P-ESDB; AAMS2347.

XX Genes and proteins involved in the upstream of the pathway of degradation

XX of a polycyclic aromatic compound.

XX Example 4; Page 18-20; 47pp; Japanese.

XX The present sequence is the coding sequence for aldehyde-dehydrogenase.

XX The enzyme is useful as a reagent for converting the metabolite

XX intermediates of polycyclic aromatic compounds such as phenanthrene and

XX anthracene

XX SQ Sequence 1461 BP; 244 A; 505 C; 505 G; 207 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 787 Length: 1461  
Score: 41.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 85.71% Mismatches: 0  
Query Match: 77.36% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABA01201 (1-1461)



PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159339P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161932P.  
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:  
Pred. No.: 897  
Score: 41.00  
Percent Similarity: 100.00%  
Best Local Similarity: 75.00%  
Query Match: 77.36%  
DB: 3  
Length: 1650  
Matches: 6  
Conservative: 2  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-029-756-6 (1-8) x AAC51462 (1-1650)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8  
:::|||||:::|||||:::|||||

Db 675 TACATAGTCACGATTCTGGTCAT 698  
RESULT 96  
AAC33846  
ID AAC33846 standard; DNA; 1650 BP.  
XX  
AC AAC33846;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 4526.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127482P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
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PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
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PR 16-JUN-1999; 99US-0139452P.  
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PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
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PR 18-JUN-1999; 99US-0139457P.  
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PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
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PR 22-JUN-1999; 99US-0139859P.  
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PR 24-JUN-1999; 99US-0140695P.  
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PR 30-JUN-1999; 99US-0141287P.  
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PR 23-JUL-1999; 99US-01451145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
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PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
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PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
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PR 10-SEP-1999; 99US-0153070P.  
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PR 21-OCT-1999; 99US-0160741P.  
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PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.:	897	Length:	1650
Score:	41.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	75.00%	Mismatches:	0
Query Match:	77.36%	Indels:	0
DB:	3	Gaps:	0

US-10-029-756-6 (1-8) x AAC33846 (1-1650)

Qy	1	TrpIleclYHisaspAlaGlyHis	8
Db	673	TACATAGGTCACGATTCTGGTCAT	696

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RESULT 97
AAZ44833
ID AAZ44833 standard; DNA; 1678 BP.
XX
AC AAZ44833;
XX
DT 27-APR-2000 (first entry)
XX
DE A. thaliana sld1 DNA.
XX
KW Spingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 172..1521
FT FT /*tag= a
FT FT /product= "sphingolipid desaturase"
XX
PN DE19828850-A1.
XX
PD 30-DEC-1999.
XX
PF 27-JUN-1998; 98DE-01028850.
XX
PR 27-JUN-1998; 98DE-01028850.
XX
PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
PI Heinz E, Zaehrer U, Schmidt H, Sperling P;
XX
DR WPI; 2000-127549/12.
DR P-PSDB; AAY51334.
XX
PT New sphingolipid desaturase that selectively introduces double bond into
PT sphingolipids and capnoids.
XX
PS Claim 11; Fig 3; 62pp; German.
XX
CC This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered delta
CC -8-unsaturated long-chain base cis/trans ratio, especially to compensate
CC for a delta-8-unsaturated long-chain base deficiency, to exclude
CC production of delta-8-unsaturated bases, to increase tolerance or
CC resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence encodes the Arabidopsis thaliana sphingolipid
CC desaturase sld1 protein described in the method of the invention
XX
SQ Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 914 Length: 1678
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAZ44833 (1-1678)
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QY 1 TrpIleGlyHisAspAlaGlyHis 8  
:::|||||:::|||||  
Db 640 TACATAGGTCCAGGATTCGTGCAT 663

RESULT 98  
AAK86044/c  
ID AAK86044 standard; DNA; 1756 BP.  
XX  
AC AAK86044;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40856.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001354.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
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PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 06-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.

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PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
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PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
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PR 08-NOV-2000; 2000US-0246525P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
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PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 40856; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention
XX
XX SQ Sequence 1756 BP; 368 A; 460 C; 418 G; 510 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 960 Length: 1756
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAK86044 (1-1756)

Qy 1 TrpIleGlyHisaspAlaGlyHis 8
| | | | | | | |
Db 844 TGGATTGGACATCGAGGAGGTCC 821

RESULT 99
AAK86045/c
ID AAK86045 standard; DNA; 1757 BP.
XX
AC AAK86045;
XX
DT 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40857.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
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XX OS	Homo sapiens.	PR 26-SEP-2000; 2000US-0235484P.
XX PN	WO200157182-A2.	PR 27-SEP-2000; 2000US-0235834P.
XX PD	09-AUG-2001.	PR 27-SEP-2000; 2000US-0235836P.
XX PF	17-JAN-2001; 2001WO-US001354.	PR 29-SEP-2000; 2000US-0236327P.
XX PR	31-JAN-2000; 2000US-0179065P.	PR 29-SEP-2000; 2000US-0236367P.
PR	04-FEB-2000; 2000US-0180628P.	PR 29-SEP-2000; 2000US-0236368P.
PR	24-FEB-2000; 2000US-0184664P.	PR 29-SEP-2000; 2000US-0236369P.
PR	02-MAR-2000; 2000US-0186350P.	PR 29-SEP-2000; 2000US-0236370P.
PR	16-MAR-2000; 2000US-0189874P.	PR 02-OCT-2000; 2000US-0236802P.
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PR	14-AUG-2000; 2000US-0225266P.	PR 08-NOV-2000; 2000US-0246476P.
PR	14-AUG-2000; 2000US-0225267P.	PR 08-NOV-2000; 2000US-0246477P.
PR	14-AUG-2000; 2000US-0225268P.	PR 08-NOV-2000; 2000US-0246478P.
PR	14-AUG-2000; 2000US-0225270P.	PR 08-NOV-2000; 2000US-0246523P.
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PR	14-AUG-2000; 2000US-0225757P.	PR 08-NOV-2000; 2000US-0246525P.
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PR	14-AUG-2000; 2000US-0225759P.	PR 08-NOV-2000; 2000US-0246527P.
PR	18-AUG-2000; 2000US-0226279P.	PR 08-NOV-2000; 2000US-0246611P.
PR	22-AUG-2000; 2000US-0226681P.	PR 08-NOV-2000; 2000US-0246613P.
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PR	08-SEP-2000; 2000US-0232080P.	PR 17-NOV-2000; 2000US-0249300P.
PR	08-SEP-2000; 2000US-0232081P.	PR 01-DEC-2000; 2000US-0250160P.
PR	12-SEP-2000; 2000US-0231968P.	PR 01-DEC-2000; 2000US-0250391P.
PR	14-SEP-2000; 2000US-0232397P.	PR 05-DEC-2000; 2000US-0251030P.
PR	14-SEP-2000; 2000US-0232398P.	PR 05-DEC-2000; 2000US-0251988P.
PR	14-SEP-2000; 2000US-0232399P.	PR 06-DEC-2000; 2000US-0256719P.
PR	14-SEP-2000; 2000US-0232400P.	PR 08-DEC-2000; 2000US-0251479P.
PR	14-SEP-2000; 2000US-0232401P.	PR 08-DEC-2000; 2000US-0251856P.
PR	14-SEP-2000; 2000US-0233063P.	PR 08-DEC-2000; 2000US-0251866P.
PR	14-SEP-2000; 2000US-0233064P.	PR 08-DEC-2000; 2000US-0251869P.
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PR	21-SEP-2000; 2000US-0234223P.	PR 11-DEC-2000; 2000US-0251990P.
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PR	25-SEP-2000; 2000US-0234997P.	
PR	25-SEP-2000; 2000US-0234998P.	XX

PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-483426/52.  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
XX Disclosure; SEQ ID NO 40857; 3071pp + Sequence Listing; English.  
PS  
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention  
XX  
XX Sequence 1757 BP; 368 A; 464 C; 417 G; 508 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 960 Length: 1757  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAK86045 (1-1757)  
Qy 1 TrrileGlyHisAspAlaGlyHis 8  
Db 843 TGGATTGGACATCGAGGAGTTCAC 820

RESULT 100  
AD007822/c  
ID AD007822 standard; cDNA; 1962 BP.  
XX  
XX AD007822;  
AC  
XX 01-JUL-2004 (first entry)  
DT  
XX Mouse polynucleotide #40.  
DE  
XX Mouse; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
KW anorectic; antidiabetic.  
XX  
XX Mus sp.  
OS  
XX US2004071700-A1.  
PN  
XX 15-APR-2004.  
PD  
XX 09-OCT-2002; 2002US-00267502.  
XX  
XX 09-OCT-2002; 2002US-00267502.  
XX  
XX (LIFE-) LIFE SCI DEV CORP.  
PA  
XX Kim J, Galant R;  
PI  
XX WPI; 2004-328526/30.  
DR

DR P-PSDB; ADO08039.  
XX  
XX Identifying compounds that influence fat cell number or size for treating  
PT or preventing obesity or diabetes by exposing the cell to the agent and  
PT identifying fat cell number or size relative to cells not exposed to the  
PT agent.  
XX  
XX Claim 1; SEQ ID NO 148; 275pp; English.  
PS  
XX The invention relates to a method of identifying compounds that influence  
CC fat cell number or size comprising providing a cell that expresses a gene  
CC and an agent, exposing the cell to the agent and identifying fat cell  
CC number or size relative to cells not exposed to the agent. The method  
CC also comprises providing an expression vector and an agent, exposing the  
CC vector to the agent, detecting a change in expression of the gene  
CC relative to expression of the gene in an expression vector not exposed to  
CC the agent, treating a subject with the agent and identifying fat cell  
CC number or size in the subject. The agent comprises an antisense  
CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
CC method also comprises providing a polypeptide and an agent, exposing the  
CC polypeptide to the agent, detecting binding of the agent to the  
CC polypeptide or a change in an activity of the polypeptide, treating a  
CC subject with the agent and identifying fat cell number or size in the  
CC subject. The agent comprises an antibody. A method of regulating fat cell  
CC number or size comprises providing a subject containing fat cells and an  
CC agent that changes the expression of a gene, and treating the subject  
CC with the agent under conditions so that fat cell size or number in the  
CC subject is altered. The method is useful for identifying compounds that  
CC influence fat cell number or size, for preparing a composition for  
CC treating or preventing obesity or diabetes. This sequence represents  
CC mouse cDNA used in the scope of the invention.  
XX  
XX Sequence 1962 BP; 497 A; 575 C; 468 G; 422 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 1.08e+03 Length: 1962  
Score: 41.00 Matches: 5  
Percent Similarity: 75.00% Conservative: 1  
Best Local Similarity: 62.50% Mismatches: 2  
Query Match: 77.36% Indels: 0  
DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ADO07822 (1-1962)  
Qy 1 TrrileGlyHisAspAlaGlyHis 8  
Db 1566 TGGTAGGGCATCCCGTTGGCCAC 1543

Search completed: June 8, 2005, 11:57:21  
Job time : 554.596 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 09:39:06 ; Search time 1030.26 Seconds  
(without alignments)  
235.159 Million cell updates/sec

Title: US-10-029-756-12

Perfect score: 34

Sequence: 1 HNAHH 5

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgm2/US10029756/runat\_07062005\_122750\_28779/app\_query.fasta\_1.597  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10029756 @CGN 1 5965 @runat\_07062005\_122750\_28779 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_ets.\*

12: gb\_ey.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	34	100.0	17	6	AX273053 Sequence
C 2	34	100.0	17	6	AX273276 Sequence
C 3	34	100.0	82	6	AR503335 Sequence
4	34	100.0	82	6	AR518617 Sequence

206	6	AR523914	Sequence
224	9	HSAS55925	Homo sapi
234	6	CQ611508	Sequence
240	8	AF171953	Lindheime
255	8	AF479986	Saccharom
261	8	AY688473	Balduina
311	6	AX801775	Sequence
313	14	AY208086	Human cox
315	8	AY558170	Saccharom
316	6	AR358244	Sequence
321	6	AR539800	Sequence
323	14	AY208082	Human cox
325	6	AX312622	Sequence
329	11	GI6708	Sequence
329	11	G34525	human STS S
333	6	AR378808	Sequence
343	6	CQ415760	Sequence
345	6	CQ425403	Sequence
348	6	AR358018	Sequence
348	6	AR539574	Sequence
358	8	AF154077	Rhizopogo
366	6	AX413277	Sequence
366	6	AX415103	Sequence
380	6	AR074124	Sequence
380	6	BD224309	Materials
380	6	BD273006	Materials
380	6	AR216359	Sequence
380	6	AR432761	Sequence
380	6	BD005672	Materials
380	11	HS272X09	H. sapiens (
394	11	HSPE48H04	Sequence
395	5	AF333188	Oncorhync
400	6	AR357625	Sequence
400	6	AR539181	Sequence
413	6	AX801776	Sequence
420	6	BD224391	Materials
420	6	AR216441	Sequence
420	6	AR432843	Sequence
428	6	AX896634	Sequence
428	6	BD032167	Sequence
432	6	AR381260	Sequence
437	5	AF221557	Gallus ga
437	5	AF221558	Gallus ga
443	1	HPUEXPRT1	Helicobacte
500	6	CQ681194	Sequence
519	9	AF449188S1	Homo sapi
561	6	BD162240	Novel pol
561	6	AX120123	Sequence
561	11	G88098	Sequence
562	6	AR499461	Sequence
562	6	AR514743	Sequence
562	11	BV022000	S212P6803
578	6	AX411835	Sequence
631	3	AF064367	Herpetomo
638	6	AX283845	Sequence
645	8	AF229270	Balduina
646	9	HUMYR86G04	Homo sapi
647	8	AJ606025	Triticum
647	9	AY454951	Alouatta
648	6	AX055282	Sequence
650	5	AY113693	Oncorhync
653	6	AR273654	Sequence
653	6	AR277235	Sequence
653	6	AR407510	Sequence
653	6	AR441360	Sequence
653	6	AX544171	Sequence
653	6	AX368687	Sequence
662	8	AY329324	Alterinari
666	6	CQ715174	Sequence
675	9	AY454977	Trachypit
679	6	CQ610128	Sequence
686	6	BD010644	Helicobac

c 78	34	100.0	686	6	BD092839	BD092839 Identific	151	34	100.0	1450	8	AY055118	AY055118 Echium pi
c 79	34	100.0	713	6	AX414104	AX414104 Sequence	152	34	100.0	1478	8	AY055117	AY055117 Echium ge
c 80	34	100.0	723	11	PMWE2G	AL685153 Penicilli	c 153	34	100.0	1479	6	AY055117	AY055117 Echium ge
c 81	34	100.0	741	8	AF352352	AF352352 Cryptoper	c 154	34	100.0	1482	6	ER387938	ER387938 Sequence
c 82	34	100.0	824	6	AR253310	AR253310 Sequence	c 155	34	100.0	1482	3	E34355	E34355 Human prote
c 83	34	100.0	824	6	BD131771	BD131771 Genetic v	c 156	34	100.0	1483	3	AF042380	AF042380 Homo sapi
c 84	34	100.0	826	6	BD147586	BD147586 Primer fo	c 157	34	100.0	1491	8	AY089693	AY089693 Drosophil
c 85	34	100.0	826	6	AX867524	AX867524 Sequence	c 158	34	100.0	1491	8	BT003379	BT003379 Arabidops
c 86	34	100.0	838	6	AX451702	AX451702 Sequence	c 159	34	100.0	1494	10	AF142759	AF142759 Rattus no
c 87	34	100.0	847	11	BV208715	BV208715 NRXN2 101	c 159	34	100.0	1499	6	CQ726426	CQ726426 Sequence
c 88	34	100.0	881	6	AR508033	AR508033 Sequence	c 160	34	100.0	1500	9	HUMCAPPRO	M98474 Human CAP p
c 89	34	100.0	895	6	AX790445	AX790445 Sequence	c 161	34	100.0	1517	6	AR559274	AR559274 Sequence
c 90	34	100.0	900	6	CNS01BZ5	AL114873 Botrytis	c 162	34	100.0	1517	9	HSU02390	HSU02390 Human adeny
c 91	34	100.0	922	3	AY061549	AY061549 Drosophil	c 163	34	100.0	1518	1	AB012621	AB012621 Aeropyrum
c 92	34	100.0	948	9	HS424083	AJ324083 Homo sapi	c 164	34	100.0	1533	9	AF236119	AF236119 Homo sapi
c 93	34	100.0	979	5	CR523245	CR523245 Gallus ga	c 165	34	100.0	1541	6	CQ492274	CQ492274 Sequence
c 94	34	100.0	990	9	CR541849	CR541849 Homo sapi	c 166	34	100.0	1546	8	YSCARSX	YSCARSX
c 95	34	100.0	993	6	BD235644	BD235644 GRIP and	c 167	34	100.0	1551	3	AK116721	AK116721 Clona int
c 96	34	100.0	993	6	BD235645	BD235645 GRIP and	c 168	34	100.0	1554	6	AX618808	AX618808 Sequence
c 97	34	100.0	993	6	AF236120	AF236120 Homo sapi	c 169	34	100.0	1558	9	AY069959	AY069959 Homo sapi
c 98	34	100.0	993	9	CR536524	CR536524 Homo sapi	c 170	34	100.0	1563	10	MUSCAP	L12367 Mus musculu
c 99	34	100.0	1026	6	AX925033	AX925033 Sequence	c 171	34	100.0	1572	6	BD179626	BD179626 Highly th
c 100	34	100.0	1027	5	AF034693	AF034693 Coturnix	c 172	34	100.0	1574	6	AX402400	AX402400 Sequence
c 101	34	100.0	1085	8	AK059000	AK059000 Oryza sat	c 173	34	100.0	1591	8	HACVTBSRN	X87143 Hellanthus
c 102	34	100.0	1086	6	AK319425	AK319425 Sequence	c 174	34	100.0	1594	6	AX007239	AX007239 Sequence
c 103	34	100.0	1088	8	AK104597	AK104597 Oryza sat	c 175	34	100.0	1596	9	BC025692	BC025692 Homo sapi
c 104	34	100.0	1089	9	HSY18051	Y18051 Homo sapien	c 176	34	100.0	1599	3	DME344344	AJ344344 Drosophil
c 105	34	100.0	1103	9	CR456498	CR456498 Homo sapi	c 177	34	100.0	1599	6	CQ586995	CQ586995 Sequence
c 106	34	100.0	1112	8	AK101345	AK101345 Oryza sat	c 178	34	100.0	1606	6	AX007273	AX007273 Sequence
c 107	34	100.0	1134	6	CQ579477	CQ579477 Sequence	c 179	34	100.0	1610	9	BNJA4160	AY224160 Brassica
c 108	34	100.0	1161	8	AF308454	CQ579477 Sequence	c 180	34	100.0	1611	9	BC026002	BC026002 Homo sapi
c 109	34	100.0	1179	6	AF376026	AB308454 Medicago	c 181	34	100.0	1612	6	AX780624	AX780624 Sequence
c 110	34	100.0	1206	6	BD061976	AB376026 Sequence	c 182	34	100.0	1614	1	ECOHPA2	M61963 Escherichia
c 111	34	100.0	1208	6	BD061687	BD061976 Antigenic	c 183	34	100.0	1616	6	CQ614706	CQ614706 Sequence
c 112	34	100.0	1209	6	CQ734784	BD061687 Antigenic	c 184	34	100.0	1618	8	AF234127	AF234127 Primula v
c 113	34	100.0	1214	14	AY208085	CQ734784 Sequence	c 185	34	100.0	1633	8	AF001394	AF001394 Arabidops
c 114	34	100.0	1236	6	AF110794	AY208085 Human cox	c 186	34	100.0	1637	3	ECGTUB2	X85235 E.crassus g
c 115	34	100.0	1241	6	CQ730418	AF110794 Volvox ca	c 187	34	100.0	1652	6	AR217930	AY087345 Arabidops
c 116	34	100.0	1255	9	AF102694	CQ730418 Sequence	c 188	34	100.0	1661	6	AR217930	AY087345 Arabidops
c 117	34	100.0	1258	9	AF129476	AF102694 Homo sapi	c 189	34	100.0	1661	6	BD057812	AR217930 Sequence
c 118	34	100.0	1266	6	CQ831420	AF129476 Homo sapi	c 190	34	100.0	1665	6	AX042048	BD057812 Growth fa
c 119	34	100.0	1275	6	BD242779	CQ831420 Sequence	c 191	34	100.0	1678	6	AX007241	AX042048 Sequence
c 120	34	100.0	1275	6	AF139720	BD242779 Desaturas	c 192	34	100.0	1681	8	AY234124	AX007241 Sequence
c 121	34	100.0	1293	6	AR450683	AF139720 Euglena g	c 193	34	100.0	1684	6	AR076814	AY234124 Primula f
c 122	34	100.0	1298	6	A04377	AR450683 Sequence	c 194	34	100.0	1684	6	AR084177	AR076814 Sequence
c 123	34	100.0	1303	9	HS4011736	A04377 E.coli phoE	c 195	34	100.0	1684	6	BD062571	AR084177 Sequence
c 124	34	100.0	1311	9	AF121002	AJ011736 Homo sapi	c 196	34	100.0	1684	6	BD070919	BD062571 A sunflow
c 125	34	100.0	1322	9	AF090456	AF121002 Homo sapi	c 197	34	100.0	1685	6	AR020904	BD070919 An oleosi
c 126	34	100.0	1323	6	AR545311	AF090456 Homo sapi	c 198	34	100.0	1685	6	I38430	AR020904 Sequence 4
c 127	34	100.0	1328	3	DROSH2P	AR545311 Sequence	c 199	34	100.0	1685	6	AR200408	I38430 Sequence
c 128	34	100.0	1340	6	AX653094	M95199 Drosophila	c 200	34	100.0	1685	6	AR455421	AR200408 Sequence
c 129	34	100.0	1341	8	AF406816	AX653094 Sequence	c 201	34	100.0	1685	6	AR455421	AR455421 Sequence
c 130	34	100.0	1341	8	AF536525	AF406816 Aquilegia	c 202	34	100.0	1687	6	AF007561	AR455421 Borago of
c 131	34	100.0	1347	8	AF513128	AF536525 Anemone l	c 203	34	100.0	1687	8	BOU79010	AF007561 Sequence
c 132	34	100.0	1350	6	AX505863	AY131238 Argania s	c 204	34	100.0	1689	8	AX402397	AX951561 Sequence
c 133	34	100.0	1362	6	AX824969	AX505863 Sequence	c 205	34	100.0	1698	8	ATU19537	U19537 Arabidopsis
c 134	34	100.0	1362	6	AX824971	AX824969 Sequence	c 206	34	100.0	1702	6	AR200409	U19537 Arabidopsis
c 135	34	100.0	1363	6	CQ491332	AX824971 Sequence	c 207	34	100.0	1702	6	AR455422	AR200409 Sequence
c 136	34	100.0	1363	6	CQ497201	CQ491332 Sequence	c 208	34	100.0	1704	8	AF428420	AR455422 Sequence
c 137	34	100.0	1385	8	AY234126	CQ497201 Sequence	c 209	34	100.0	1705	8	AF428420	AF428420 Arabidops
c 138	34	100.0	1410	8	AY234125	AY234126 Primula v	c 210	34	100.0	1708	8	AK064680	AJ224161 Arabidops
c 139	34	100.0	1419	6	CQ608955	AY234125 Primula f	c 211	34	100.0	1715	6	AX402398	AK064680 Oryza sat
c 140	34	100.0	1419	6	AX058721	CQ608955 Sequence	c 212	34	100.0	1716	6	AX402392	AX402398 Sequence
c 141	34	100.0	1420	6	CQ600930	AX058721 Sequence	c 213	34	100.0	1727	10	BC050752	AX402392 Sequence
c 142	34	100.0	1421	1	ECOGADB	CQ600930 Sequence	c 214	34	100.0	1727	1	HHISH26	BC050752 Mus muscu
c 143	34	100.0	1421	1	ECOGADB	M84025 E. coli glu	c 215	34	100.0	1737	6	AX617772	X04832 Halobacteri
c 144	34	100.0	1425	6	AR451014	M84025 E. coli glu	c 216	34	100.0	1743	8	BT000442	AX617772 Sequence
c 145	34	100.0	1428	9	BT007152	AR451014 Sequence	c 217	34	100.0	1748	8	AK103193	BT000442 Arabidops
c 146	34	100.0	1428	9	CR457409	BT007152 Homo sapi	c 218	34	100.0	1757	6	AX402399	AK103193 Oryza sat
c 147	34	100.0	1428	12	BT008195	CR457409 Homo sapi	c 219	34	100.0	1757	6	AX402405	AX402399 Sequence
c 148	34	100.0	1434	3	AF208540	BT008195 Synthetic	c 220	34	100.0	1758	6	AX402390	AX402405 Sequence
c 149	34	100.0	1439	3	AF208540	CR457022 Homo sapi	c 221	34	100.0	1765	6	AX402401	AX402390 Sequence
c 150	34	100.0	1445	3	ECGAWTUB2	AF208540 Trypanoso	c 222	34	100.0	1766	6	AX402389	AX402401 Sequence
	34	100.0				Y09551 E.crassus m	c 223	34	100.0	1766	6	AX402394	AX402389 Sequence

224	34	100.0	1767	6	AX402393	Sequence	297	34	100.0	2000	6	AX831670	Sequence
225	34	100.0	1767	6	AX402402	Sequence	298	34	100.0	2000	6	AX831836	Sequence
226	34	100.0	1767	6	AX402403	Sequence	299	34	100.0	2000	6	AX832184	Sequence
227	34	100.0	1767	6	AX402404	Sequence	300	34	100.0	2000	6	AX832320	Sequence
228	34	100.0	1767	6	AX402406	Sequence	301	34	100.0	2000	6	AX832324	Sequence
229	34	100.0	1767	6	AX402409	Sequence	302	34	100.0	2000	6	AX832452	Sequence
230	34	100.0	1770	6	AX098422	Sequence	c 303	34	100.0	2029	3	AX116692	Sequence
231	34	100.0	1800	6	AR389150	Sequence	c 304	34	100.0	2060	6	CQ593385	Sequence
232	34	100.0	1825	10	BC013606	Sequence	c 305	34	100.0	2065	3	AY058347	Drosophil
233	34	100.0	1825	10	BC013606	Sequence	c 306	34	100.0	2083	11	BV177634	sgm95874
234	34	100.0	1869	8	AF133728	Sequence	c 307	34	100.0	2110	8	AF428316	Arabidops
235	34	100.0	1875	6	AX505999	Sequence	c 308	34	100.0	2111	9	BC008481	Homo sapi
236	34	100.0	1875	6	AX505999	Sequence	c 309	34	100.0	2118	3	AX113085	Ciona int
237	34	100.0	1879	10	BC005803	Sequence	c 310	34	100.0	2122	8	AY098893	Citrus hy
238	34	100.0	1879	10	BC005803	Sequence	c 311	34	100.0	2124	8	AK099028	Oryza sat
239	34	100.0	1909	3	AF139008	Sequence	c 312	34	100.0	2125	9	BC019877	Homo sapi
240	34	100.0	1916	5	BC075928	Sequence	c 313	34	100.0	2146	5	AF034570	Gallus ga
241	34	100.0	1934	6	CQ716584	Sequence	c 314	34	100.0	2151	8	AY045903	Arabidops
242	34	100.0	1958	6	CQ052068	Sequence	c 315	34	100.0	2170	6	AX451705	Arabidops
243	34	100.0	1958	6	CQ067112	Sequence	c 316	34	100.0	2176	14	NHP74X	Choristoneu
244	34	100.0	1958	6	CQ71531	Sequence	c 317	34	100.0	2181	8	ATANTMR	249227 A. thaliana
245	34	100.0	1958	6	CQ216159	Sequence	c 318	34	100.0	2191	3	AF045790	Drosophil
246	34	100.0	1958	6	CQ254724	Sequence	c 319	34	100.0	2196	3	AF045791	Drosophil
247	34	100.0	1958	6	CQ328864	Sequence	c 320	34	100.0	2197	3	AF045788	Drosophil
248	34	100.0	1975	8	AX155462	Physcomit	c 321	34	100.0	2199	3	AF045792	Drosophil
249	34	100.0	1980	1	ECPHOE	BD157976	c 322	34	100.0	2202	3	AF045793	Drosophil
250	34	100.0	1985	6	AX879700	Sequence	c 323	34	100.0	2205	3	AF045789	Drosophil
251	34	100.0	1985	6	AX879700	Sequence	c 324	34	100.0	2209	3	AF045795	Drosophil
252	34	100.0	1985	9	AX022735	Sequence	c 325	34	100.0	2210	9	AK096193	Homo sapi
253	34	100.0	2000	6	AX509561	Sequence	c 326	34	100.0	2212	9	BC013963	Homo sapi
254	34	100.0	2000	6	AX509847	Sequence	c 327	34	100.0	2214	3	AY044166	Drosophil
255	34	100.0	2000	6	AX594424	Sequence	c 328	34	100.0	2220	3	AF0445787	Drosophil
256	34	100.0	2000	6	AX594700	Sequence	c 329	34	100.0	2230	3	AF045794	Drosophil
257	34	100.0	2000	6	AX595136	Sequence	c 330	34	100.0	2231	3	AF045796	Drosophil
258	34	100.0	2000	6	AX595184	Sequence	c 331	34	100.0	2234	6	CQ611507	Sequence
259	34	100.0	2000	6	AX595462	Sequence	c 332	34	100.0	2265	3	AF061538	Drosophil
260	34	100.0	2000	6	AX595786	Sequence	c 333	34	100.0	2268	5	CR760497	Xenopus t
261	34	100.0	2000	6	AX596038	Sequence	c 334	34	100.0	2342	6	AX833224	Sequence
262	34	100.0	2000	6	AX596344	Sequence	c 335	34	100.0	2342	9	AK094797	Homo sapi
263	34	100.0	2000	6	AX596348	Sequence	c 336	34	100.0	2344	5	AK098211	Homo sapi
264	34	100.0	2000	6	AX596572	Sequence	c 337	34	100.0	2358	5	BC045402	Danio rer
265	34	100.0	2000	6	AX596760	Sequence	c 338	34	100.0	2361	14	HS5WIEP	M60321 Human cytom
266	34	100.0	2000	6	AX596862	Sequence	c 339	34	100.0	2373	6	AR528299	Sequence
267	34	100.0	2000	6	AX596866	Sequence	c 340	34	100.0	2384	3	AY061234	Drosophil
268	34	100.0	2000	6	AX596980	Sequence	c 341	34	100.0	2417	8	KLDNAMI31	Z50017 K. lactis DN
269	34	100.0	2000	6	AX596507	Sequence	c 342	34	100.0	2422	6	CQ595866	Sequence
270	34	100.0	2000	6	AX556340	Sequence	c 343	34	100.0	2453	8	AK065590	Oryza sat
271	34	100.0	2000	6	AX818546	Sequence	c 344	34	100.0	2528	10	BC005472	Mus muscu
272	34	100.0	2000	6	AX819140	Sequence	c 345	34	100.0	2543	10	BC005446	Mus muscu
273	34	100.0	2000	6	AX819196	Sequence	c 346	34	100.0	2543	10	AK128889	AK128889 Mus muscu
274	34	100.0	2000	6	AX819202	Sequence	c 347	34	100.0	2550	3	PLINTB	X38852 P. leniuscul
275	34	100.0	2000	6	AX819580	Sequence	c 348	34	100.0	2591	6	AR380455	AX8180455 Sequence
276	34	100.0	2000	6	AX819946	Sequence	c 349	34	100.0	2591	6	AX775123	Sequence
277	34	100.0	2000	6	AX819982	Sequence	c 350	34	100.0	2591	9	HUMADCY	L12168 Homo sapien
278	34	100.0	2000	6	AX820296	Sequence	c 351	34	100.0	2614	6	CQ800917	Sequence
279	34	100.0	2000	6	AX820472	Sequence	c 352	34	100.0	2614	6	AX779813	Sequence
280	34	100.0	2000	6	AX820636	Sequence	c 353	34	100.0	2664	6	CQ583305	Sequence
281	34	100.0	2000	6	AX820640	Sequence	c 354	34	100.0	2669	8	SCU73805	Saccharomyc
282	34	100.0	2000	6	AX820806	Sequence	c 355	34	100.0	2683	5	BC076869	BC076869 Xenopus l
283	34	100.0	2000	6	AX821154	Sequence	c 356	34	100.0	2694	10	AK172943	AK172943 Mus muscu
284	34	100.0	2000	6	AX821290	Sequence	c 357	34	100.0	2724	6	CQ654002	Sequence
285	34	100.0	2000	6	AX821294	Sequence	c 358	34	100.0	2731	8	AK110399	AK110399 Oryza sat
286	34	100.0	2000	6	AX821422	Sequence	c 359	34	100.0	2781	6	CQ646530	Sequence
287	34	100.0	2000	6	AX829576	Sequence	c 360	34	100.0	2784	1	AY050492	AY050492 Streptoco
288	34	100.0	2000	6	AX830170	Sequence	c 361	34	100.0	2784	6	AX608470	Sequence
289	34	100.0	2000	6	AX830226	Sequence	c 362	34	100.0	2796	3	S57693	S57693 fat body pr
290	34	100.0	2000	6	AX830232	Sequence	c 363	34	100.0	2800	8	AF107116	AF107116 Candida g
291	34	100.0	2000	6	AX830610	Sequence	c 364	34	100.0	2814	8	AB126946	AB126946 Colicium
292	34	100.0	2000	6	AX830976	Sequence	c 365	34	100.0	2818	10	AF202994	AF202994 Mus muscu
293	34	100.0	2000	6	AX831012	Sequence	c 366	34	100.0	2888	10	MMU19860	U19860 Mus muscu
294	34	100.0	2000	6	AX831326	Sequence	c 367	34	100.0	2970	6	AR449553	AR449553 Sequence
295	34	100.0	2000	6	AX831502	Sequence	c 368	34	100.0	3025	3	BT015203	BT015203 Drosophil
296	34	100.0	2000	6	AX831666	Sequence	c 369	34	100.0	3041	1	ECPROAB	X00786 E. coli gen

C 370	34	100.0	3051	6	CQ604893	CQ604893 Sequence	443	34	100.0	4328	6	AR137192	AR137192 Sequence
C 371	34	100.0	3079	8	AK100579	AK100579 Oryza sat	444	34	100.0	4328	6	AR158346	AR158346 Sequence
C 372	34	100.0	3095	9	BC030156	BC030156 Homo sapi	445	34	100.0	4328	6	AR241208	AR241208 Sequence
C 373	34	100.0	3107	6	CQ608461	CQ608461 Sequence	446	34	100.0	4328	6	AR338179	AR338179 Sequence
C 374	34	100.0	3108	8	SCYDL239C	Z74287 S. cerevisia	447	34	100.0	4328	6	AR340481	AR340481 Sequence
C 375	34	100.0	3109	9	BC007671	BC007671 Homo sapi	C 448	34	100.0	4336	6	AR354428	AR354428 Sequence
C 376	34	100.0	3162	9	AB060844	AB060844 Macaca fa	C 449	34	100.0	4336	6	AR535984	AR535984 Sequence
C 377	34	100.0	3168	3	THO278945	AJ278945 Trachiple	C 450	34	100.0	4346	5	BC077819	BC077819 Xenopus 1
C 378	34	100.0	3176	3	DRONCX	LJ9835 Drosophila	C 451	34	100.0	4357	8	AY072188	AY072188 Arabidops
C 379	34	100.0	3194	5	AF134320	AF134320 Drosostic	C 452	34	100.0	4380	6	CQ721015	CQ721015 Sequence
C 380	34	100.0	3247	6	CQ610127	CQ610127 Sequence	C 453	34	100.0	4395	6	CQ606464	CQ606464 Sequence
C 381	34	100.0	3258	14	PVU09508	U09508 Potato viru	C 454	34	100.0	4523	8	AY346360	AY346360 Rhizopus
C 382	34	100.0	3269	6	CQ608907	CQ608907 Sequence	C 455	34	100.0	4546	6	CQ584196	CQ584196 Sequence
C 383	34	100.0	3278	6	CQ610625	CQ610625 Sequence	C 456	34	100.0	4575	6	AX801769	AX801769 Sequence
C 384	34	100.0	3291	6	CQ804192	CQ804192 Sequence	C 457	34	100.0	4622	6	AX299128	AX299128 Sequence
C 385	34	100.0	3304	6	CQ879476	CQ879476 Sequence	C 458	34	100.0	4666	1	ECOFOLBDA	ECOFOLBDA
C 386	34	100.0	3304	6	AR447355	AR447355 Sequence	C 459	34	100.0	4755	6	AX801767	AX801767 Sequence
C 387	34	100.0	3331	6	CQ607811	CQ607811 Sequence	C 460	34	100.0	4779	6	AX800955	AX800955 Sequence
C 388	34	100.0	3391	1	SAAJ3164	AJ003164 Streptoco	C 461	34	100.0	4818	6	A92668	A92668 Sequence 4
C 389	34	100.0	3391	1	TPALAS	X95571 T. ferrooxid	C 462	34	100.0	4818	6	AR158348	AR158348 Sequence
C 390	34	100.0	3391	1	AY429663	AY429663 Streptoco	C 463	34	100.0	4818	6	AR241210	AR241210 Sequence
C 391	34	100.0	3395	1	SAG251493	AJ251493 Streptoco	C 464	34	100.0	4828	6	CQ608954	CQ608954 Sequence
C 392	34	100.0	3395	1	SAG251494	AJ251494 Streptoco	C 465	34	100.0	4912	6	BD271227	BD271227 Nucleic a
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C 395	34	100.0	3408	1	SAG251497	AJ251497 Streptoco	C 468	34	100.0	4928	6	CQ870784	CQ870784 Sequence
C 396	34	100.0	3408	1	SAG251498	AJ251498 Streptoco	C 469	34	100.0	4928	6	I49890	I49890 Sequence 1
C 397	34	100.0	3409	1	SAG251499	AJ251499 Streptoco	C 470	34	100.0	4928	6	AR212221	AR212221 Sequence
C 398	34	100.0	3419	5	AB100021	AB100021 Leionath	C 471	34	100.0	4949	8	AF135863	AF135863 Neurospor
C 399	34	100.0	3438	6	AX416597	AX416597 Sequence	C 472	34	100.0	5089	6	AX776820	AX776820 Sequence
C 400	34	100.0	3469	10	AK129370	AK129370 Mus muscu	C 473	34	100.0	5089	6	AX776823	AX776823 Sequence
C 401	34	100.0	3483	6	CQ585131	CQ585131 Sequence	C 474	34	100.0	5107	6	A92667	A92667 Sequence 3
C 402	34	100.0	3514	6	CQ849717	CQ849717 Sequence	C 475	34	100.0	5107	6	AR158347	AR158347 Sequence
C 403	34	100.0	3514	9	AK126758	AK126758 Homo sapi	C 476	34	100.0	5107	6	CQ607805	CQ607805 Sequence
C 404	34	100.0	3539	9	AK096417	AK096417 Homo sapi	C 477	34	100.0	5107	6	AR241209	AR241209 Sequence
C 405	34	100.0	3580	4	CFU55029	U55029 Canis fami	C 478	34	100.0	5108	6	AR562804	AR562804 Sequence
C 406	34	100.0	3581	6	CQ851210	CQ851210 Sequence	C 479	34	100.0	5108	6	AR562805	AR562805 Sequence
C 407	34	100.0	3581	9	AK128436	AK128436 Homo sapi	C 480	34	100.0	5108	6	AX138932	AX138932 Sequence
C 408	34	100.0	3602	8	AK110173	AK110173 Oryza sat	C 481	34	100.0	5108	6	AX138933	AX138933 Sequence
C 409	34	100.0	3701	6	AX327334	AX327334 Sequence	C 482	34	100.0	5108	6	BD000697	BD000697 Growth ho
C 410	34	100.0	3726	10	AY274810	AY274810 Rattus no	C 483	34	100.0	5108	6	BD000698	BD000698 Growth ho
C 411	34	100.0	3743	3	AY118680	AY118680 Drosophil	C 484	34	100.0	5111	6	AR562808	AR562808 Sequence
C 412	34	100.0	3747	3	BT011420	BT011420 Drosophil	C 485	34	100.0	5111	6	AX138936	AX138936 Sequence
C 413	34	100.0	3785	8	AF411833	AF411833 Arabidops	C 486	34	100.0	5111	6	BD000701	BD000701 Growth ho
C 414	34	100.0	3797	6	CQ591686	CQ591686 Sequence	C 487	34	100.0	5128	6	AX154497	AX154497 Sequence
C 415	34	100.0	3874	6	CQ612372	CQ612372 Sequence	C 488	34	100.0	5130	12	AF286076	AF286076 Expressio
C 416	34	100.0	3875	9	HSPGTER2G1	AF134201 Homo sapi	C 489	34	100.0	5185	6	AR562800	AR562800 Sequence
C 417	34	100.0	3879	1	ECOMPP	X74278 E.coli ompf	C 490	34	100.0	5185	6	AX138928	AX138928 Sequence
C 418	34	100.0	3884	6	BD159728	BD159728 Primer fo	C 491	34	100.0	5185	6	BD000693	BD000693 Growth ho
C 419	34	100.0	3884	6	AX882444	AX882444 Sequence	C 492	34	100.0	5188	6	AR562812	AR562812 Sequence
C 420	34	100.0	3884	9	AK022953	AK022953 Homo sapi	C 493	34	100.0	5188	6	AX138940	AX138940 Sequence
C 421	34	100.0	3886	3	DMU07595	U07595 Drosophila	C 494	34	100.0	5188	6	BD000705	BD000705 Growth ho
C 422	34	100.0	3893	12	AF425299	AF425299 Expressio	C 495	34	100.0	5215	6	AR231278	AR231278 Sequence
C 423	34	100.0	3898	12	AF425297	AF425297 Expressio	C 496	34	100.0	5215	6	BD008823	BD008823 Compositi
C 424	34	100.0	3934	10	AF323987	AF323987 Mus muscu	C 497	34	100.0	5254	6	AX562813	AX562813 Sequence
C 425	34	100.0	3948	4	AB121737	AB121737 Bos tauru	C 498	34	100.0	5254	6	AX138941	AX138941 Sequence
C 426	34	100.0	3960	9	BC043258	BC043258 Homo sapi	C 499	34	100.0	5254	6	BD000706	BD000706 Growth ho
C 427	34	100.0	3974	5	XU373733	U373733 Xenopus lae	C 500	34	100.0	5254	8	AK120962	AK120962 Oryza sat
C 428	34	100.0	3989	6	AK354698	AK354698 Sequence	C 501	34	100.0	5259	6	CQ847548	CQ847548 Sequence
C 429	34	100.0	3989	6	AR536254	AR536254 Sequence	C 502	34	100.0	5259	6	CQ847552	CQ847552 Sequence
C 430	34	100.0	4039	5	AY152408	AY152408 Gallus ga	C 503	34	100.0	5259	6	BD086100	BD086100 Cytokine-
C 431	34	100.0	4040	6	CQ586994	CQ586994 Sequence	C 504	34	100.0	5259	6	BD086104	BD086104 Cytokine-
C 432	34	100.0	4051	1	HU26665	U26665 Haemophilus	C 505	34	100.0	5287	6	CQ595865	CQ595865 Sequence
C 433	34	100.0	4060	6	CQ593384	CQ593384 Sequence	C 506	34	100.0	5287	6	E03599	E03599 E. coli polB
C 434	34	100.0	4081	1	ECFOLB	X54847 E. coli pol	C 507	34	100.0	5303	6	CQ583304	CQ583304 Sequence
C 435	34	100.0	4152	8	AY133875	AY133875 Arabidops	C 508	34	100.0	5310	6	AX080989	AX080989 Sequence
C 436	34	100.0	4156	9	AK092387	AK092387 Homo sapi	C 509	34	100.0	5322	6	CQ847550	CQ847550 Sequence
C 437	34	100.0	4233	8	OSU26660	U26660 Oryza sativ	C 510	34	100.0	5322	6	AX080956	AX080956 Sequence
C 438	34	100.0	4247	10	BC023757	BC023757 Mus muscu	C 511	34	100.0	5322	8	BD086102	BD086102 Cytokine-
C 439	34	100.0	4276	6	AX154496	AX154496 Sequence	C 512	34	100.0	5325	8	AY583466	AY583466 Marchanti
C 440	34	100.0	4282	6	AX164583	AX164583 Sequence	C 513	34	100.0	5386	6	AX743953	AX743953 Sequence
C 441	34	100.0	4315	3	AY075567	AY075567 Drosophil	C 514	34	100.0	5408	3	AF009897	AF009897 Drosophil
C 442	34	100.0	4328	6	A92666	A92666 Sequence 2	C 515	34	100.0	5422	6	CQ847551	CQ847551 Sequence

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518	34	100.0	5428	6	BD086099	Cytokine-	BD086099	591	34	100.0	6613	6	AX427830	Sequence
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587	34	100.0	6608	6	AX427884	Sequence	AX427884	660	34	100.0	6787	6	AX427820	Sequence
588	34	100.0	6609	6	AX427846	Sequence	AX427846	661	34	100.0	6790	6	AX427904	Sequence

662	34	100.0	6790	6	AX427914	Sequence	AX427914	Sequence	735	34	100.0	9620	6	AX164581	Sequence	AX164581	Sequence
663	34	100.0	6797	6	AX427888	Sequence	AX427888	Sequence	c 736	34	100.0	9647	14	AJ585342	Potato vi	AJ585342	Potato vi
664	34	100.0	6800	6	AX427855	Sequence	AX427855	Sequence	c 737	34	100.0	9653	14	AJ585197	Potato vi	AJ585197	Potato vi
665	34	100.0	6808	6	AX427817	Sequence	AX427817	Sequence	c 738	34	100.0	9653	14	AJ585198	Potato vi	AJ585198	Potato vi
666	34	100.0	6824	6	AX427874	Sequence	AX427874	Sequence	c 739	34	100.0	9700	14	AY166866	Potato vi	AY166866	Potato vi
667	34	100.0	6829	6	AX427858	Sequence	AX427858	Sequence	c 740	34	100.0	9700	14	AY166867	Potato vi	AY166867	Potato vi
668	34	100.0	6836	6	AX427854	Sequence	AX427854	Sequence	c 741	34	100.0	9701	14	PVYGEN	Potato viru	PVYGEN	Potato viru
669	34	100.0	6846	6	AX427851	Sequence	AX427851	Sequence	c 742	34	100.0	9703	14	PVPOLYP	Potato viru	PVPOLYP	Potato viru
670	34	100.0	6853	6	AX427852	Sequence	AX427852	Sequence	c 743	34	100.0	9782	6	AX427935	Sequence	AX427935	Sequence
671	34	100.0	6856	6	AX427776	Sequence	AX427776	Sequence	c 744	34	100.0	9783	6	AX427934	Sequence	AX427934	Sequence
672	34	100.0	6859	6	AX427772	Sequence	AX427772	Sequence	c 745	34	100.0	9785	6	AX427938	Sequence	AX427938	Sequence
673	34	100.0	6861	6	AX427848	Sequence	AX427848	Sequence	c 746	34	100.0	9788	6	AX427936	Sequence	AX427936	Sequence
674	34	100.0	6872	6	AX427856	Sequence	AX427856	Sequence	c 747	34	100.0	9792	6	AX427932	Sequence	AX427932	Sequence
c 675	34	100.0	6921	10	AB093297	Mus muscu	AB093297	Mus muscu	c 748	34	100.0	9918	12	AF430344	Synthetic	AF430344	Synthetic
676	34	100.0	6965	6	AX427773	Sequence	AX427773	Sequence	c 749	34	100.0	10056	2	AC015418	Drosophil	AC015418	Drosophil
677	34	100.0	6970	6	AX427768	Sequence	AX427768	Sequence	c 750	34	100.0	10138	1	AE003902	Xylella f	AE003902	Xylella f
678	34	100.0	7003	6	AX427835	Sequence	AX427835	Sequence	c 751	34	100.0	10150	1	AE005393	Escherich	AE005393	Escherich
679	34	100.0	7015	6	AR222043	Sequence	AR222043	Sequence	c 752	34	100.0	10290	1	AE015194	Shigella	AE015194	Shigella
680	34	100.0	7015	6	AX205071	Sequence	AX205071	Sequence	c 753	34	100.0	10298	1	AE009596	Brucella	AE009596	Brucella
681	34	100.0	7037	6	AX427775	Sequence	AX427775	Sequence	c 754	34	100.0	10367	1	AE005521	Escherich	AE005521	Escherich
682	34	100.0	7042	6	AX427771	Sequence	AX427771	Sequence	c 755	34	100.0	10371	1	AE015063	Shigella	AE015063	Shigella
c 683	34	100.0	7086	6	AX743955	Sequence	AX743955	Sequence	c 756	34	100.0	10533	1	AE008007	Agrobacte	AE008007	Agrobacte
684	34	100.0	7096	6	AX411806	Sequence	AX411806	Sequence	c 757	34	100.0	10542	1	AE010881	Methanosa	AE010881	Methanosa
685	34	100.0	7181	6	AX427832	Sequence	AX427832	Sequence	c 758	34	100.0	10826	1	AE015367	Shigella	AE015367	Shigella
686	34	100.0	7186	6	AX427834	Sequence	AX427834	Sequence	c 759	34	100.0	10934	1	AE005577	Escherich	AE005577	Escherich
687	34	100.0	7186	6	AX427836	Sequence	AX427836	Sequence	c 760	34	100.0	10938	1	AE001818	Thermotog	AE001818	Thermotog
688	34	100.0	7186	6	AX427837	Sequence	AX427837	Sequence	c 761	34	100.0	11163	1	AE001500	Helicobac	AE001500	Helicobac
689	34	100.0	7207	3	U23411	Caenorhabdi	U23411	Caenorhabdi	c 762	34	100.0	11270	1	AE004185	Vibrio ch	AE004185	Vibrio ch
690	34	100.0	7315	6	AX427839	Sequence	AX427839	Sequence	c 763	34	100.0	11380	6	CQ614705	Sequence	CQ614705	Sequence
c 691	34	100.0	7334	6	AX743956	Sequence	AX743956	Sequence	c 764	34	100.0	11434	1	AE004191	Vibrio ch	AE004191	Vibrio ch
c 692	34	100.0	7334	9	AB040896	Homo sapi	AB040896	Homo sapi	c 765	34	100.0	11448	5	AF394166	Tetraodon	AF394166	Tetraodon
693	34	100.0	7351	6	AX427766	Sequence	AX427766	Sequence	c 766	34	100.0	11612	1	AE004001	Xylella f	AE004001	Xylella f
c 694	34	100.0	7395	10	AF267848	Mus muscu	AF267848	Mus muscu	c 767	34	100.0	12261	1	AE015042	Shigella	AE015042	Shigella
c 695	34	100.0	7403	6	CQ579467	Sequence	CQ579467	Sequence	c 768	34	100.0	12272	10	F255566S22	Mus muscu	F255566S22	Mus muscu
696	34	100.0	7493	6	AX427833	Sequence	AX427833	Sequence	c 769	34	100.0	12411	6	AX427927	Sequence	AX427927	Sequence
697	34	100.0	7498	6	AX427838	Sequence	AX427838	Sequence	c 770	34	100.0	12441	1	SERFBC2	X1917 S. enterica	X1917 S. enterica	
698	34	100.0	7498	6	AX427840	Sequence	AX427840	Sequence	c 771	34	100.0	12441	6	BD085556	Nucleic a	BD085556	Nucleic a
699	34	100.0	7498	6	AX427841	Sequence	AX427841	Sequence	c 772	34	100.0	12446	6	AX029263	Sequence	AX029263	Sequence
700	34	100.0	7547	6	AX427763	Sequence	AX427763	Sequence	c 773	34	100.0	12490	1	U39712	Mycoplasma	U39712	Mycoplasma
701	34	100.0	7552	6	AX427849	Sequence	AX427849	Sequence	c 774	34	100.0	12563	1	AE001346	Chlamydia	AE001346	Chlamydia
702	34	100.0	7558	6	AX427765	Sequence	AX427765	Sequence	c 775	34	100.0	12607	1	AE010082	Streptoco	AE010082	Streptoco
703	34	100.0	7807	6	CQ855141	Sequence	CQ855141	Sequence	c 776	34	100.0	12641	1	AE014731	Bifidobac	AE014731	Bifidobac
704	34	100.0	7897	6	AX427923	Sequence	AX427923	Sequence	c 777	34	100.0	12920	6	CQ608906	Sequence	CQ608906	Sequence
705	34	100.0	7913	6	CQ855142	Sequence	CQ855142	Sequence	c 778	34	100.0	13116	1	AF213680	Actinobac	AF213680	Actinobac
706	34	100.0	7984	6	AX427924	Sequence	AX427924	Sequence	c 779	34	100.0	13208	9	AB028893	Homo sapi	AB028893	Homo sapi
707	34	100.0	7995	12	CVU64448	Sequence	CVU64448	Sequence	c 780	34	100.0	13429	2	AC019610	Drosophil	AC019610	Drosophil
708	34	100.0	8001	6	CQ855137	Sequence	CQ855137	Sequence	c 781	34	100.0	13464	6	CQ855143	Sequence	CQ855143	Sequence
709	34	100.0	8008	6	AX427767	Sequence	AX427767	Sequence	c 782	34	100.0	13466	6	CQ872949	Sequence	CQ872949	Sequence
710	34	100.0	8009	6	AX427764	Sequence	AX427764	Sequence	c 783	34	100.0	13579	1	AE005182	Escherich	AE005182	Escherich
c 711	34	100.0	8758	6	AX346020	Sequence	AX346020	Sequence	c 784	34	100.0	13848	1	AE009041	Agrobacte	AE009041	Agrobacte
c 712	34	100.0	8777	6	CQ604892	Sequence	CQ604892	Sequence	c 785	34	100.0	13915	9	AL589705	Human DNA	AL589705	Human DNA
c 713	34	100.0	8826	3	AF114152	Drosophil	AF114152	Drosophil	c 786	34	100.0	13930	1	AE014709	Bifidobac	AE014709	Bifidobac
c 714	34	100.0	9021	6	CQ584825	Sequence	CQ584825	Sequence	c 787	34	100.0	13960	1	AE015177	Shigella	AE015177	Shigella
c 715	34	100.0	9083	1	AE005356	Escherich	AE005356	Escherich	c 788	34	100.0	14224	1	AE000543	Helicobac	AE000543	Helicobac
c 716	34	100.0	9114	6	CQ573815	Sequence	CQ573815	Sequence	c 789	34	100.0	14250	1	AE014343	Brucella	AE014343	Brucella
717	34	100.0	9166	6	AX427930	Sequence	AX427930	Sequence	c 790	34	100.0	15073	2	AC019677	Drosophil	AC019677	Drosophil
718	34	100.0	9167	6	AX427933	Sequence	AX427933	Sequence	c 791	34	100.0	15090	9	CR759911	Human DNA	CR759911	Human DNA
719	34	100.0	9169	6	AX427931	Sequence	AX427931	Sequence	c 792	34	100.0	15158	1	AE001705	Thermotog	AE001705	Thermotog
720	34	100.0	9170	6	AX427928	Sequence	AX427928	Sequence	c 793	34	100.0	15378	14	AY141760	Fer-de-la	AY141760	Fer-de-la
721	34	100.0	9188	1	AE005202	Escherich	AE005202	Escherich	c 794	34	100.0	15418	6	BD226816	Alphaviru	BD226816	Alphaviru
722	34	100.0	9189	6	AX427921	Sequence	AX427921	Sequence	c 795	34	100.0	15538	6	AR243299	Sequence	AR243299	Sequence
723	34	100.0	9194	6	AX427925	Sequence	AX427925	Sequence	c 796	34	100.0	15627	9	HS786C22	Human DNA	HS786C22	Human DNA
724	34	100.0	9194	6	AX427926	Sequence	AX427926	Sequence	c 797	34	100.0	16408	8	AY083607	Candida g	AY083607	Candida g
c 725	34	100.0	9215	1	U32785	Haemophilus	U32785	Haemophilus	c 798	34	100.0	16616	4	AF010406	Ovis arie	AF010406	Ovis arie
726	34	100.0	9236	1	AE009727	Brucella	AE009727	Brucella	c 799	34	100.0	16658	6	CQ363842	Sequence	CQ363842	Sequence
727	34	100.0	9280	6	AX427929	Sequence	AX427929	Sequence	c 800	34	100.0	16832	4	MTC5XX	Y07726 Ceratotheri	Y07726 Ceratotheri	
728	34	100.0	9285	6	AX427922	Sequence	AX427922	Sequence	c 801	34	100.0	18013	1	D90790	E.coli geno	D90790 E.coli geno	
729	34	100.0	9407	6	AX427937	Sequence	AX427937	Sequence	c 802	34	100.0	18346	2	AC015345	Drosophil	AC015345	Drosophil
c 730	34	100.0	9497	2	AC014604	Drosophil	AC014604	Drosophil	c 803	34	100.0	18791	2	AC017940	Drosophil	AC017940	Drosophil
731	34	100.0	9600	6	A32665	Sequence 1	A32665	Sequence 1	c 804	34	100.0	19079	1	AE005229	Escherich	AE005229	Escherich
732	34	100.0	9600	6	AR158345	Sequence	AR158345	Sequence	c 805	34	100.0	19929	1	D90791	E.coli geno	D90791 E.coli geno	
733	34	100.0	9600	6	AR241207	Sequence	AR241207	Sequence	c 806	34	100.0	20178	1	AE008893	Salmonell	AE008893	Salmonell
734	34	100.0	9620	6	AX164579	Sequence	AX164579	Sequence	c 807	34	100.0	20855	2	AC017786	Drosophil	AC017786	Drosophil

C 808	34	100.0	21411	1	AB041266	AB041266 Actinobac	C 881	34	100.0	56458	8	AC148880	AC148880 Chlamydom
C 809	34	100.0	21752	2	AC014105	AC014105 Drosophil	C 882	34	100.0	57198	2	AC020115	AC020115 Drosophil
C 810	34	100.0	22130	6	AX702431	AX702431 Sequence	C 883	34	100.0	57250	2	AC083997	AC083997 Homo sapi
C 811	34	100.0	22622	6	C0612248	C0612248 Sequence	C 884	34	100.0	57303	2	AC020240	AC020240 Drosophil
C 812	34	100.0	22690	1	AB0310032	AB0310032 Actinobac	C 885	34	100.0	57402	2	AC127888_3	Continuation (4 of
C 813	34	100.0	24126	1	AB014208	AB014208 Streptoco	C 886	34	100.0	57730	2	AC014848	AC014848 Drosophil
C 814	34	100.0	24221	6	C0584195	C0584195 Sequence	C 887	34	100.0	57840	8	AF359361	AF359361 Gibberell
C 815	34	100.0	24907	1	AB002668	AB002668 Actinobac	C 888	34	100.0	58288	2	AC101021	AC101021 Mus muscu
C 816	34	100.0	25165	6	AR204143	AR204143 Sequence	C 889	34	100.0	58811	2	AC136094	AC136094 Rattus no
C 817	34	100.0	25473	6	BD184781	BD184781 NuclLeic a	C 890	34	100.0	60040	2	AC005128	AC005128 Drosophil
C 818	34	100.0	25530	14	AY446869	AY446869 Human her	C 891	34	100.0	61258	2	AC023082	AC023082 Homo sapi
C 819	34	100.0	25595	3	AF039045	AF039045 Caenorhab	C 892	34	100.0	62456	2	AC099992	AC099992 Mus muscu
C 820	34	100.0	26336	9	AC034208	AC034208 Homo sapi	C 893	34	100.0	63170	10	AL645799	AL645799 Mouse DNA
C 821	34	100.0	26621	2	AC020878	AC020878 Mus muscu	C 894	34	100.0	63779	3	AL845322	AL845322 Zebrafish
C 822	34	100.0	27022	8	AF336366	AF336366 Gibberell	C 895	34	100.0	64674	3	AC004247	AC004247 Drosophil
C 823	34	100.0	27974	9	HSL174G8A	Z69638 Human DNA s	C 896	34	100.0	64919	2	AC100902	AC100902 Mus muscu
C 824	34	100.0	29120	3	AF016446	AF016446 Caenorhab	C 897	34	100.0	65900	9	EX005209	EX005209 Human DNA
C 825	34	100.0	29795	3	US8742	US8742 Caenorhabdi	C 898	34	100.0	66795	2	AC110584	AC110584 Homo sapi
C 826	34	100.0	30159	8	AF336365	AF336365 Gibberell	C 899	34	100.0	67188	2	AC104364	AC104364 Homo sapi
C 827	34	100.0	30168	3	DMC114D9	AL031640 Drosophil	C 900	34	100.0	67473	1	AB016854	AB016854 Pseudomon
C 828	34	100.0	30197	8	AB060689	AB060689 Gibberell	C 901	34	100.0	68025	5	BX510960	BX510960 Zebrafish
C 829	34	100.0	30670	1	MSGB1229CS	L78812 Mycobacteri	C 902	34	100.0	68092	2	AC025634	AC025634 Homo sapi
C 830	34	100.0	30866	3	L09634	L09634 Caenorhabdi	C 903	34	100.0	68108	2	AC113994	AC113994 Homo sapi
C 831	34	100.0	32872	6	CQ575591	CQ575591 Sequence	C 904	34	100.0	68418	2	AC018990	AC018990 Drosophil
C 832	34	100.0	33200	3	CF5F4B3	Z49583 Caenorhabdi	C 905	34	100.0	68914	2	AC024970	AC024970 Homo sapi
C 833	34	100.0	34267	6	AX602190	AX602190 Sequence	C 906	34	100.0	69596	2	AC101647	AC101647 Mus muscu
C 834	34	100.0	34796	5	BX005325	BX005325 Zebrafish	C 907	34	100.0	69619	2	AC103638	AC103638 Mus muscu
C 835	34	100.0	36003	3	CF313B12	Z70683 Caenorhabdi	C 908	34	100.0	69706	9	AL445592	AL445592 Human DNA
C 836	34	100.0	36457	2	AC107968	AC107968 Homo sapi	C 909	34	100.0	70163	2	AC014829	AC014829 Drosophil
C 837	34	100.0	37810	9	AC022153	AC022153 Homo sapi	C 910	34	100.0	70175	8	NC13E11	AL353820 Neurospor
C 838	34	100.0	37991	9	AF000565	AF000565 Homo sapi	C 911	34	100.0	70387	3	AC087075	AC087075 Caenorhab
C 839	34	100.0	38181	3	AF016685	AF016685 Caenorhab	C 912	34	100.0	70394	2	AC023011	AC023011 Homo sapi
C 840	34	100.0	38429	9	AC000035	AC000035 Homo sapi	C 913	34	100.0	70752	2	AC113148	AC113148 Homo sapi
C 841	34	100.0	38717	9	AC005357	AC005357 Homo sapi	C 914	34	100.0	71190	2	AC130384	AC130384 Homo sapi
C 842	34	100.0	39177	3	CRAC8	Z83097 Caenorhabdi	C 915	34	100.0	71456	10	WMA298054	AL298054 Mus muscu
C 843	34	100.0	39324	9	HSL27H9	Z49237 Human DNA s	C 916	34	100.0	71504	3	AC002473	AC002473 Drosophil
C 844	34	100.0	39757	14	AF110004	AF110004 Ranid her	C 917	34	100.0	71506	9	AC092452	AC092452 Homo sapi
C 845	34	100.0	39929	2	AC014373	AC014373 Drosophil	C 918	34	100.0	71774	8	NCB9K17	BX294016 Neurospor
C 846	34	100.0	40068	3	CBRG44F10	AC084614 Caenorhab	C 919	34	100.0	72137	9	AL356795	AL356795 Human DNA
C 847	34	100.0	40221	1	MSGY154	AD000002 Mycobacte	C 920	34	100.0	72360	2	AC101329	AC101329 Mus muscu
C 848	34	100.0	40597	3	CBG22A1	ZB1038 Caenorhabdi	C 921	34	100.0	72735	8	AP004487	AP004487 Lotus cor
C 849	34	100.0	40850	9	AC012723	AB012723 Homo sapi	C 922	34	100.0	73656	2	AC027536	AC027536 Homo sapi
C 850	34	100.0	41115	3	CEC46C2	Z68296 Caenorhabdi	C 923	34	100.0	73721	2	AC020007	AC020007 Drosophil
C 851	34	100.0	41571	2	AC145660	AC145660 Homo sapi	C 924	34	100.0	73794	2	AC101544	AC101544 Mus muscu
C 852	34	100.0	41820	8	AP004479	AP004479 Lotus cor	C 925	34	100.0	73794	2	AC101544	AC101544 Mus muscu
C 853	34	100.0	43500	8	AP028608	AP028608 Arabidops	C 926	34	100.0	74084	2	AF322451	AF322451 Homo sapi
C 854	34	100.0	44477	2	CR589923	CR589923 Homo sapi	C 927	34	100.0	74355	1	AY120853	AY120853 Synchoco
C 855	34	100.0	44993	2	AC014424	AC014424 Drosophil	C 928	34	100.0	76529	2	AC090202	AC090202 Homo sapi
C 856	34	100.0	45428	3	AY190963	AY190963 Drosophil	C 929	34	100.0	77167	5	BX248235	BX248235 Zebrafish
C 857	34	100.0	45512	2	AC137269	AC137269 Ciona sav	C 930	34	100.0	77551	9	HS7H11	AL035209 Human DNA
C 858	34	100.0	45911	9	AC005688	AC005688 Homo sapi	C 931	34	100.0	79564	9	BX649443	BX649443 Human DNA
C 859	34	100.0	46152	9	AC005530	AC005530 Homo sapi	C 932	34	100.0	80106	9	AL645634	AL645634 Human DNA
C 860	34	100.0	46851	2	AC012391	AC012391 Drosophil	C 933	34	100.0	80240	9	AC010330	AC010330 Homo sapi
C 861	34	100.0	46894	9	AC114729	AC114729 Homo sapi	C 934	34	100.0	80264	6	CQ870452	CQ870452 Sequence
C 862	34	100.0	47127	2	AC020157	AC020157 Drosophil	C 935	34	100.0	80438	9	AL133552	AL133552 Homo sapi
C 863	34	100.0	47147	3	AF077536	AF077536 Caenorhab	C 936	34	100.0	80955	9	AL133552	AL133552 Homo sapi
C 864	34	100.0	47739	1	AF017113	AF017113 Bacillus	C 937	34	100.0	81100	2	AC019838	AC019838 Drosophil
C 865	34	100.0	48119	2	AC130493	AC130493 Homo sapi	C 938	34	100.0	81602	3	AC004349	AC004349 Drosophil
C 866	34	100.0	48279	9	AC093662	AC093662 Homo sapi	C 939	34	100.0	81735	2	AC022230	AC022230 Mus muscu
C 867	34	100.0	49433	9	AL157707	AL157707 Human DNA	C 940	34	100.0	81866	8	NC64C2	BX294009 Neurospor
C 868	34	100.0	50885	2	AC014946	AC014946 Drosophil	C 941	34	100.0	81905	1	LISINP100	AL592102 Listeria
C 869	34	100.0	51289	3	AC005717	AC005717 Drosophil	C 942	34	100.0	81905	6	AX415066	AX415066 Sequence
C 870	34	100.0	51677	9	AL133288	AL133288 Human DNA	C 943	34	100.0	82081	8	AY371490	AY371490 Aspergill
C 871	34	100.0	52259	2	AC017309	AC017309 Drosophil	C 944	34	100.0	82400	10	AC090495	AC090495 Genomic s
C 872	34	100.0	52525	1	AB014164	AB014164 Streptoco	C 945	34	100.0	82654	9	AL353713	AL353713 Human DNA
C 873	34	100.0	52707	2	AC017288	AC017288 Drosophil	C 946	34	100.0	82689	6	AX413020	AX413020 Sequence
C 874	34	100.0	53124	2	AC012698	AC012698 Drosophil	C 947	34	100.0	82728	2	AC115478_4	Continuation (5 of
C 875	34	100.0	53951	9	AC092866	AC092866 Homo sapi	C 948	34	100.0	83703	5	AL732635	AL732635 Zebrafish
C 876	34	100.0	54115	2	AC018149	AC018149 Drosophil	C 949	34	100.0	83958	9	AF334828	AF334828 Homo sapi
C 877	34	100.0	54152	10	AL645749	AL645749 Mouse DNA	C 950	34	100.0	84182	9	AC110763	AC110763 Homo sapi
C 878	34	100.0	54375	9	AC011377	AC011377 Homo sapi	C 951	34	100.0	84562	2	AC140700	AC140700 Homo sapi
C 879	34	100.0	55956	9	AL772202	AL772202 Human DNA	C 952	34	100.0	84724	9	AC022084	AC022084 Homo sapi
C 880	34	100.0	56315	2	AC137140	AC137140 Homo sapi	C 953	34	100.0	84928	2	AC141231	AC141231 Homo sapi

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954 34 100.0 85214 8 AC005396 Arabidops
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958 34 100.0 86661 10 AP001294 AP001294 Mus muscu
959 34 100.0 87323 2 CR762433 CR762433 Homo sapi
960 34 100.0 87340 1 AP005224 AP005224 Corynebac
961 34 100.0 87428 3 CRV64G10A AL110498 Caenorhab
962 34 100.0 87847 6 CQ870457 CQ870457 Sequence
963 34 100.0 88483 2 AC079591 AC079591 Homo sapi
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965 34 100.0 88824 2 AC105453 AC105453 Rattus no
966 34 100.0 88933 2 AC017870 AC017870 Drosophil
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971 34 100.0 91040 2 AC017292 AC017292 Drosophil
972 34 100.0 91430 1 ECOTSF BX545912 Zebrafish
973 34 100.0 92169 5 BX545912 BX545912 Zebrafish
974 34 100.0 92948 8 AC069551 AC069551 Genomic s
975 34 100.0 92969 9 HSJ687F11 AL117334 Human DNA
976 34 100.0 93351 2 AC020335 AC020335 Drosophil
977 34 100.0 94015 2 AC012223 AC012223 Homo sapi
978 34 100.0 94162 9 AL450322 AL450322 Human DNA
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981 34 100.0 95115 8 AC146746 AC146746 Medicago
982 34 100.0 95119 8 AC146682 AC146682 Medicago
983 34 100.0 95327 8 AC013354 AC013354 Genomic s
984 34 100.0 95993 8 ATF2A19 AL132962 Arabidops
985 34 100.0 96202 9 AL138824 AL138824 Human DNA
986 34 100.0 96283 8 NC208H10 BX294024 Neurospor
987 34 100.0 96560 9 AC090582 AC090582 Homo sapi
988 34 100.0 96694 9 AC090470 AC090470 Homo sapi
989 34 100.0 96792 9 HSU95741 U95741 Human chrom
990 34 100.0 98360 9 AC008473 AC008473 Homo sapi
991 34 100.0 98472 6 AX706975 AX706975 Sequence
992 34 100.0 98472 6 AX707905 AX707905 Sequence
993 34 100.0 98472 9 AC005068 AC005068 Homo sapi
994 34 100.0 98494 9 AC087763 AC087763 Homo sapi
995 34 100.0 99159 1 AP001918 AP001918 F plasmid
996 34 100.0 99163 2 AL356436 AL356436 Homo sapi
997 34 100.0 99369 9 AC112140 AC112140 Homo sapi
998 34 100.0 99629 6 AR408758 AR408758 Sequence
999 34 100.0 99629 6 AX067462 AX067462 Sequence
1000 34 100.0 99795 8 AC113332 AC113332 Oryza sat
Continuation (4 of
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## ALIGNMENTS

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RESULT 1
LOCUS AX273053/c 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 622 from Patent WO0162911.
ACCESSION AX273053
VERSION AX273053.1 GI:16545790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
METHOD Method and reagent for the inhibition of grid
PATENT Patent: WO 0162911-A 622 30-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
TITLE Location/Qualifiers
JOURNAL 1..17
FEATURES
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/organism="Homo sapiens"
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ORIGIN
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Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-12 (1-5) x AX273053 (1-17)
Qy 1 HisaenAlahisHis 5
Db 16 CACAATGCCCATCAT 2

RESULT 2
AX273276/c 17 bp RNA linear PAT 29-OCT-2001
LOCUS AX273276
DEFINITION Sequence 845 from Patent WO0162911.
ACCESSION AX273276
VERSION AX273276.1 GI:16546013
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
METHOD Method and reagent for the inhibition of grid
PATENT Patent: WO 0162911-A 845 30-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
TITLE Location/Qualifiers
FEATURES
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ORIGIN
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Pred. No.: 34.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-12 (1-5) x AX273276 (1-17)
Qy 1 HisaenAlahisHis 5
Db 17 CACAATGCCCATCAT 3

RESULT 3
AR503335 82 bp DNA linear PAT 22-SEP-2004
LOCUS AR503335
DEFINITION Sequence 8295 from patent US 6703491.
ACCESSION AR503335
VERSION AR503335.1 GI:52438810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 82)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 8295 09-MAR-2004;
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 239 Length: 82
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR503335 (1-82)

Qy 1 HisAenAlaHisHis 5
Db 2 CACAACGCCACCAC 16

RESULT 4
AR518617
LOCUS AR518617 82 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 23577 from patent US 6703491.
ACCESSION AR518617
VERSION AR518617.1 GI:52454092
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 82)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 23577 09-MAR-2004;
FEATURES
source
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/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 239 Length: 82
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR518617 (1-82)

Qy 1 HisAenAlaHisHis 5
Db 2 CACAACGCCACCAC 16

RESULT 5
AR523914
LOCUS AR523914 206 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 28874 from patent US 6703491.
ACCESSION AR523914
VERSION AR523914.1 GI:52459389
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 206)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 28874 09-MAR-2004;
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:

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Pred. No.: 565 Length: 206
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR523914 (1-206)

Qy 1 HisAenAlaHisHis 5
Db 183 CACAATGCCACCAC 197

RESULT 6
HSA555925/c
LOCUS HSA555925 224 bp DNA linear PRI 16-APR-2003
DEFINITION Homo sapiens rearranged immunoglobulin gene DNA, isolate case 1,
cell 40.
ACCESSION AJ555925
VERSION AJ555925.1 GI:29836815
KEYWORDS immunoglobulin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brauning,A., Spieker,T., Mottok,A., Baur,A., Koppers,R. and
Hansmann,M.L.
TITLE Epstein Barr virus (EBV)-positive lymphoproliferations in
posttransplant patients show immunoglobulin V gene mutation
patterns suggesting interference of EBV with normal B cell
differentiation processes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 224)
AUTHORS Brauning,A.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2003) Brauning,A., Pathology, University of
Frankfurt, Theodor Stern Kai 7, 60590, GERMANY
FEATURES
source
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/isolate="case 1, cell 40"
/db_xref="taxon:9606"
/tissue type="posttransplantation lymphoproliferative
disease"
/rearranged

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Alignment Scores:
Pred. No.: 611 Length: 224
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA555925 (1-224)

Qy 1 HisAenAlaHisHis 5
Db 216 CATATGCTCATCAC 202

RESULT 7
CQ611508
LOCUS CQ611508 234 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 39286 from Patent WO0171042.
ACCESSION CQ611508
VERSION CQ611508.1 GI:41662985
KEYWORDS
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.  
TITLE Detection kits, such as nucleic acid arrays, for detecting the  
expression of 10,000 or more Drosophila genes and uses thereof  
JOURNAL Patent: WO 0171042-A 39266 27-SEP-2001;  
PE Corporation (US)  
FEATURES Location/Qualifiers  
source  
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Pred. No.: 636 Length: 234  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ611508 (1-234)

Qy 1 HisAenAlaHisHis 5  
Db 90 CATACGCGCACAC 104

## RESULT 8

AF171953/ C AF171953 240 bp DNA linear PLN 01-MAY-2000  
LOCUS Lindheimera texana internal transcribed spacer 1, complete  
DEFINITION sequence.  
ACCESSION AF171953  
VERSION AF171953.1 GI:7673204  
KEYWORDS Lindheimera texana  
ORGANISM Lindheimera texana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Lindheimera.

REFERENCE  
AUTHORS Cleveringer, J.A. and Panero, J.L.  
TITLE Phylogenetic analysis of Silphium and subtribe Engelmanniinae  
(Asteraceae: Heliantheae) based on ITS and ETS sequence data  
JOURNAL Am. J. Bot. 87 (4), 565-572 (2000)  
PUBMED 10766728

REFERENCE 2 (bases 1 to 240)  
AUTHORS Cleveringer, J.A. and Panero, J.L.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-1999) Biology, James Madison University, MSC  
7801, Harrisonburg, Virginia 22807, USA  
LOCATION/Qualifiers

## FEATURES

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## ORIGIN

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Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF171953 (1-240)

Qy 1 HisAenAlaHisHis 5  
Db 222 CACAATGCGCACAC 208  
RESULT 9  
AF479986  
LOCUS Saccharomyces cerevisiae YAL068W-A gene, complete cds.  
DEFINITION  
ACCESSION AF479986  
VERSION AF479986.1 GI:18767167  
KEYWORDS  
SOURCE Saccharomyces cerevisiae (baker's yeast)  
ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE  
AUTHORS Kumar, A., Harrison, P.M., Cheung, K.H., Lan, N., Echols, N.,  
Bertone, P., Miller, P., Gerstein, M.B. and Snyder, M.  
TITLE An integrated approach for finding overlooked genes in yeast  
JOURNAL Nat. Biotechnol. 20 (1), 58-63 (2002)  
MEDLINE 21624570  
PUBMED 11753363

REFERENCE 2 (bases 1 to 255)  
AUTHORS Kumar, A., Paul, H.M., Cheung, K.H., Lan, N., Echols, N., Bertone, P.,  
Miller, P., Gerstein, M.B. and Snyder, M.  
TITLE Direct Submission  
JOURNAL Submitted (01-FEB-2002) MCD Biology, Yale University, P.O. Box  
208103, New Haven, CT 06520-8103, USA  
LOCATION/Qualifiers

## FEATURES

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IPLHLHLLTTFYTYVNVITEKSPQKSPKHNILLFNNT"

## ORIGIN

Alignment Scores:  
Pred. No.: 689 Length: 255  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF479986 (1-255)

Qy 1 HisAenAlaHisHis 5  
Db 46 CATACGCGCACAT 60

## RESULT 10

AF688473S1/ c AF688473S1 261 bp DNA linear PLN 14-AUG-2004  
LOCUS Balduina uniflora clone BUI1S1 internal transcribed spacer 1,  
DEFINITION partial sequence.  
ACCESSION AF688473  
VERSION AF688473.1 GI:51039204  
KEYWORDS  
SEGMENT 1 of 2  
SOURCE Balduina uniflora

ORGANISM Balduina uniflora  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Helenieae; Balduina.  
REFERENCE 1 (bases 1 to 261)  
AUTHORS Simurda, M.C., Marshall, D.C. and Knox, J.S.  
TITLE Phylogeography of the narrow endemic, *Helenium virginicum*  
(Asteraceae), based upon ITS sequence comparisons  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 261)  
AUTHORS Simurda, M.C., Marshall, D.C. and Knox, J.S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2004) Biology, Washington and Lee University,  
Lexington, VA 24450-0303, USA  
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source  
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misc\_RNA  
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/product="internal transcribed spacer 1"  
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Pred. No.: 705 Length: 261  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0  
US-10-029-756-12 (1-5) x AY688473S1 (1-261)  
Qy 1 HisAenAlaHisHis 5  
Db 142 CACAATGCCCATCAT 128  
RESULT 11  
LOCUS AX801775 311 bp DNA linear PAT 24-NOV-2003  
DEFINITION Sequence 9 from Patent WO03057867.  
ACCESSION AX801775  
VERSION AX801775.1 GI:38500699  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Xiao, Y.  
TITLE Regulation of human fatty acid CoA ligase-like AMP-binding enzyme  
JOURNAL Patent: WO 03057867-A 9 17-JUL-2003;  
Bayer Aktiengesellschaft (DE)  
FEATURES  
source  
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Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-029-756-12 (1-5) x AX801775 (1-311)  
Qy 1 HisAenAlaHisHis 5

Db 264 CACAATGCCCATCAT 250  
RESULT 12  
LOCUS AY208086 313 bp RNA linear VRL 19-APR-2003  
DEFINITION Human coxsackievirus A16 strain C6292-115/99 VPI gene, partial cds.  
ACCESSION AY208086  
VERSION AY208086.1 GI:30025149  
KEYWORDS  
SOURCE Human coxsackievirus A16  
ORGANISM Human coxsackievirus A16  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 313)  
AUTHORS Norder, H., Bjerregaard, L., Magnus, L.O., Lina, B., Aymard, M. and  
Chomel, J.J.  
TITLE Sequencing of 'untypable' enteroviruses reveals two new types,  
EV-77 and EV-78, within human enterovirus type B and substitutions  
in the BC loop of the VP1 protein for known types  
JOURNAL J. Gen. Virol. 84 (Pt 4), 827-836 (2003)  
MEDLINE 22541853  
PUBMED 12655083  
REFERENCE 2 (bases 1 to 313)  
AUTHORS Norder, H., Bjerregaard, L., Magnus, L.O., Lina, B., Aymard, M. and  
Chomel, J.J.  
TITLE Direct Submission  
JOURNAL Submitted (27-DEC-2002) Virological Department, Swedish Institute  
for Infectious Disease Control, Hepatitis Section, Solna SE- 171  
82, Sweden  
FEATURES  
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/mol\_type="genomic RNA"  
/strain="C6292-115/99"  
/db\_xref="taxon:31704"  
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/product="VP1"  
/protein\_id="AAP04537.1"  
/db\_xref="GI:30025150"  
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GTQNTGVDVNDIDLMDGYAQRKRCLEFTYMRFAEFTFVVKENGELVPLLQTMFV  
PP"  
ORIGIN  
Alignment Scores:  
Pred. No.: 835 Length: 313  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0  
US-10-029-756-12 (1-5) x AY208086 (1-313)  
Qy 1 HisAenAlaHisHis 5  
Db 117 CACAATGCCCATCAT 131  
RESULT 13  
LOCUS AY558170 315 bp DNA linear PLN 14-MAR-2004  
DEFINITION Saccharomyces cerevisiae clone PLH110982.01X YAL069W gene, complete  
cds.  
ACCESSION AY558170  
VERSION AY558170.1 GI:45270229  
KEYWORDS Yeast ORF Project.  
SOURCE Saccharomyces cerevisiae (baker's yeast)  
ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
REFERENCE 1 (bases 1 to 315)

**AUTHORS** Marsischky, G., Rolfs, A., Richardson, A., Kane, M., Baqui, M., Taycher, E., Hu, Y., Vamberg, F., Weger, J., Kramer, J., Moreira, D., Kelley, F., Zuo, D., Raphael, J., Hogle, C., Jepsen, D., Williamson, J., Camargo, A., Gonzaga, L., Vasconcelos, A.T., Simpson, A., Kolodner, R., Harlow, E. and LaBaer, J.

**TITLE** Creation of the YFLX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system

**JOURNAL** Unpublished

**REFERENCE** 2 (bases 1 to 315)

**AUTHORS** Marsischky, G., Rolfs, A., Richardson, A., Kane, M., Baqui, M., Taycher, E., Hu, Y., Vamberg, F., Weger, J., Kramer, J., Moreira, D., Kelley, F., Zuo, D., Raphael, J., Hogle, C., Jepsen, D., Williamson, J., Camargo, A., Gonzaga, L., Vasconcelos, A.T., Simpson, A., Kolodner, R., Harlow, E. and LaBaer, J.

**TITLE** Direct Submission

**JOURNAL** Submitted (17-FEB-2004) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA

**COMMENT** This clone is part of a collection of Saccharomyces cerevisiae full-length ORF clones generated by the Harvard Institute of Proteomics. Each CDS has been cloned with its native stop-codon. The CDS has been directionally cloned using the Gateway cloning system into the donor vectors pDONR 201 or pDONR 221. Additional sequences in the clone: 'TCCAGCTGACCAC' after the attL1 site and before the 'ATG' (from Research Genetics primers used to amplify the ORFs, including a Kozak consensus sequence); 'ATCCCGGAATGCCATG' after the stop codon and before the attL2 site (from the Research Genetics primers used to amplify the ORFs).

**FEATURES** Location/Qualifiers

source

1..315

/organism="Saccharomyces cerevisiae"

/mol\_type="genomic DNA"

/db\_xref="taxon:4932"

/clone="FLH10982.01X"

/lab\_host="Escherichia coli DH5alpha T1 resistant"

<1..>315

/product="YAL069W"

1..315

/codon\_start=1

/product="YAL069W"

/protein\_id="AAS56496.1"

/db\_xref="GI:45270230"

/translation="MIVNTHVLPLPLVTTTCTHPLHTDFTYAGCYSIYHLKLTLLSDSTSLHGSPSLTESVFNALSLTALASAVYTLCHLPITPIIIHLISHSVFNIV"

**ORIGIN**

Alignment Scores:

Pred. No.: 840 Length: 315

Score: 840 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AY558170 (1-315)

**Qy** 1 HisAenAlaHisHis 5

**Db** 249 CATAACGCCCATCAT 263

**RESULT 14** AR358244/c

**LOCUS** AR358244

**DEFINITION** Sequence 4362 from patent US 6593114.

**ACCESSION** AR358244

**VERSION** AR358244.1 GI:33764328

**KEYWORDS** Unknown.

**SOURCE** Unknown.

**ORGANISM** Unknown.

**REFERENCE** 1 (bases 1 to 316)

**AUTHORS** Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and

**TITLE** Rosen, C.A.

**JOURNAL** Staphylococcus aureus polynucleotides and sequences

**FEATURES** Patent: US 6593114-A 4362 15-JUL-2003; Location/Qualifiers

source

1..316

/organism="unknown"

/mol\_type="genomic DNA"

**ORIGIN**

Alignment Scores:

Pred. No.: 842 Length: 316

Score: 842 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR358244 (1-316)

**Qy** 1 HisAenAlaHisHis 5

**Db** 205 CATAACGCCCATCAT 191

**RESULT 15** AR539800/c

**LOCUS** AR539800

**DEFINITION** Sequence 4362 from patent US 6737248.

**ACCESSION** AR539800

**VERSION** AR539800.1 GI:53931017

**KEYWORDS** Unknown.

**SOURCE** Unknown.

**ORGANISM** Unknown.

**REFERENCE** 1 (bases 1 to 316)

**AUTHORS** Kunsch, C.A., Choi, G.A., Barash, S., Dillon, P.J., Fannon, M.R. and Rosen, C.A.

**TITLE** Staphylococcus aureus polynucleotides and sequences

**JOURNAL** Patent: US 6737248-A 4362 18-MAY-2004; Location/Qualifiers

source

1..316

/organism="unknown"

/mol\_type="genomic DNA"

**ORIGIN**

Alignment Scores:

Pred. No.: 842 Length: 316

Score: 842 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR539800 (1-316)

**Qy** 1 HisAenAlaHisHis 5

**Db** 205 CATAACGCCCATCAT 191

**RESULT 16** CQ433519

**LOCUS** CQ433519

**DEFINITION** Sequence 18553 from Patent WO0151629.

**ACCESSION** CQ433519

**VERSION** CQ433519.1 GI:41385748

**KEYWORDS** Homo sapiens (human)

**SOURCE** Homo sapiens

**ORGANISM** Homo sapiens

**REFERENCE** 1

**AUTHORS** Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.

**TITLE** Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer

JOURNAL Patent: WO 0151628-A 18553 19-JUL-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..321  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 855 Length: 321  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ433519 (1-321)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 83 CACAATGCACATCAT 97  
|||||

RESULT 17  
AY208082 AY208082 323 bp RNA linear VRL 19-APR-2003  
LOCUS Human coxsackievirus A16 strain 98/01154-39/99 VP1 gene, partial  
DEFINITION cds,  
ACCESSION AY208082  
VERSION AY208082.1 GI:30025142  
KEYWORDS Human coxsackievirus A16  
SOURCE Viruses; ssRNA positive-strand viruses, no DNA stage;  
ORGANISM Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 323)  
AUTHORS Norder, H., Bjerregaard, L., Magnus, L.O., Lina, B., Aymard, M. and Chomel, J.J.  
TITLE Sequencing of 'untypable' enteroviruses reveals two new types, EV-77 and EV-78, within human enterovirus type B and substitutions in the BC loop of the VP1 protein for known types  
JOURNAL J. Gen. Virol. 84 (Pt 4), 827-836 (2003)  
MEDLINE 22541853  
PUBMED 12655083  
REFERENCE 2 (bases 1 to 323)  
AUTHORS Norder, H., Bjerregaard, L., Magnus, L.O., Lina, B., Aymard, M. and Chomel, J.J.  
TITLE Direct Submission  
JOURNAL Submitted (27-DEC-2002) Virological Department, Swedish Institute for Infectious Disease Control, Hepatitis Section, Solna SE- 171 82, Sweden  
FEATURES Location/Qualifiers  
source 1..323  
/organism="Human coxsackievirus A16"  
/mol\_type="genomic RNA"  
/strain="98/01154-39/99"  
/db\_xref="taxon:31704"  
<1\_->323  
/codon\_start=1  
/product="VP1"  
/protein\_id="AAP04534.1"  
/db\_xref="GI:30025143"  
/translation="QAARTGASNASDKNLIETRCVLNHHSTQETAIQNFPSRAGLVSLIITWPTGTQNTDGVNWDIDLMGVQLRRKCELFYMRFDATFFVAKENGELVPLVQLQYM"

CDS  
860 Length: 323  
34.00 Matches: 5  
100.00% Conservative: 0  
100.00% Mismatches: 0  
100.00% Indels: 0

ORIGIN

Alignment Scores:  
Pred. No.: 860 Length: 323  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0

US-10-029-756-12 (1-5) x AY208082 (1-323)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 138 CACAATGCCACCAC 152  
|||||

RESULT 18  
AX312622 AX312622 325 bp DNA linear PAT 14-DEC-2001  
LOCUS Sequence 5607 from Patent WO0190366.  
DEFINITION AX312622  
ACCESSION AX312622  
VERSION AX312622.1 GI:17897541  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Leach, M.D. and Shinkets, R.A.  
TITLE Human polynucleotides and polypeptides encoded thereby  
JOURNAL Patent: WO 0190366-A 5607 29-NOV-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..325  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 865 Length: 325  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX312622 (1-325)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 217 CACAATGCCACCAC 231  
|||||

RESULT 19  
GI6708/c GI6708 329 bp DNA linear STS 06-MAR-1996  
LOCUS human STS SHGC-3920 clone pg-1554, sequence tagged site.  
DEFINITION GI6708  
ACCESSION GI6708  
VERSION GI6708.1 GI:1214134  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 329)  
AUTHORS Myers, R.M.  
JOURNAL Unpublished (1996)  
COMMENT Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu  
Primer A: TCTTGTCCCTTTTCGTCCATCC  
Primer B: ATAAGTAGATTTCATATGCACACC  
STS size: 176  
PCR Profile:  
Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30  
 Thermal Cycler: Perkin Elmer 9600

Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3

Chromosome 4.  
 Location/Qualifiers  
 source  
 1..329  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /map="4"  
 3..178  
 3..25  
 complement (154..178)

STS  
 primer\_bind  
 primer\_bind

Alignment Scores:  
 Pred. No.: 875 Length: 329  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x G16708 (1-329)

Qy 1 HisAenAlaHisHis 5  
 |||||  
 Db 166 CATAATGCACCAT 152

RESULT 20  
 G34525/c  
 LOCUS human STS SHGC-60109, sequence tagged site. STS 01-JUL-1997  
 DEFINITION  
 G34525  
 G34525  
 G34525.1 GI:2227829  
 VERSION STS; STS sequence; primer; sequence tagged site.  
 KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 329)  
 Myers,R.M.  
 Unpublished (1997)

Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu

Primer A: TTGTGTCCTCTTATGTTGTC  
 Primer B: CTCATAACAGTGACTTCACCC  
 STS size: 121  
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30  
 Thermal Cycler: Perkin Elmer 9600

Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3

Redeveloped chromosome 21 markers for scoring on oligonucleotide arrays. Designed and developed at the Stanford Human Genome Center on sequences previously developed as STSs at the Stanford Human Genome Center, the Whitehead Institute or TIGR, as well as sequence available in the public databases for chromosome 21.

FEATURES  
 source  
 1..329  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /map="4"  
 139..259  
 139..160  
 complement (236..259)

STS  
 primer\_bind  
 primer\_bind

Alignment Scores:  
 Pred. No.: 875 Length: 329  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x G34525 (1-329)

Qy 1 HisAenAlaHisHis 5  
 |||||  
 Db 166 CATAATGCACCAT 152

RESULT 21  
 AR378808/c  
 LOCUS AR378808 333 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 3814 from patent US 6605709.  
 ACCESSION AR378808  
 VERSION AR378808.1 GI:40081990

KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 333)  
 Breton,G.L.

TITLE  
 Nucleic acid and amino acid sequences relating to Proteus mirabilis  
 for diagnostics and therapeutics  
 JOURNAL Patent: US 6605709-A 3814 12-AUG-2003;  
 FEATURES Location/Qualifiers  
 source  
 1..333  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 885 Length: 333  
 Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR378808 (1-333)

Qy 1 HisaenAlahisHis 5  
Db 205 CACAATGCGCACCAC 191

RESULT 22  
CQ415760 343 bp DNA linear PAT 28-JAN-2004  
LOCUS  
DEFINITION Sequence 794 from Patent WO0151628.  
ACCESSION CQ415760  
VERSION CQ415760.1 GI:41367989  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.  
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer  
JOURNAL Patent: WO 0151628-A 794 19-JUL-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
source  
1. 343  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 909 Length: 343  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ415760 (1-343)

Qy 1 HisaenAlahisHis 5  
Db 104 CACAATGCGCACCAC 118

RESULT 23  
CQ425403 345 bp DNA linear PAT 28-JAN-2004  
LOCUS  
DEFINITION Sequence 10437 from Patent WO0151628.  
ACCESSION CQ425403  
VERSION CQ425403.1 GI:41377632  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.  
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer  
JOURNAL Patent: WO 0151628-A 10437 19-JUL-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
source  
1. 345  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 914 Length: 345  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ425403 (1-345)

Qy 1 HisaenAlahisHis 5  
Db 104 CACAATGCGCACCAC 118

RESULT 24  
CQ4158018 348 bp DNA linear PAT 17-AUG-2003  
LOCUS  
DEFINITION Sequence 4136 from patent US 6593114.  
ACCESSION AR358018  
VERSION AR358018.1 GI:33764102  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 348)  
AUTHORS Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and Rosen, C.A.  
TITLE Staphylococcus aureus polynucleotides and sequences  
JOURNAL Patent: US 6593114-A 4136 15-JUL-2003;  
Location/Qualifiers  
source  
1. 348  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 922 Length: 348  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR358018 (1-348)

Qy 1 HisaenAlahisHis 5  
Db 144 CACAATGCGCACCAC 158

RESULT 25  
AR539574 348 bp DNA linear PAT 08-OCT-2004  
LOCUS  
DEFINITION Sequence 4136 from patent US 6737248.  
ACCESSION AR539574  
VERSION AR539574.1 GI:53930791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 348)  
AUTHORS Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and Rosen, C.A.  
TITLE Staphylococcus aureus polynucleotides and sequences  
JOURNAL Patent: US 6737248-A 4136 18-MAY-2004;  
Location/Qualifiers  
source  
1. 348  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 922 Length: 348  
Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR539574 (1-348)

QY 1 HisAsnAlaHis 5  
 Db 144 CATAACGCATCAT 158

RESULT 26  
 AF154077/c  
 LOCUS AF154077 358 bp DNA linear PLN 16-FEB-2001  
 DEFINITION Rhizopogon vinicolor clone Rv15 microsatellite sequence.  
 ACCESSION AF154077  
 VERSION AF154077.1 GI:8347141  
 KEYWORDS  
 SOURCE Rhizopogon vinicolor  
 ORGANISM Rhizopogon vinicolor  
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 Boletales; Suillineae; Rhizopogonaceae; Rhizopogon.  
 REFERENCE 1 (bases 1 to 358)  
 AUTHORS Kretzer,A.M., Molina,R. and Spatafora,J.W.  
 TITLE Microsatellite markers for the ectomycorrhizal basidiomycete  
 Rhizopogon vinicolor  
 JOURNAL Mol. Ecol. 9 (8), 1190-1191 (2000)  
 MEDLINE 20427187  
 PUBMED 10964248  
 REFERENCE 2 (bases 1 to 358)  
 AUTHORS Kretzer,A.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-MAY-1999) Botany and Plant Pathology, Oregon State  
 University, 2082 Cordley Hall, Corvallis, OR 97331, USA

FEATURES  
 source 1..358  
 repeat\_region 1..358  
 /organism="Rhizopogon vinicolor"  
 /mol\_type="genomic DNA"  
 /strain="T20787"  
 /db\_xref="taxon:80600"  
 /clone="Rv15"  
 /note="microsatellite"  
 /rpt\_type=tandem

ORIGIN  
 Alignment Scores:  
 Pred. No.: 947 Length: 358  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF154077 (1-358)

QY 1 HisAsnAlaHis 5  
 Db 84 CATAATGCCATCAT 70

RESULT 27  
 AX413277/c  
 LOCUS AX413277 366 bp DNA linear PAT 02-SEP-2002  
 DEFINITION Sequence 268 from Patent WO0228891.  
 ACCESSION AX413277  
 VERSION AX413277.1 GI:21445734  
 KEYWORDS  
 SOURCE Listeria innocua  
 ORGANISM Listeria innocua  
 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 REFERENCE 1  
 AUTHORS Kunst,F. and Glaser,P.  
 TITLE Listeria innocua, genome and applications

JOURNAL Patent: WO 0228891-A 268 11-APR-2002;  
 INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE  
 SCIENTIFIQUE (CNRS) (FR)

FEATURES  
 source 1..366  
 /organism="Listeria innocua"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:1642"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 966 Length: 366  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX413277 (1-366)

QY 1 HisAsnAlaHis 5  
 Db 94 CACACGCTCACCAC 80

RESULT 28  
 AX415103/c  
 LOCUS AX415103 366 bp DNA linear PAT 02-SEP-2002  
 DEFINITION Sequence 2094 from Patent WO0228891.  
 ACCESSION AX415103  
 VERSION AX415103.1 GI:21447560  
 KEYWORDS  
 SOURCE Listeria innocua  
 ORGANISM Listeria innocua  
 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 REFERENCE 1  
 AUTHORS Kunst,F. and Glaser,P.  
 TITLE Listeria innocua, genome and applications  
 JOURNAL Patent: WO 0228891-A 2094 11-APR-2002;  
 INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE  
 SCIENTIFIQUE (CNRS) (FR)

FEATURES  
 source 1..366  
 /organism="Listeria innocua"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:1642"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 966 Length: 366  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX415103 (1-366)

QY 1 HisAsnAlaHis 5  
 Db 94 CACACGCTCACCAC 80

RESULT 29  
 AR074124/c  
 LOCUS AR074124 380 bp DNA linear PAT 28-AUG-2000  
 DEFINITION Sequence 33 from patent US 5952486.  
 ACCESSION AR074124  
 VERSION AR074124.1 GI:10000884  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 380)  
 AUTHORS Bloksberg,L.N., Havukkala,I. and Grierson,A.W.



TITLE Materials and methods for the modification of plant lignin content  
JOURNAL Patent: US 5952486-A 33 14-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..380  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1e+03 Length: 380  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR074124 (1-380)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 50 CACAACGCTCACCAT 36

RESULT 30  
BD224309/c  
LOCUS BD224309 380 bp DNA linear PAT 17-JUL-2003  
DEFINITION Materials and methods for the modification of plant lignin content.  
ACCESSION BD224309  
VERSION BD224309.1 GI:33034079  
KEYWORDS JP 2002527058-A/33.  
SOURCE Eucalyptus grandis  
ORGANISM Eucalyptus grandis

REFERENCE 1 (bases 1 to 380)  
AUTHORS Bloksberg,L.N. and Havukkala,I.J.  
TITLE Materials and methods for the modification of plant lignin content  
JOURNAL Patent: JP 2002527058-A 33 27-AUG-2002;  
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE  
FORESTS LTD

COMMENT OS Eucalyptus grandis  
PN JP 2002527058-A/33  
PD 27-AUG-2002  
PF 06-OCT-1999 JP 2000575991  
PR 09-OCT-1998 US 09/169789,14-JUL-1999 US 60/143811 PI  
LEONARD NATHAN BLOKSBERG,ILKKA JAAKKO HAVUKKALA PC  
C12N15/09,A01H5/00,C12N5/10,C12N9/02,C12N9/04,C12N9/ PC  
10,C12N9/24,  
PC C12N9/88,C12N15/00,C12N5/00  
CC Materials and methods for the modification of plant lignin CC

FH Key Location/Qualifiers  
FT source 1..380  
/organism='Eucalyptus grandis'.  
FT Location/Qualifiers

FEATURES  
source 1..380  
/organism="Eucalyptus grandis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:71139"

## ORIGIN

Alignment Scores:  
Pred. No.: 1e+03 Length: 380  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD224309 (1-380)

Qy 1 HisAenAlaHisHis 5  
|||||

Db 50 CACAACGCTCACCAT 36

RESULT 31  
BD273006/c

LOCUS BD273006 380 bp DNA linear PAT 17-JUL-2003  
DEFINITION Materials and methods for the modification of isoprenoid content,  
composition and metabolism.  
ACCESSION BD273006  
VERSION BD273006.1 GI:33082774  
KEYWORDS JP 2002541764-A/73.  
SOURCE Eucalyptus grandis  
ORGANISM Eucalyptus grandis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Myrtales; Myrtaceae; Eucalyptus.  
REFERENCE 1 (bases 1 to 380)  
AUTHORS Havukkala,I.J.  
TITLE Materials and methods for the modification of isoprenoid content,  
composition and metabolism  
JOURNAL Patent: JP 2002541764-A 73 10-DEC-2002;  
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE  
FORESTS INDUSTRIES LTD

COMMENT OS Eucalyptus grandis (flooded gum)  
PN JP 2002541764-A/73  
PD 10-DEC-2002  
PF 16-DEC-1999 JP 2000588332  
PR 17-DEC-1998 US 09/215504,29-JUL-1999 US 60/146441 PI  
ILKKA JAAKKO HAVUKKALA

PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/  
PC 10,C12N9/00,  
PC C12Q1/69,C12N15/00,C12N5/00,C12N5/00  
CC Materials and methods for the modification of isoprenoid CC  
content,  
CC composition and metabolism  
FH Key Location/Qualifiers  
FT source 1..380  
/organism='Eucalyptus grandis (flooded gum)'.  
FT Location/Qualifiers

FEATURES  
source 1..380  
/organism="Eucalyptus grandis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:71139"

## ORIGIN

Alignment Scores:  
Pred. No.: 1e+03 Length: 380  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD273006 (1-380)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 50 CACAACGCTCACCAT 36

RESULT 32  
AR216359/c

LOCUS AR216359 380 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 33 from patent US 6410718.  
ACCESSION AR216359  
VERSION AR216359.1 GI:23314839  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 380)  
AUTHORS Bloksberg,L.N. and Havukkala,I.  
TITLE Materials and methods for the modification of plant lignin content  
JOURNAL Patent: US 6410718-A 33 25-JUN-2002;  
FEATURES Location/Qualifiers

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source      1. .380
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      1e+03      Length:      380
Score:          34.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%  Indels:      0
DB:            6          Gaps:      0

US-10-029-756-12 (1-5) x AR216359 (1-380)

Qy      1 HisAenAlaHisHis 5
Db      50 CACAACGCTCACCAT 36

RESULT 33
AR432761/c      AR432761      380 bp      DNA      linear      PAT 18-DEC-2003
LOCUS
DEFINITION      Sequence 33 from patent US 6653528.
ACCESSION      AR432761
VERSION      AR432761.1 GI:40195364
KEYWORDS
SOURCE      unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 380)
AUTHORS      Bloksberg,L.N. and Havukkala,I.
TITLE      Pinus radiata nucleic acids encoding O-methyl transferase and
            methods for the modification of plant lignin content therewith
JOURNAL      Patent: US 6653528-A 33 25-NOV-2003;
FEATURES
            Location/Qualifiers
            source      1. .380
                        /organism="unknown"
                        /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      1e+03      Length:      380
Score:          34.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%  Indels:      0
DB:            6          Gaps:      0

US-10-029-756-12 (1-5) x AR432761 (1-380)

Qy      1 HisAenAlaHisHis 5
Db      50 CACAACGCTCACCAT 36

RESULT 34
BD005672/c      BD005672      380 bp      DNA      linear      PAT 31-JAN-2002
LOCUS
DEFINITION      Materials and methods for the modification of plant lignin content.
ACCESSION      BD005672
VERSION      BD005672.1 GI:18634043
KEYWORDS      JP 2001500378-A/33.
SOURCE      unidentified
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 380)
AUTHORS      Bloksberg,L.N., Grierson,A.W. and Havukkala,I.J.
TITLE      Materials and methods for the modification of plant lignin content
JOURNAL      Patent: JP 2001500378-A 33 16-JAN-2001;
            GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS
            LTD
COMMENT      OS      Unidentified
            PN      JP 2001500378-A/33
            PD      16-JAN-2001

```

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PF      10-SEP-1997 JP 1998513535
PR      11-SEP-1996 US      08/713000
PI      LEONARD NATHAN BLOKSBERG,ALISTAIR WALLACE GRIERSON, PI      ILKKA
JAAKKO HAVUKKALA
PC      C12N15/53,C12N15/54,C12N15/52,C12N15/60,C12N15/82,A01H5/00 CC
Strandedness: Single;
CC      Topology: Linear;
FH      Key      Location/Qualifiers
FT      source      1. .380
            Location/Qualifiers
            1. .380
            /organism="Unidentified".
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.:      1e+03      Length:      380
Score:          34.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%  Indels:      0
DB:            6          Gaps:      0

US-10-029-756-12 (1-5) x BD005672 (1-380)

Qy      1 HisAenAlaHisHis 5
Db      50 CACAACGCTCACCAT 36

RESULT 35
HSA272XC9      H.sapiens (D1S2682) DNA segment containing (CA) repeat; clone
LOCUS
DEFINITION      AFMa272xc9; single read, sequence tagged site.
ACCESSION      Z52721
VERSION      Z52721.1 GI:1234021
KEYWORDS      STS; CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA;
            microsatellite marker; repeat polymorphism.
SOURCE      Homo sapiens
            Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 380)
AUTHORS      Dib,C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A.,
            Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyapay,G.,
            Morissette,J. and Weissenbach,J.
            A comprehensive genetic map of the human genome based on 5,264
            microsatellites
            Nature 380 (6570), 152-154 (1996)
JOURNAL
MEDLINE      96176476
PUBMED      8600387
REFERENCE      2 (bases 1 to 380)
AUTHORS      Weissenbach,J.
TITLE      Direct Submission
JOURNAL      Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
COMMENT      E-mail: Jean.Weissenbach@genethon.fr
            full automatic.
FEATURES
            Location/Qualifiers
            source      1. .380
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="1"
                        /cell_line="CEPH 134702"
                        /clone_lib="genomic DNA"
                        /note="Cloning vector is M13mp18"

ORIGIN
Alignment Scores:
Pred. No.:      1e+03      Length:      380
Score:          34.00      Matches:      5

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x HSA272XC9 (1-380)

Qy 1 HisAenAlaHis 5
| | | | | | | | | |
Db 290 CACAATGCATCAT 304

RESULT 36
HSP48H04 394 bp DNA linear STS 21-MAY-1998
DEFINITION H.sapiens flow-sorted chromosome 1 HindIII fragment, SCIP48H04,
sequence tagged site.
ACCESSION AL010086
VERSION AL010086.1 GI:2665248
KEYWORDS STS; single read.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 394)
AUTHORS Gregory,S., Kettleborough,R., Langford,C., Ross,M.T. and Hunt,S.E.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1997) E-mail contact: humquery@sanger.ac.uk
COMMENT Vector: pBS1ISK+
Marker stS3252FS (Primer A : TCTCTGAGTCCCAACATC; Primer B :
AGGCGGTATCCAGCTG; amplimer size : 134 bp) was mapped to
chromosome 1 using Radiation Hybrid
panel Genebridge 4 (GB4).
FEATURES
source
1..394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="SCIP48H04"
/sex="female"
/tissue_type="EBV lymphoblastoid cell line"
/clone_lib="SCIPe"
/dev_stage="adult"

ORIGIN
Alignment Scores: 1.04e+03 Length: 394
Pred. No.: 34.00 Matches: 5
Score: 34.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 11

US-10-029-756-12 (1-5) x HSP48H04 (1-394)

Qy 1 HisAenAlaHis 5
| | | | | | | | | |
Db 118 CACAATGCATCAT 132

RESULT 37
AF333188/c 395 bp mRNA linear VRT 24-JUL-2001
LOCUS AF333188
DEFINITION Oncorhynchus mykiss fructose-1,6-bisphosphatase mRNA, partial cds.
ACCESSION AF333188
VERSION AF333188.1 GI:15004314
KEYWORDS Oncorhynchus mykiss (rainbow trout)
SOURCE Oncorhynchus mykiss
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 395)
AUTHORS Panseerat,S., Plagnes-Juan,E. and Kaushik,S.

Nutritional regulation and tissue specificity of gene expression
for proteins involved in hepatic glucose metabolism in rainbow
trout (Oncorhynchus mykiss)
J. Exp. Biol. 204 (Pt 13), 2351-2360 (2001)
MEDLINE 21398391
PUBMED 11507117
REFERENCE 2 (bases 1 to 395)
AUTHORS Panseerat,S., Plagnes-Juan,E. and Kaushik,S.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2001) INRA-IFREMER Fish Nutrition Laboratory,
INRA, St-Pee-sur-Nivelle 64310, France
FEATURES
source
1..395
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
<1_>395
/EC_number="3.1.3.11"
/note="FBPase"
/codon_start=1
/product="fructose-1,6-bisphosphatase"
/protein_id="AAK77025.1"
/db_xref="GI:15004315"
/translation="PLDSSNIDCLVSGITFAIYRKTDDPNERDALQSGRHIVAA
GYALYGSATMMVLSTGGVNCFLMDPSIGEFILTDKDVKKIKRGKIYSLNEGFAOHFY
PDVTEYLKKKKYPEDSGAPYGRYVGSMAV"

ORIGIN
Alignment Scores: 1.04e+03 Length: 395
Pred. No.: 34.00 Matches: 5
Score: 34.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 5

US-10-029-756-12 (1-5) x AF333188 (1-395)

Qy 1 HisAenAlaHis 5
| | | | | | | | | |
Db 379 CATACGCCACCAT 365

RESULT 38
AR357625 400 bp DNA linear PAT 17-AUG-2003
LOCUS AR357625
DEFINITION Sequence 3743 from patent US 6593114.
ACCESSION AR357625
VERSION AR357625.1 GI:33763709
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 400)
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 3743 15-JUL-2003;
FEATURES
source
1..400
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores: 1.05e+03 Length: 400
Pred. No.: 34.00 Matches: 5
Score: 34.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-12 (1-5) x AR357625 (1-400)

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```

Qy      1 HisAenAlaHisHis 5
Db      79 CATAACGCACATCAT 93

RESULT 39
LOCUS   AR539181
DEFINITION Sequence 3743 from patent US 6737248.
ACCESSION AR539181
VERSION   AR539181.1 GI:53930398
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 400)
AUTHORS   Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
           Rosen,C.A.
TITLE     Staphylococcus aureus polynucleotides and sequences
JOURNAL   Patent: US 6737248-A 3743 18-MAY-2004;
FEATURES   Location/Qualifiers
            source
              1..400
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      1.05e+03      Length:      400
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              6           Gaps:        0

US-10-029-756-12 (1-5) x AR539181 (1-400)

Qy      1 HisAenAlaHisHis 5
Db      79 CATAACGCACATCAT 93

RESULT 40
LOCUS   AX801776
DEFINITION Sequence 10 from Patent WO03057867.
ACCESSION AX801776
VERSION   AX801776.1 GI:38500700
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS   Xiao,X.
TITLE     Regulation of human fatty acid CoA ligase-like AMP-binding enzyme
JOURNAL   Patent: WO 03057867-A 10 17-JUL-2003;
           Bayer Aktiengesellschaft (DE)
FEATURES   Location/Qualifiers
            source
              1..413
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:      1.08e+03      Length:      413
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              6           Gaps:        0

US-10-029-756-12 (1-5) x AX801776 (1-413)

Qy      1 HisAenAlaHisHis 5

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```

Db      138 CACAATGCACATCAT 152

RESULT 41
LOCUS   BD224391/c
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD224391
VERSION   BD224391.1 GI:33034161
KEYWORDS
SOURCE   Eucalyptus grandis
ORGANISM
REFERENCE 1 (bases 1 to 420)
AUTHORS   Bloksberg,L.N. and Havukkala,I.J.
TITLE     Materials and methods for the modification of plant lignin content
JOURNAL   Patent: JP 2002527058-A 115 27-AUG-2002;
           GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
           FORESTS LTD
COMMENT   OS Eucalyptus grandis
           PN JP 2002527058-A/115
           PD 27-AUG-2002
           PF 06-OCT-1999 JP 2000575991
           PR 09-OCT-1998 US 09/169789, 14-JUL-1999 US 60/143811 PI
           LEONARD NATHAN BLOKSBERG,ILKKA JAAKKO HAVUKKALA PC
           C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/02,C12N9/04,C12N9/04,
           10,C12N9/24,
           PC C12N9/88,C12N15/00,C12N5/00
           CC Materials and methods for the modification of plant lignin CC
           content
           FH Key
           FT source
           Location/Qualifiers
           1..420
           /organism="Eucalyptus grandis"
           /mol_type="genomic DNA"
           /db_xref="taxon:71139"

ORIGIN
Alignment Scores:
Pred. No.:      1.1e+03      Length:      420
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              6           Gaps:        0

US-10-029-756-12 (1-5) x BD224391 (1-420)

Qy      1 HisAenAlaHisHis 5
Db      80 CACAACGCCTCACCAT 66

RESULT 42
LOCUS   AR216441/c
DEFINITION Sequence 115 from patent US 6410718.
ACCESSION AR216441
VERSION   AR216441.1 GI:23314921
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 420)
AUTHORS   Bloksberg,L.N. and Havukkala,I.
TITLE     Materials and methods for the modification of plant lignin content
JOURNAL   Patent: US 6410718-A 115 25-JUN-2002;
           Location/Qualifiers
           1..420
           /organism="unknown"

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/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.1e+03 Length: 420  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR216441 (1-420)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 80 CACAACGCTCACCAT 66

## RESULT 43

AR432843/c  
LOCUS AR432843 420 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 115 from patent US 6653528.

ACCESSION AR432843

VERSION AR432843.1 GI:40195446

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 420)

Blosberg,J.N. and Havukkala,I.

Pinus radiata nucleic acids encoding O-methyl transferase and

methods for the modification of plant lignin content therewith

Patent: US 6653528-A 115 25-NOV-2003;

JOURNAL Location/Qualifiers

FEATURES

source

1..420

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.1e+03 Length: 420  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR432843 (1-420)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 80 CACAACGCTCACCAT 66

## RESULT 44

AX896634  
LOCUS AX896634 428 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 12497 from Patent EP1033401.

ACCESSION AX896634

VERSION AX896634.1 GI:40051518

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.

Expressed sequence tags and encoded human proteins

Patent: EP 1033401-A 12497 06-SEP-2000;

JOURNAL Genset (FR)

FEATURES

source

1..428

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.12e+03 Length: 428  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX896634 (1-428)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 109 CACAATGCACACCAC 123

## RESULT 45

BD032167  
LOCUS BD032167 428 bp DNA linear PAT 27-AUG-2002

DEFINITION Sequence tag and encoded human protein.

ACCESSION BD032167

VERSION BD032167.1 GI:22573909

KEYWORDS JP 2001269182-A/8413.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 428)

Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 8413 02-OCT-2001;

JOURNAL GENSET

COMMENT

OS Homo sapiens (human)

PN JP 2001269182-A/8413

PD 02-OCT-2001

PF 24-FEB-2000 JP 2000118773

PR 26-FEB-1999 US 60/122487

PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES

PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC

PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC

CC G06F15/40

FH Key

Location/Qualifiers.

FEATURES

source

1..428

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.12e+03 Length: 428  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD032167 (1-428)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 109 CACAATGCACACCAC 123

## RESULT 46

AR381260/c  
LOCUS AR381260 432 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 7 from patent US 6607914.

ACCESSION AR381260

VERSION AR381260.1 GI:40089066

KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 432)
AUTHORS      Belyavsky,A.V., Luchinskaya,N.N. and Popsueva,A.E.
TITLE        Camello gene family and uses thereof
JOURNAL      Patent: US 6607914-A 7 19-AUG-2003;
FEATURES     Location/Qualifiers
             source
               1..432
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      1.13e+03      Length:      432
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6            Gaps:        0

US-10-029-756-12 (1-5) x AR381260 (1-432)

Qy           1 HisAenAlaHisHis 5
Db           216 CACAATGCCACCAC 202

RESULT 47
AF221557
LOCUS        AF221557      437 bp      mRNA      linear      VRT 07-JUN-2001
DEFINITION   Gallus gallus bZIP transcription factor L-MAF mRNA, partial cds.
ACCESSION    AF221557
VERSION      AF221557.1 GI:7960153
KEYWORDS     .
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 437)
AUTHORS      Zhou,H., Liu,W. and Lamont,S.J.
TITLE        Genetic variation among chicken lines and mammalian species in
              specific genes
JOURNAL      Poult. Sci. 80 (3), 284-288 (2001)
MEDLINE      21158006
PUBMED       11261557
REFERENCE    2 (bases 1 to 437)
AUTHORS      Zhou,H. and Lamont,S.J.
TITLE        Direct Submission
JOURNAL      Submitted (06-JAN-2000) Animal Science, Iowa State University, 2255
              Kildee Hall, Ames, IA 50011, USA
FEATURES     Location/Qualifiers
             source
               1..437
               /organism="Gallus gallus"
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               /strain="breed G-B1 Leghorn"
               /db_xref="taxon:9031"
               /sex="female"
               /tissue type="spleen"
               <1..>437
               /note="MAFL"
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               /product="bZIP transcription factor L-MAF"
               /protein_id="AAF71239.1"
               /db_xref="GI:7960154"
               /translation="EALIGAPHHHHHHQSVESPRQPFQGEELPPAAHHHNAHHHH
               HHHLRERFSDQLVSMVRELNRQLRGFSKEVIRLKKRRTLKNRGYAQCRCYKR
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CDS
Alignment Scores:
Pred. No.:      1.14e+03      Length:      437
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             5            Gaps:        0

US-10-029-756-12 (1-5) x AF221558 (1-437)

Qy           1 HisAenAlaHisHis 5
Db           109 CACAACGCCACCAC 123

RESULT 49
HPUEXPRT1/c
LOCUS        HPUEXPRT1     443 bp      DNA      linear      BCT 10-OCT-2003
DEFINITION   Helicobacter pylori ORF1 for hypothetical protein, isolate PI-50.
ACCESSION    Z68311

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Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:        100.00%   Indels:      0
DB:                 5         Gaps:        0

US-10-029-756-12 (1-5) x AF221557 (1-437)

Qy           1 HisAenAlaHisHis 5
Db           109 CACAACGCCACCAC 123

RESULT 48
AF221558
LOCUS        AF221558      437 bp      mRNA      linear      VRT 07-JUN-2001
DEFINITION   Gallus gallus bZIP transcription factor L-MAF mRNA, partial cds.
ACCESSION    AF221558
VERSION      AF221558.1 GI:7960155
KEYWORDS     .
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 437)
AUTHORS      Zhou,H., Liu,W. and Lamont,S.J.
TITLE        Genetic variation among chicken lines and mammalian species in
              specific genes
JOURNAL      Poult. Sci. 80 (3), 284-288 (2001)
MEDLINE      21158006
PUBMED       11261557
REFERENCE    2 (bases 1 to 437)
AUTHORS      Zhou,H. and Lamont,S.J.
TITLE        Direct Submission
JOURNAL      Submitted (06-JAN-2000) Animal Science, Iowa State University, 2255
              Kildee Hall, Ames, IA 50011, USA
FEATURES     Location/Qualifiers
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               /mol_type="mRNA"
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               /tissue type="spleen"
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               /db_xref="GI:7960156"
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ORIGIN
Alignment Scores:
Pred. No.:      1.14e+03      Length:      437
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             5            Gaps:        0

US-10-029-756-12 (1-5) x AF221558 (1-437)

Qy           1 HisAenAlaHisHis 5
Db           109 CACAACGCCACCAC 123

RESULT 49
HPUEXPRT1/c
LOCUS        HPUEXPRT1     443 bp      DNA      linear      BCT 10-OCT-2003
DEFINITION   Helicobacter pylori ORF1 for hypothetical protein, isolate PI-50.
ACCESSION    Z68311

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VERSION      Z68311.1  GI:1419554
KEYWORDS     ORF1.
SOURCE       Helicobacter pylori
ORGANISM     Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
              Helicobacteraceae; Helicobacter.
REFERENCE    1 (bases 1 to 443)
AUTHORS     Odenbreit,S., Till,M. and Haas,R.
TITLE       Optimized Blam-transposon shuttle mutagenesis of Helicobacter
              pylori allows the identification of novel genetic loci involved in
              bacterial virulence
JOURNAL      Mol. Microbiol. 20 (2), 361-373 (1996)
MEDLINE      96310373
PUBMED       8733234
REFERENCE    2 (bases 1 to 422)
AUTHORS     Haas,R.
TITLE       Direct Submission
JOURNAL      Submitted (18-DEC-1995) Rainer Haas, Abteilung Infektionsbiologie,
              Max-Planck-Institut, fuer Biologie, Spemannstr. 34, Tuebingen,
              72076, GERMANY
FEATURES     source
              1..443
              /organism="Helicobacter pylori"
              /mol_type="genomic DNA"
              /strain="P1"
              /isolate="P1-50"
              /db_xref="taxon:210"
              /clone="pMu50"
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              /function="involved in flagellar motility"
              /note="ORF1"
              /codon_start=1
              /transl_table=11
              /product="hypothetical protein"
              /protein_id="CAA92653.1"
              /db_xref="GI:141955"
              /translation="MKKPKRIQSYAIIVGGLSALVMSIVGCKSNADPKPEQSSLSQ
              SVQKGAFLVLEQDKSKYKVVEYPSSTNTHIVRDQLQGNRVLSNEEIQKLKEEAK
              IDNGTSKLQVPNGSGNESS"
CDS          1..155+03 Length: 443
              Score: 34.00 Matches: 5
              Percent Similarity: 100.00% Conservative: 0
              Best Local Similarity: 100.00% Mismatches: 0
              Query Match: 100.00% Indels: 0
              DB: 1 Gaps: 0
US-10-029-756-12 (1-5) x HPUXPRT1 (1-443)
Qy          1 HisAenAlaHisHis 5
Db          154 CACAATGCTCCACAT 140
RESULT 50   CQ681194/c Q681194 500 bp DNA linear PAT 03-FEB-2004
LOCUS       CQ681194 Sequence 26120 from Patent WO02070737.
DEFINITION  CQ681194
ACCESSION   CQ681194
VERSION     CQ681194.1 GI:42198347
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE       Compositions and methods relating to osteoarthritis
JOURNAL      Patent: WO 02070737-A 26120 12-SEP-2002;
              Chondrogene Inc. (CA)
FEATURES     Location/Qualifiers
              1..155+03 Length: 500
              Score: 34.00 Matches: 5
              Percent Similarity: 100.00% Conservative: 0
              Best Local Similarity: 100.00% Mismatches: 0
              Query Match: 100.00% Indels: 0
              DB: 9 Gaps: 0
US-10-029-756-12 (1-5) x AF449188S1 (1-519)
Qy          1 HisAenAlaHisHis 5
Db          92 CACAATGCCACCAC 78
RESULT 51   AF449188S1 AF449188S1 519 bp DNA linear PRI 28-MAY-2002
LOCUS       AF449188S1 Homo sapiens hypothetical BLOCK27 gene, exon 1.
DEFINITION  AF449188S1
ACCESSION   AF449188S1
VERSION     AF449188.1 GI:21218162
KEYWORDS    1 of 4
SEGMENT     1
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 519)
AUTHORS     Cortelli,J.R., Pallos,D. and Hart,T.C.
TITLE       Physical/Genetic Map of the 2p22-2p21 Region on Chromosome 2
JOURNAL      Unpublished
KEYWORDS    2 (bases 1 to 519)
AUTHORS     Gorry,M.C., Zhang,Y., Marks,J.J., Suppe,B., Hart,P.S.,
              Cortelli,J.R., Pallos,D. and Hart,T.C.
TITLE       Direct Submission
JOURNAL      Submitted (20-NOV-2001) Oral Medicine/Pathology, University of
              Pittsburgh, School of Dental Medicine, 3501 Terrace Street, 614
              Salk Hall, Pittsburgh, PA 15261, USA
FEATURES     Location/Qualifiers
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              /evidence=not experimental
              complement(495..519)
              /note="X01-R"
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Alignment Scores:
Pred. No.: 1.34e+03 Length: 519
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-029-756-12 (1-5) x AF449188S1 (1-519)
Qy          1 HisAenAlaHisHis 5
Db          92 CACAATGCCACCAC 78
RESULT 51   AF449188S1 AF449188S1 519 bp DNA linear PRI 28-MAY-2002
LOCUS       AF449188S1 Homo sapiens hypothetical BLOCK27 gene, exon 1.
DEFINITION  AF449188S1
ACCESSION   AF449188S1
VERSION     AF449188.1 GI:21218162
KEYWORDS    1 of 4
SEGMENT     1
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 519)
AUTHORS     Cortelli,J.R., Pallos,D. and Hart,T.C.
TITLE       Physical/Genetic Map of the 2p22-2p21 Region on Chromosome 2
JOURNAL      Unpublished
KEYWORDS    2 (bases 1 to 519)
AUTHORS     Gorry,M.C., Zhang,Y., Marks,J.J., Suppe,B., Hart,P.S.,
              Cortelli,J.R., Pallos,D. and Hart,T.C.
TITLE       Direct Submission
JOURNAL      Submitted (20-NOV-2001) Oral Medicine/Pathology, University of
              Pittsburgh, School of Dental Medicine, 3501 Terrace Street, 614
              Salk Hall, Pittsburgh, PA 15261, USA
FEATURES     Location/Qualifiers
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              1..24
              /note="X01-F"
              276..409
              /gene="hypothetical BLOCK27"
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              complement(495..519)
              /note="X01-R"
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Alignment Scores:
Pred. No.: 1.34e+03 Length: 519
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-029-756-12 (1-5) x AF449188S1 (1-519)
Qy          1 HisAenAlaHisHis 5
Db          92 CACAATGCCACCAC 78
RESULT 51   AF449188S1 AF449188S1 519 bp DNA linear PRI 28-MAY-2002
LOCUS       AF449188S1 Homo sapiens hypothetical BLOCK27 gene, exon 1.
DEFINITION  AF449188S1
ACCESSION   AF449188S1
VERSION     AF449188.1 GI:21218162
KEYWORDS    1 of 4
SEGMENT     1
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 519)
AUTHORS     Cortelli,J.R., Pallos,D. and Hart,T.C.
TITLE       Physical/Genetic Map of the 2p22-2p21 Region on Chromosome 2
JOURNAL      Unpublished
KEYWORDS    2 (bases 1 to 519)
AUTHORS     Gorry,M.C., Zhang,Y., Marks,J.J., Suppe,B., Hart,P.S.,
              Cortelli,J.R., Pallos,D. and Hart,T.C.
TITLE       Direct Submission
JOURNAL      Submitted (20-NOV-2001) Oral Medicine/Pathology, University of
              Pittsburgh, School of Dental Medicine, 3501 Terrace Street, 614
              Salk Hall, Pittsburgh, PA 15261, USA
FEATURES     Location/Qualifiers
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              /db_xref="taxon:9606"
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              1..24
              /note="X01-F"
              276..409
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              complement(495..519)
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Db 46 CACAACGGCATCAC 60

RESULT 52  
BD162240/c  
LOCUS  
DEFINITION Novel polynucleotide.  
ACCESSION BD162240  
VERSION BD162240.1 GI:27867997  
KEYWORDS JP 2002191370-A/39.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 561)  
AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.  
TITLE Novel polynucleotide  
JOURNAL Patent: JP 2002191370-A 39 09-JUL-2002;  
KYOWA HAKKO KOGYO CO LTD  
COMMENT OS Corynebacterium glutamicum  
PN JP 2002191370-A/39  
PD 09-JUL-2002  
PF 15-DEC-2000 JP 2000405096  
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,  
PI KEIKO OCHIAI,  
PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO  
PI OZAKI  
PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC  
C12N1/15,  
PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12P7/40, C12P13/  
PC 04, C12P13/08,  
PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC  
G01N33/566,  
PC G01N33/569, G01N33/68, G01N37/00, C12P21/08, (C12N1/21, C12R1:15),  
PC (C12N1/21, C12R1:13), (C12N1/21, C12R1:01), (C12P13/08, C12R1:15),  
PC C12N5/00, C12N15/00  
CC Novel polynucleotide  
FH Key Location/Qualifiers  
FT source 1..561  
FT source /organism="Corynebacterium glutamicum".  
FEATURES  
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1..561  
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ORIGIN

Alignment Scores:  
Pred. No.: 1.44e+03 Length: 561  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 6

US-10-029-756-12 (1-5) x BD162240 (1-561)

Qy 1 HisAenAlaHisHis 5  
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Db 42 CATAACGCCCATCATC 28

RESULT 53  
AX120123/c  
LOCUS  
DEFINITION Sequence 39 from Patent EP1108790.  
ACCESSION AX120123  
VERSION AX120123.1 GI:14036838  
KEYWORDS  
SOURCE Corynebacterium glutamicum  
ORGANISM Corynebacterium glutamicum  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
REFERENCE 1

AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.  
TITLE Novel polynucleotides  
JOURNAL Patent: EP 1108790-A 39 20-JUN-2001;  
KYOWA HAKKO KOGYO CO., LTD. (JP)  
FEATURES  
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/organism="Corynebacterium glutamicum"  
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ORIGIN

Alignment Scores:  
Pred. No.: 1.44e+03 Length: 561  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 6

US-10-029-756-12 (1-5) x AX120123 (1-561)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 42 CATAACGCCCATCATC 28

RESULT 54  
G88098  
LOCUS  
DEFINITION S209P6437RG4.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged site.  
ACCESSION G88098  
VERSION G88098.1 GI:22738854  
KEYWORDS STS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 561)  
AUTHORS Wade, C.  
TITLE Polymorphism Structure in the Mouse  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kerstin Lindblad-Toh  
Whitehead Institute for Biomedical Research, Center for Genome Research  
320 Charles Street, Cambridge, MA 02141, USA  
Tel: 6172521477  
Fax: 6172580903  
Email: kersli@genome.wi.mit.edu  
Primer A: None  
Primer B: None  
STS size: 561  
Protocol:  
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvimJ C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the WGSv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

FEATURES  
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/map="3 22-508 48067552-48068038"  
/clone\_lib="C3H/HeJ"  
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STS  
ORIGIN



Alignment Scores:  
Pred. No.: 1.44e+03  
Score: 34.00  
Length: 561  
Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Query Match: 100.00%  
Indels: 0  
Gaps: 0  
DB: 11

US-10-029-756-12 (1-5) x G88098 (1-561)

Qy 1 HisaenAlaHisHis 5

Db 206 CATATGCGCCATCAT 220

RESULT 55  
LOCUS AR499461 562 bp DNA linear PAT 22-SEP-2004  
DEFINITION Sequence 4421 from patent US 6703491.

ACCESSION AR499461  
VERSION AR499461.1 GI:52434936

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 562)

AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,

Margolis,J.S., Ruddy,B.P., Ruddy,D.A. and Buchman,A.R.

TITLE Drosophila sequences

JOURNAL Patent: US 6703491-A 4421 09-MAR-2004;

FEATURES Location/Qualifiers

source 1..562

1..562

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1.44e+03  
Score: 34.00  
Length: 562  
Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Query Match: 100.00%  
Indels: 0  
Gaps: 0  
DB: 6

US-10-029-756-12 (1-5) x AR499461 (1-562)

Qy 1 HisaenAlaHisHis 5

Db 346 CATATGCGCCAC 360

RESULT 56  
LOCUS AR514743 562 bp DNA linear PAT 22-SEP-2004  
DEFINITION Sequence 19703 from patent US 6703491.

ACCESSION AR514743  
VERSION AR514743.1 GI:52450218

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 562)

AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,

Margolis,J.S., Ruddy,B.P., Ruddy,D.A. and Buchman,A.R.

TITLE Drosophila sequences

JOURNAL Patent: US 6703491-A 19703 09-MAR-2004;

FEATURES Location/Qualifiers

source 1..562

1..562

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1.44e+03  
Score: 34.00  
Length: 562  
Matches: 5

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 6  
Conservative: 0  
Indels: 0  
Gaps: 0

US-10-029-756-12 (1-5) x AR514743 (1-562)

Qy 1 HisaenAlaHisHis 5

Db 346 CATATGCGCCAC 360

RESULT 57

LOCUS BV022000

DEFINITION S212P6803PE1.TO CZECHII/Ei Mus musculus STS genomic, sequence

tagged site.

ACCESSION BV022000

VERSION BV022000.1 GI:31105895

KEYWORDS STS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 565)

AUTHORS Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C.,

Lander,E.S., Lindblad-Toh,K. and Daly,M.J.

TITLE The mosaic structure of variation in the laboratory mouse genome

JOURNAL Nature 420 (6915), 574-578 (2002)

MEDLINE 22354684

PUBMED 12466852

COMMENT

Contact: Kerstin Lindblad-Toh

Whitehead Institute for Biomedical Research, Center for Genome

Research

320 Charles Street, Cambridge, MA 02141, USA

Tel: 6172521477

Fax: 6172580903

Email: kersli@genome.wi.mit.edu

Primer A: None

Primer B: None

STS size: 565

Protocol:

WGS-discovery: Paired-end low-coverage whole genome shotgun reads

were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS

reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP

detection was carried out by SSAHA-SNP. 225,000 reads were

annotated

as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J

and the strain from which the particular read came. The validation

rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers

source 1..565

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="CZECHII/Ei"

/db\_xref="taxon:10090"

/map="12 22-498 101043540-101043062"

/clone\_lib="CZECHII/Ei"

<1..>565

STs

ORIGIN

Alignment Scores:

Pred. No.: 1.45e+03

Score: 34.00

Length: 565

Matches: 5

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Conservative: 0

Mismatches: 0

Query Match: 100.00%

Indels: 0

Gaps: 0

US-10-029-756-12 (1-5) x BV022000 (1-565)

Qy 1 HisaenAlaHisHis 5

|||||

```

Db      15  CACAATGCCACCAT 29

RESULT 58
AX411835/c
LOCUS   AX411835          578 bp    DNA        linear    PAT 14-JUN-2002
DEFINITION Sequence 15 from Patent WO224742.
ACCESSION AX411835
VERSION   AX411835.1 GI:21444323
KEYWORDS
SOURCE   Canis familiaris (dog)
ORGANISM Canis familiaris
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Krasnow,R.E. and Baughn,M.R.
TITLE   Atp-binding cassette protein
JOURNAL Patent: WO 0224742-A 15 28-MAR-2002;
          Incyte Genomics, Inc. (US)
FEATURES
source   Location/Qualifiers
          1..578
            /organism="Canis familiaris"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9615"
            /note="Incyte ID No: 702386639H1"

ORIGIN
Alignment Scores:
Pred. No.:      1.48e+03      Length:      578
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              6           Gaps:        0

US-10-029-756-12 (1-5) x AX411835 (1-578)

Qy      1  HisAenAlaHisHis 5
      |||||
Db      155 CACAATGCCACCAT 141

RESULT 59
AF064367
LOCUS   AF064367          631 bp    DNA        linear    INV 17-MAR-1999
DEFINITION Herpetomonas samuelpessoai clone her30 kinetoplast minicircle DNA,
partial sequence.
ACCESSION AF064367
VERSION   AF064367.1 GI:4092894
KEYWORDS kinetoplast Herpetomonas pessoai
SOURCE   Herpetomonas pessoai
ORGANISM Herpetomonas pessoai
          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
          Herpetomonas.
REFERENCE
AUTHORS Fu,G., Lambson,B. and Barker,D.
TITLE   Characterisation of kinetoplast DNA minicircles from Herpetomonas
samuelpessoai
JOURNAL FEMS Microbiol. Lett. 172 (1), 65-71 (1999)
MEDLINE 99179246
PUBMED   10079529
REFERENCE
AUTHORS Fu,G. and Barker,D.C.
TITLE   Direct Submission
JOURNAL Submitted (11-MAY-1998) Department of Pathology, University of
Cambridge, Tennis Court Road, Cambridge CB2 1QP, UK
FEATURES
source   Location/Qualifiers
          1..631
            /organism="Herpetomonas pessoai"
            /organalle="mitochondrion:kinetoplast"
            /mol_type="genomic DNA"
            /db_xref="taxon:5715"
            /chromosome="minicircle"
            /clone="her30"

ORIGIN
Alignment Scores:
Pred. No.:      1.62e+03      Length:      638
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              6           Gaps:        0

US-10-029-756-12 (1-5) x AX283845 (1-638)

Qy      1  HisAenAlaHisHis 5
      |||||
Db      170 CACAATGCCACCAT 156

RESULT 61
AF229270/c
LOCUS   AF229270          645 bp    DNA        linear    PLN 16-AUG-2002
DEFINITION Balduina uniflora internal transcribed spacer 1, 5.8S ribosomal RNA
Gene, and internal transcribed spacer 2, complete sequence.
ACCESSION AF229270
VERSION   AF229270.1 GI:12642289
KEYWORDS
SOURCE   Balduina uniflora
ORGANISM Balduina uniflora
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; campanulids; Asterales; Asteraceae; Asteroideae;
          Helenieae; Balduina.
REFERENCE
AUTHORS Baldwin,B.G. and Wessa,B.L.
TITLE   Phylogenetic placement of Pelucha and new subtribes in Helenieae
sensu stricto (Compositae)
JOURNAL Syst. Bot. 25 (3), 522-538 (2000)
REFERENCE
          2 (bases 1 to 645)

```

**AUTHORS** Baldwin,B.G. and Wessa,B.L.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (20-JAN-2000) Jepson Herbarium and Department of Integrative Biology, University of California, Berkeley, 1001 Valley Life Sciences Building #2465, Berkeley, CA 94720-2465, USA

**FEATURES** Location/Qualifiers  
 source 1..645 /organism="Baldauina uniflora"  
 /mol\_type="genomic DNA"  
 /specimen\_voucher="Urbatech 7579 (LSU, UC)"  
 /db\_xref="taxon:128714"  
 misc\_RNA 1..259 /product="internal transcribed spacer 1"  
 rRNA 260..423 /product="5.8S ribosomal RNA"  
 misc\_RNA 424..645 /product="internal transcribed spacer 2"

**ORIGIN**  
 Alignment Scores: 1.64e+03 Length: 645  
 Pred. No.: 34.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 8

US-10-029-756-12 (1-5) x AF229270 (1-645)  
 Qy 1 HisAenAlaHisHis 5  
 Db 141 CATAATGCCCATCAT 127

**RESULT 62**  
 HUMYR86G04/c HUMYR86G04 646 bp mRNA linear PRI 29-AUG-1998  
**LOCUS** HUMYR86G04  
**DEFINITION** Homo sapiens full length insert cDNA clone YR86G04.  
**ACCESSION** AF085955  
**VERSION** AF085955.1 GI:3483300  
**KEYWORDS** FLI CDNA.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 646)  
**AUTHORS** Woesner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J., Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B., Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R., Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymet,K., Hillier,L., Wilson,R. and Waterston,R.  
**TITLE** Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 646)  
**AUTHORS** Waterston,R.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

**COMMENT**  
 SUBMITTED BY: Genome Sequencing Center  
 Department of Genetics  
 Washington University  
 St. Louis MO 63108, USA  
 http://genome.wustl.edu/gsc  
 mailto:est@watson.wustl.edu

**NOTICE:** This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

The location of this clone is unknown.  
**FEATURES** Location/Qualifiers  
 source 1..646 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGE:212214"  
 /clone\_lib="Soares\_fetal\_liver\_spleen\_inFLS"

**ORIGIN**  
 Alignment Scores: 1.64e+03 Length: 646  
 Pred. No.: 34.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 9

US-10-029-756-12 (1-5) x HUMYR86G04 (1-646)  
 Qy 1 HisAenAlaHisHis 5  
 Db 91 CACATGACACACCAC 77

**RESULT 63**  
 AJ606025/c AJ606025 647 bp mRNA linear PLN 05-JAN-2004  
**LOCUS** AJ606025  
**DEFINITION** Triticum aestivum partial mRNA for putative integral membrane protein that regulates cation conductance (at2G03510 gene).  
**ACCESSION** AJ606025  
**VERSION** AJ606025.1 GI:40641592  
**KEYWORDS** at2G03510 gene; integral membrane protein that regulates cation conductance.  
**SOURCE** Triticum aestivum (bread wheat)  
**ORGANISM** Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
**REFERENCE** 1  
**AUTHORS** Ciaffi,M., Tanzarella,O.A., Porceddu,E., Paolacci,A.R. and d'Aloisio,E.  
**TITLE** Identification and characterization of gene sequences expressed in wheat spikelets at the heading stage  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 647)  
**AUTHORS** Ciaffi,M.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (06-NOV-2003) Ciaffi M., Dipartimento Agrobiologia e Agrochimica, University of Tuscia, Via S. Camillo De Lellis, Italy 01100, ITALY

**FEATURES** Location/Qualifiers  
 source 1..647 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clones="P71A"  
 /tissue\_type="spike at heading stage"  
 gene 1..647 /gene="at2G03510"  
 CDS <1..645 /gene="at2G03510"  
 /codon\_start=1  
 /product="putative integral membrane protein that regulates cation conductance"  
 /protein\_id="CAE54276.1"  
 /db\_xref="GI:40641593"

/translation="TSAPSTLHVPSHGVMYWRGGLLKTITPGVHLKLPITOF  
EPIQVTLQDVQKIPCGTKGGMISFDKIGVNRNLKDPFVETLLNYGVYDXTWLY  
DKIHHEINQFCSHSLQVYIDMFQDQAIATERQVAKAEATQKIALSBAEKNALV  
SKILMQMLTEKSSKRQQQIDNEMFLARERALADANYRITKEAEANKLITPE"

ORIGIN

Alignment Scores:  
Pred. No.: 1.65e+03 Length: 647  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AJ506025 (1-647)

Qy 1 HisAsnAlaHisHis 5  
|||||  
Db 289 CATATGACACCAT 275

RESULT 64

AY454951  
LOCUS AY454951 647 bp DNA linear PRI 21-JAN-2004  
DEFINITION Alouatta caraya clone 1 olfactory receptor pseudogene, partial  
sequence.  
ACCESSION AY454951  
VERSION AY454951.1 GI:38424539  
KEYWORDS  
SOURCE Alouatta caraya (black howler monkey)  
ORGANISM Alouatta caraya  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;  
Alouatta.

REFERENCE 1 (bases 1 to 647)  
AUTHORS Gilad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.  
TITLE Loss of Olfactory Receptor Genes Coincides with the Acquisition of  
Full Trichromatic Vision in Primates  
JOURNAL PLoS Biol. 2 (1), 0120-0125 (2004)

REFERENCE 2 (bases 1 to 647)  
AUTHORS Gilad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.  
TITLE Direct Submission  
JOURNAL Submitted (30-OCT-2003) Max Plank Institute for Evolutionary  
Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES

source  
1..647  
/organism="Alouatta caraya"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9502"  
/clone="1"  
gene <1..>647  
/gene="olfactory receptor"  
/pseudo

ORIGIN

Alignment Scores:  
Pred. No.: 1.65e+03 Length: 647  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x AY454951 (1-647)

Qy 1 HisAsnAlaHisHis 5  
|||||  
Db 443 CATATGCCCATCAT 457

RESULT 65

AX055282  
LOCUS AX055282 648 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 189 from Patent WO0073502.  
ACCESSION AX055282

AX055282.1 GI:12228586

KEYWORDS  
SOURCE Helicobacter sp.  
ORGANISM Helicobacter sp.  
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
Helicobacteraceae; Helicobacter.

REFERENCE

1  
AUTHORS Apfel,H., Fuchs,T.M., Gibbs,C.P., Hueck,C.J. and Meyer,T.F.  
TITLE Essential gene and gene products for identifying, developing and  
optimising immunological and pharmacological active ingredients for  
the treatment of microbial infections  
JOURNAL Patent: WO 0073502-A 189 07-DEC-2000;  
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)  
; Creatogen GmbH (DE)

FEATURES

source  
1..648  
/organism="Helicobacter sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:218"

CDS

1..648  
/note="unnamed protein product"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="CAC22068.1"  
/db\_xref="GI:12228587"  
/translation="MKPKYRKISDYAIVGGLSALVMVSIYCKSNADDPKEQSSLSQ  
SVQKGAPVILEEQDKSKYKVEYPSRTHIIVRDLOGNERVLSNEIQKLKEEAK  
IDNGTSKLQVPNGGSSGPGGLGSAIGSAGAILGSGIKLGNKLFNNPNYQNAQRT  
YKSPQAYQRQNSFSKSPASSMGSGKQSGFFGSSRPTSPAVSSGTRGFNS"

ORIGIN

Alignment Scores:  
Pred. No.: 1.65e+03 Length: 648  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX055282 (1-648)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 78 CACAATGCTCACCAT 64

RESULT 66

AY113693  
LOCUS AY113693 650 bp mRNA linear VRT 03-SEP-2002  
DEFINITION Oncorhynchus mykiss fructose-1,6-bisphosphatase-like mRNA, partial  
sequence.

ACCESSION AY113693  
VERSION AY113693.1 GI:22657376

KEYWORDS  
SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM

Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS Booth,H.L. and Mommsen,T.P.  
TITLE Characterization of fructose-1,6-bisphosphatase in rainbow trout  
JOURNAL Unpublished

REFERENCE

AUTHORS Booth,H.L. and Mommsen,T.P.  
TITLE Direct Submission

JOURNAL

Submitted (16-MAY-2002) Biochemistry and Microbiology, University  
of Victoria, P.O. Box 3055, MS 7077, Victoria, BC V8W 3P6, Canada  
NCBI staff are still waiting for submitters to provide appropriate  
coding region information.

FEATURES

source  
1..650  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"

misc\_feature /db\_xref="taxon:8022"  
<1..650  
/note="similar to fructose-1,6-bisphosphatase"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.65e+03 Length: 650  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-029-756-12 (1-5) x AY113693 (1-650)

Qy 1 HisAenAlaHisHis 5

Db 296 CATAACGCCACCAC 282

## RESULT 67

AR273654 LOCUS linear PAT 10-APR-2003

DEFINITION Sequence 1397 from patent US 6504010.

ACCESSION AR273654

VERSION AR273654.1 GI:29705539

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J., and Fan, L.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6504010-A 1397 07-JAN-2003;

FEATURES Location/Qualifiers

source 1..653

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.66e+03 Length: 653  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR273654 (1-653)

Qy 1 HisAenAlaHisHis 5

Db 448 CACAATGCCACCAC 462

## RESULT 68

AR277235 LOCUS linear PAT 10-APR-2003

DEFINITION Sequence 1397 from patent US 6509448.

ACCESSION AR277235

VERSION AR277235.1 GI:29710882

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6509448-A 1397 21-JAN-2003;

FEATURES Location/Qualifiers

source 1..653

/organism="unknown"

/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.66e+03 Length: 653  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR277235 (1-653)

Qy 1 HisAenAlaHisHis 5

Db 448 CACAATGCCACCAC 462

## RESULT 69

AR407510 LOCUS linear PAT 18-DEC-2003

DEFINITION Sequence 1397 from patent US 6630574.

ACCESSION AR407510

VERSION AR407510.1 GI:40157321

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J., and Fan, L.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6630574-A 1397 07-OCT-2003;

FEATURES Location/Qualifiers

source 1..653

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.66e+03 Length: 653  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR407510 (1-653)

Qy 1 HisAenAlaHisHis 5

Db 448 CACAATGCCACCAC 462

## RESULT 70

AR441360 LOCUS linear PAT 20-FEB-2004

DEFINITION Sequence 1397 from patent US 6667154.

ACCESSION AR441360

VERSION AR441360.1 GI:42667520

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J., and Fan, L.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6667154-A 1397 23-DEC-2003;

FEATURES Location/Qualifiers

source 1..653

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.66e+03 Length: 653  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR441360 (1-653)

Qy 1 HisAenAlaHisHis 5

Db 448 CACAATGCCACCAC 462

## RESULT 71

AR544171 AR544171 653 bp DNA linear PAT 08-OCT-2004  
 LOCUS Sequence 1397 from patent US 6746846.  
 DEFINITION AR544171

ACCESSION AR544171.1 GI:53936847

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,  
 Carter, D., Retter, M.W., Mannion, J. and Fan, L.

TITLE Methods for diagnosing lung cancer

JOURNAL Patent: US 6746846-A 1397 08-JUN-2004;

FEATURES Location/Qualifiers

source

1. .653

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.66e+03 Length: 653  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR544171 (1-653)

Qy 1 HisAenAlaHisHis 5

Db 448 CACAATGCCACCAC 462

## RESULT 72

AR368687 AR368687 653 bp DNA linear PAT 16-FEB-2002  
 LOCUS Sequence 1397 from Patent WO0204514.  
 DEFINITION AR368687

ACCESSION AR368687

VERSION AR368687.1 GI:18856760

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,

Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S.,

McNabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.

TITLE Compositions and methods for the therapy and diagnosis of lung

JOURNAL Patent: WO 0204514-A 1397 17-JAN-2002;

CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

source 1. .653

/organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.66e+03 Length: 653  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX368687 (1-653)

Qy 1 HisAenAlaHisHis 5

Db 448 CACAATGCCACCAC 462

## RESULT 73

AY329324 AY329324 662 bp DNA linear PLN 30-JUN-2004  
 LOCUS catalytic subunit A (vmaA) gene, partial cds; and vmaA-vpsA  
 DEFINITION Alternaria alternata strain EGS34-016 vacuolar membrane ATPase  
 intergenic spacer, partial sequence.

ACCESSION AY329324

VERSION AY329324.1 GI:37594436

KEYWORDS

SOURCE Alternaria alternata

ORGANISM Alternaria alternata

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;

Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria;

Alternaria alternata group.

REFERENCE 1 (bases 1 to 662)

AUTHORS Inderbitzin, P. and Berbee, M.L.

TITLE Mating type gene evolution in Pleospora, the sexual state of

Stemphylium

JOURNAL Unpublished

AUTHORS Inderbitzin, P. and Berbee, M.L.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2003) Department of Botany, University of British

Columbia, #3529-6270 University Blvd., Vancouver, British Columbia

V6T1Z4, Canada

## FEATURES

Location/Qualifiers

source 1. .662

/organism="Alternaria alternata"

/mol\_type="genomic DNA"

/strain="EGS34-016"

/db\_xref="taxon:5599"

&lt;1. .&gt;39

/gene="vmaA"

&lt;1. .&gt;39

/product="vacuolar membrane ATPase catalytic subunit A"

&lt;1. .&gt;39

/gene="vmaA"

/note="similar to Aspergillus oryzae vmaA sequence in

GenBank Accession Number AB073302"

/codon\_start=1

/product="vacuolar membrane ATPase catalytic subunit A"

/protein\_id="AA094178.1"

/db\_xref="GI:37594437"

/translation="GKLSQLLSYKC"

40. .&gt;662

/note="vmaA-vpsA intergenic spacer"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.68e+03 Length: 662  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-029-756-12 (1-5) x AY329324 (1-662)

Qy 1 HisAenAlaHisHis 5
Db 241 CACAATGCCCATCAT 255

RESULT 74
CQ715174/c
LOCUS CQ715174 666 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1108 from Patent WO02068579.
ACCESSION CQ715174
VERSION CQ715174.1 GI:42276031
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1108 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.69e+03 Length: 666
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x CQ715174 (1-666)

Qy 1 HisAenAlaHisHis 5
Db 525 CACAATGCCCATCAT 511

RESULT 75
AY454977
LOCUS AY454977 675 bp DNA linear PRI 21-JAN-2004
DEFINITION Trachypithecus auratus clone 10 olfactory receptor pseudogene,
partial sequence.
ACCESSION AY454977
VERSION AY454977.1 GI:38424583
KEYWORDS
SOURCE Trachypithecus auratus (Javan langur)
ORGANISM Trachypithecus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Colobinae; Trachypithecus.
1 (bases 1 to 675)
REFERENCE Gilad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
AUTHORS Loss of Olfactory Receptor Genes Coincides with the Acquisition of
TITLE Full Trichromatic Vision in Primates
JOURNAL PLOS Biol. 2 (1), 0120-0125 (2004)
REFERENCE Gilad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
AUTHORS Loss of Olfactory Receptor Genes Coincides with the Acquisition of
TITLE Full Trichromatic Vision in Primates
JOURNAL Submitted (30-OCT-2003) Max Plank Institute for Evolutionary
Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
FEATURES
source
1..675

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/organism="Trachypithecus auratus"
/mol_type="genomic DNA"
/db_xref="taxon:222416"
/clone="10"
<1..>675
/feature="olfactory receptor"
/pseudo

gene

ORIGIN
Alignment Scores:
Pred. No.: 1.71e+03 Length: 675
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-029-756-12 (1-5) x AY454977 (1-675)

Qy 1 HisAenAlaHisHis 5
Db 40 CACAATGCCCATCAT 54

RESULT 76
CQ610128/c
LOCUS CQ610128 679 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 37886 from Patent WO0171042.
ACCESSION CQ610128
VERSION CQ610128.1 GI:41662065
KEYWORDS
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1
REFERENCE Venter,J.C., Adams,M., Li,P.W. and Myers,B.W.
AUTHORS Detection kits, such as nucleic acid arrays, for detecting the
TITLE expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL Patent: WO 0171042-A 37886 27-SEP-2001;
PE Corporation (NY) (US)
FEATURES
source
1..679
Location/Qualifiers
/organism="Drosophila sp."
/mol_type="unassigned DNA"
/db_xref="taxon:7242"

ORIGIN
Alignment Scores:
Pred. No.: 1.72e+03 Length: 679
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x CQ610128 (1-679)

Qy 1 HisAenAlaHisHis 5
Db 559 CACAATGCCCATCAT 545

RESULT 77
BD010644/c
LOCUS BD010644 686 bp DNA linear PAT 31-JAN-2002
DEFINITION Helicobacter polypeptides and corresponding polynucleotide
molecules.
ACCESSION BD010644
VERSION BD010644.1 GI:18639017
KEYWORDS JP 2001503637-A/82.
SOURCE unidentified
ORGANISM unidentified
unclassified.

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```

REFERENCE 1 (bases 1 to 686)
AUTHORS Haas,R., Kleanthous,H., Tomb,J.F., Miller,C., Garawi,A.A.,
Odenbreit,S. and Meyer,T.
TITLE Helicobacter polypeptides and corresponding polynucleotide
molecules
JOURNAL Patent: JP 2001503637-A 82 21-MAR-2001;
MERIEUX ORAVAX, MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER
WISSENSCHAFTEN EV BERLIN, HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2001503637-A/82
PD 21-MAR-2001
PR 14-NOV-1997 JP 1998522949
PR 14-NOV-1996 US 08/749051,01-APR-1997 US 08/831309 PR
01-APR-1997 US 08/834705,01-APR-1997 US 08/833457 PR
24-JUN-1997 US 08/881227,29-JUL-1997 US 08/902615 PI RAINER
HAAS,HAROLD KLEANTHOS,JEAN FRANCOIS TOMB, PI CHARLES MILLER,
PI AMAL AL GARAWI,STEFAN ODENBREIT,THOMAS MEYER
PC C07H21/02,C07K1/00,A61K39/02,A01N37/18
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..686
FT /organism="Unidentified".
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32644"

FEATURES source
ORIGIN
Alignment Scores:
Pred. No.: 1.74e+03 Length: 686
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD010644 (1-686)

Qy 1 HisAsnAlaHisHis 5
Db 93 CACAATGCTCACCAT 79

RESULT 78
BD092839/c
LOCUS BD092839 686 bp DNA linear PAT 27-AUG-2002
DEFINITION Identification of polynucleotides encoding novel helicobacter
polypeptides in the helicobacter genome.
ACCESSION BD092839
VERSION BD092839.1 GI:22638450
KEYWORDS JP 2001527393-A/620.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
1 (bases 1 to 686)
REFERENCE Kleanthous,H., Garawi,A.A., Miller,C., Tomb,J.F. and Oomen,R.P.
AUTHORS Identification of polynucleotides encoding novel helicobacter
TITLE polypeptides in the helicobacter genome
JOURNAL Patent: JP 2001527393-A 620 25-DEC-2001;
MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCINS AGROBIOLOGICAL RESOURCES MINISTRY O SA, HUMAN GENOME
SCIENCES INC
COMMENT PN JP 2001527393-A/620
PD 25-DEC-2001
PF 01-APR-1998 JP 1998541947
PR 01-APR-1997 US 08/833457,24-JUN-1997 US 08/881227 PR
29-JUL-1997 US 08/902615
PI HAROLD KLEANTHOS,AMAL AL GARAWI,CHARLES MILLER,JEAN FRANCOIS
TOMB,
PI RAYMOND PETER OOMEN
PC A01N43/04,A61K31/70
CC Strandedness: Single;

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CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES source
ORIGIN
Alignment Scores:
Pred. No.: 1.74e+03 Length: 686
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD092839 (1-686)

Qy 1 HisAsnAlaHisHis 5
Db 93 CACAATGCTCACCAT 79

RESULT 79
AX414104/c
LOCUS AX414104 713 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 1095 from Patent WO0228891.
ACCESSION AX414104
VERSION AX414104.1 GI:21446561
KEYWORDS Listeria monocytogenes ATCC 19115
SOURCE Listeria monocytogenes ATCC 19115
ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Kunst,F. and Glaser,P.
TITLE Listeria innocua, genome and applications
JOURNAL Patent: WO 0228891-A 1095 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES source
ORIGIN
Alignment Scores:
Pred. No.: 1.8e+03 Length: 713
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX414104 (1-713)

Qy 1 HisAsnAlaHisHis 5
Db 407 CATAATGCACACCAC 393

RESULT 80
PM7E2G/c
LOCUS PM7E2G 723 bp DNA linear STS 29-MAY-2003
DEFINITION Penicillium marneffeii STS, clone pm7e2.g, sequence tagged site.
ACCESSION AL685153
VERSION AL685153.1 GI:19336504
KEYWORDS STS.
SOURCE Penicillium marneffeii
ORGANISM Penicillium marneffeii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE 1
AUTHORS Yuen,K.Y., Pascal,G., Wong,S.S., Glaser,P., Woo,P.C., Kunst,F.,

```



Cai, J.J., Cheung, E.Y., Medigue, C. and Danchin, A.  
 Exploring the Penicillium marneffei genome  
 Arch. Microbiol. 179 (5), 339-353 (2003)

TITLE  
 JOURNAL  
 MEDLINE  
 22595073  
 PUBMED  
 12640520  
 REFERENCE  
 2 (bases 1 to 723)  
 AUTHORS  
 Danchin, A. and Pascal, G.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,  
 Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong  
 FEATURES  
 Location/Qualifiers  
 source  
 1..723  
 /organism="Penicillium marneffei"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3772"  
 /clone="pm7e2.g"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.83e+03 Length: 723  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x PM7E2G (1-723)

Qy 1 HisAenAlaHisHis 5  
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 Db 393 CACAATGCTCATCAT 379

RESULT 81  
 AF352352/c  
 LOCUS  
 DEFINITION  
 Cryptoperidinopsoid sp. clone V14 ChrVIMS14ITS1\_3\_6\_12 internal  
 transcribed spacer 1, 5.8S ribosomal RNA gene and internal  
 transcribed spacer 2, complete sequence; and large subunit  
 ribosomal RNA gene, partial sequence.

ACCESSION  
 AF352352  
 VERSION  
 AF352352.1 GI:18462188  
 KEYWORDS  
 cryptoperidinopsoid sp. clone V14  
 SOURCE  
 cryptoperidinopsoid sp. clone V14  
 ORGANISM  
 Eukaryota; Alveolata; Dinophyceae; unclassified Dinophyceae.  
 REFERENCE  
 1 (bases 1 to 741)  
 AUTHORS  
 Litaker, R.W., Reece, K.S., Stokes, N.A., Yonish, B.A., Vandersea, M.W.,  
 Steidinger, K. and Tester, P.A.  
 TITLE  
 Genetic Variability in Dinoflagellate ITS Regions: Implications for  
 species identification and phylogenetic analysis  
 JOURNAL  
 Unpublished  
 REFERENCE  
 2 (bases 1 to 741)  
 AUTHORS  
 Reece, K.S. and Stokes, N.A.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (21-FEB-2001) Molecular Biology and Biotechnology,  
 University of North Carolina at Chapel Hill, 442 Taylor Hall, CB  
 7100, Chapel Hill, NC 27599, USA  
 FEATURES  
 Location/Qualifiers  
 source  
 1..741  
 /organism="cryptoperidinopsoid sp. clone V14"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:155772"  
 /clone="ChrVIMS14ITS1\_3\_6\_12"  
 /country="USA: Great Wicomico River, Virginia"  
 /note="isolated in 1998"  
 1..262  
 /product="internal transcribed spacer 1"  
 /note="ITS1"  
 263..421  
 /product="5.8S ribosomal RNA"  
 422..716  
 /product="internal transcribed spacer 2"  
 /note="ITS2"

misc\_RNA  
 1..262  
 /product="internal transcribed spacer 1"  
 /note="ITS1"

rRNA  
 263..421  
 /product="5.8S ribosomal RNA"

misc\_RNA  
 422..716  
 /product="internal transcribed spacer 2"  
 /note="ITS2"

rRNA  
 717..741  
 /product="large subunit ribosomal RNA"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.87e+03 Length: 741  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF352352 (1-741)

Qy 1 HisAenAlaHisHis 5  
 |||||  
 Db 333 CACAATGCTCATCAC 319

RESULT 82  
 AR253310  
 LOCUS  
 DEFINITION  
 Sequence 56 from patent US 6479258.  
 ACCESSION  
 AR253310  
 VERSION  
 AR253310.1 GI:27301733  
 KEYWORDS  
 SOURCE  
 Unknown.  
 ORGANISM  
 Unclassified.  
 REFERENCE  
 1 (bases 1 to 824)  
 AUTHORS  
 Short, J.M.  
 TITLE  
 Non-stochastic generation of genetic vaccines  
 JOURNAL  
 Patent: US 6479258-A 56 12-NOV-2002;  
 FEATURES  
 Location/Qualifiers  
 source  
 1..824  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.06e+03 Length: 824  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR253310 (1-824)

Qy 1 HisAenAlaHisHis 5  
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 Db 523 CACAATGCCACCAC 537

RESULT 83  
 BD131771  
 LOCUS  
 DEFINITION  
 Genetic vaccine vector engineering.  
 ACCESSION  
 BD131771  
 VERSION  
 BD131771.1 GI:23236716  
 KEYWORDS  
 JP 2002503461-A/5.  
 SOURCE  
 Human herpesvirus 5  
 ORGANISM  
 Human herpesvirus 5  
 REFERENCE  
 1 (bases 1 to 824)  
 AUTHORS  
 Punnonen, J., Stemmer, W.P.C., Whalen, R.G. and Howard, R.  
 TITLE  
 Betaherpesvirinae; Cytomegalovirus.  
 JOURNAL  
 Patent: JP 2002503461-A 5 05-FEB-2002;  
 COMMENT  
 OS Human cytomegalovirus  
 PN JP 2002503461-A/5  
 PD 05-FEB-2002  
 PF 10-FEB-1999 JP 2000531550  
 PR 11-FEB-1998 US 60/074294, 11-FEB-1998 US 09/021769 PI

JUHA PUNNONEN, WILLEM P C STEMMER, ROBERT GERALD WHALEN, RUSSELL PI  
 HOWARD  
 PC C12N15/09, A61K39/00, A61K48/00, A61P11/06, A61P29/00, A61P31/00,  
 PC A61P35/00,  
 PC A61P37/06, A61P37/08, A61K35/76, C12N15/00  
 CC Introns A from human cytomegalovirus (CMV) AD169 strain FH  
 Key Location/Qualifiers  
 FT intron (1)..(824).

FEATURES  
 source  
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 /organism="Human herpesvirus 5"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10359"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.06e+03 Length: 824  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD131771 (1-824)

Qy 1 HisAsnAlaHisHis 5  
 |||||  
 Db 523 CACAATGCCACCCAC 537

## RESULT 84

BD147586 826 bp DNA linear PAT 17-JAN-2003  
 LOCUS  
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD147586  
 VERSION BD147586.1 GI:27853344  
 KEYWORDS JP 2002191363-A/2429.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,  
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.  
 TITLE Primer for synthesizing full-length cDNA and use thereof  
 JOURNAL Patent: JP 2002191363-A 2429 09-JUL-2002;  
 COMMENT HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002191363-A/2429  
 PD 09-JUL-2002  
 PF 28-JUL-2000 JP 2000280990  
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU  
 PI SAITO,  
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
 PI KEIICHI NAGAI, TETSUJI OTSUKI  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/16, C12N5/18, C12N5/19, C12N5/20, C12N5/21, C12N5/22, C12N5/23, C12N5/24, C12N5/25, C12N5/26, C12N5/27, C12N5/28, C12N5/29, C12N5/30, C12N5/31, C12N5/32, C12N5/33, C12N5/34, C12N5/35, C12N5/36, C12N5/37, C12N5/38, C12N5/39, C12N5/40, C12N5/41, C12N5/42, C12N5/43, C12N5/44, C12N5/45, C12N5/46, C12N5/47, C12N5/48, C12N5/49, C12N5/50, C12N5/51, C12N5/52, C12N5/53, C12N5/54, C12N5/55, C12N5/56, C12N5/57, C12N5/58, C12N5/59, C12N5/60, C12N5/61, C12N5/62, C12N5/63, C12N5/64, C12N5/65, C12N5/66, C12N5/67, C12N5/68, C12N5/69, C12N5/70, C12N5/71, C12N5/72, C12N5/73, C12N5/74, C12N5/75, C12N5/76, C12N5/77, C12N5/78, C12N5/79, C12N5/80, C12N5/81, C12N5/82, C12N5/83, C12N5/84, C12N5/85, C12N5/86, C12N5/87, C12N5/88, C12N5/89, C12N5/90, C12N5/91, C12N5/92, C12N5/93, C12N5/94, C12N5/95, C12N5/96, C12N5/97, C12N5/98, C12N5/99, C12N5/100, C12N5/101, C12N5/102, C12N5/103, C12N5/104, C12N5/105, C12N5/106, C12N5/107, 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Score: 34.00 Matches: 5  
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US-10-029-756-12 (1-5) x AX451702 (1-838)

Qy 1 HisAenAlaHisHis 5  
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Db 523 CACAATGCCACCAC 537

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VERSION BV208715.1 GI:49533398  
KEYWORDS STS.  
SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM  
Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
1 (bases 1 to 847)  
Spindel, E.R., Pauley, M., Jia, Y., Boyle, N., Jiang, S., Gravett, C.,  
Lupo, S.L., Ali, H., Ojeda, S.R. and Norgren, R.B.  
Targeted amplification of the 3' end of rhesus macaque orthologs of  
human genes  
Unpublished (2004)

Contact: Spindel ER  
Division of Neuroscience  
Oregon National Primate Research Center  
505 NW 185th Avenue, Beaverton, OR 97006, USA  
Tel: 403-690-5388  
Fax: 503-690-5384  
Email: spindel@ohsu.edu  
Primer A: aacctcaggacagatgg  
Primer B: cagtggacactttacaaaac  
STS size: 847  
PCR Profile:  
Hot Start: 95 degrees C for 2.00 min  
Denaturation: 95 degrees C for 0.50 min  
Annealing: 48 degrees C for 0.50 min  
Polymerization: 72 degrees C for 1.00 min  
PCR Cycles: 35  
Extension: 72 degrees C for 7.0 min  
Thermal Cycler: MJ Instruments PTC100

Protocol:  
Template: 200 ng  
Primer: each 1uM  
dNTP's: each 200 uM  
Taq Polymerase: 0.05 units/ul (Fast Start High  
Fidelity, Roche)  
Total Vol: 50 ul

Buffer: MgCl2: 1.8 mM  
Fast Start polymerase reaction buffer (Roche)

Bases 1-847 are 98% homologous (Blast) to bases 1999-2844 of  
NM\_138734.1. Primers were chosen to amplify genomic DNA in the 3'  
region of NRXN2. As human sequence was used to design the primers,  
the primer sequences are not included in the rhesus sequence  
provided below. To obtain additional information regarding  
primers or clones contact: Dr. Robert Norgren; Dept of Genetics,  
Cell Biology & Anatomy; University of Nebraska Medical Center;  
986395 Nebraska Medical Center; Omaha, NE 68198. Email:  
rnorgren@unmc.edu  
A database containing sequences associated with this project can be  
found at: <http://rhesusgenomechip.unomaha.edu/index.html>.

FEATURES  
source  
Location/Qualifiers  
1. .847  
/organism="Macaca mulatta"  
/mol\_type="genomic DNA"  
/strain="Indian origin"  
/db\_xref="taxon:9544"  
/clone="MMA1011"  
/clone\_lib="Rhesus macaque genomic DNA"  
/dev\_stage="Adult"  
/note="Organ: Liver; Vector: pGEM-T Easy; V-type: Plasmid;  
cDNA amplified from rhesus genomic DNA with the human  
forward and reverse primers listed above and subcloned  
into pGEM-T Easy-"  
1. .847  
/gene="NRXN2"  
/note="neurexin 2"  
<1. .>847  
/gene="NRXN2"

gene  
STS  
ORIGIN

Alignment Scores:  
Pred. No.: 2.12e+03 Length: 847  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x BV208715 (1-847)

Qy 1 HisAenAlaHisHis 5  
|||||

Db 304 CACAATGCCACCAC 290

RESULT 88  
AR508033  
LOCUS  
DEFINITION Sequence 12993 from patent US 6703491.  
ACCESSION AR508033  
VERSION AR508033.1 GI:52443508  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 881)  
AUTHORS Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L.,  
Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.  
Drosophila sequences  
Patent: US 6703491-A 12993 09-MAR-2004;  
JOURNAL Location/Qualifiers  
FEATURES  
source  
1. .881  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 2.2e+03 Length: 881  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR508033 (1-881)

Qy 1 HisAenAlaHisHis 5  
|||||

Db 858 CACAATGCCACCAC 872

RESULT 89  
AX790445/c  
LOCUS  
DEFINITION Sequence 2909 from Patent WO02066501.  
PAT 22-SEP-2004  
PAT 17-JUL-2003

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ACCESSION AX790445
VERSION AX790445.1 GI:32956066
KEYWORDS
SOURCE
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
REFERENCE
1 Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A.
AUTHORS Protein-protein interactions in Helicobacter pylori
TITLE Patent: WO 0206501-A 2909 29-AUG-2002;
JOURNAL Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
FEATURES
source
Location/Qualifiers
1..895
/organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"
ORIGIN
Alignment Scores: 2.23e+03 Length: 895
Pred. No.: 34.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x AX790445 (1-895)
Qy 1 HisAenAlaHisHis 5
Db 881 CACATGCTCACCAT 867
RESULT 90
CNS01BZ5 900 bp mRNA linear PLN 20-MAR-2004
LOCUS Botrytis cinerea strain T4 cDNA library.
ACCESSION AL114873
VERSION AL114873.1 GI:5829492
KEYWORDS cDNA library; EST, nitrate deprivation.
SOURCE Botryotinia fuckeliana
ORGANISM Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE
1 (bases 1 to 900)
AUTHORS Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
REFERENCE
2 (bases 1 to 900)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT The cDNA library was made by using Botrytis cinerea T4 strain grown
under nitrate deprivation conditions. The cDNA were cloned
directionally in the pBSII vector.
FEATURES
source
Location/Qualifiers
1..900
/organism="Botryotinia fuckeliana"
/mol_type="mRNA"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W11H121"
ORIGIN
Alignment Scores: 2.24e+03 Length: 900
Pred. No.: 34.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%

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```

DB: 8 Gaps: 0
US-10-029-756-12 (1-5) x CNS01BZ5 (1-900)
Qy 1 HisAenAlaHisHis 5
Db 241 CACAACGCACACCAC 255
RESULT 91
AY061549/c 922 bp mRNA linear INV 22-JAN-2003
LOCUS Drosophila melanogaster LP07806 full insert cDNA.
DEFINITION
ACCESSION AY061549
VERSION AY061549.1 GI:16769755
KEYWORDS FLY_CDNA.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 922)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,
Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K.,
Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
REFERENCE
2 (bases 1 to 922)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
and Celniker, S.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
FEATURES
source
Location/Qualifiers
1..922
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/strain="Y; cn bw sp"
/db_xref="taxon:7227"
1..922
/gene="Fbp2"
/db_xref="FLYBASE:FBgn0000640"
64..834
/gene="Fbp2"
/note="Longest ORF"
/codon_start=1

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/product="LP07806p"
/protein_id="AAL29097.1"
/db_xref="GI:16769756"
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/tranlation="MEDWTGNNVYVGSFSGIGHQMMMLWOKDKIMGIMHMRNVK
MKKQLQALNPSVKVVFQMNLMKMSIQANKKQGMGHIDVINGEGVLLDKDDET
FTGNNLTGMIQSTWAMPYMDKTOGMGMGVNNSVYGLPEPAFAFSAAMHGILG
PTRSGMDMYIYKGTGVPMFMAFCPLTNSMIMNLNRDNTVTHHSSEWVEIASAKRQMP
EEAAMQIHAMENMKMGSMWIVSMGQLKEVTPPTMHQW"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e+03 Length: 922
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x AY061549 (1-922)

Qy 1 HisAenLaHisH1s 5
|||||
Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI:15868462
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
Podowski,R.M., Matushkin,Y.G., Gvanchandani,A., Muravenko,O.V.,
Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 948)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
source Location/Qualifiers
1..948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NLI-VL24C"

ORIGIN
Alignment Scores:
Pred. No.: 2.35e+03 Length: 948
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA324083 (1-948)

Qy 1 HisAenLaHisH1s 5
|||||

Db 138 CACAATGCCATCATC 152

RESULT 93
CR523245 979 bp mRNA linear VRT 15-JUN-2004
LOCUS Gallus gallus finished cDNA, clone CHEST966g24.
DEFINITION CR523245
ACCESSION CR523245
VERSION CR523245.1 GI:48841907
KEYWORDS Gallus gallus (chicken)
SOURCE ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauiria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 979)
REFERENCE Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V.,
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
Tickle,C. and Wilson,S.A.
Direct Submission
TITLE Submitted (15-JUN-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickest@sanger.ac.uk
JOURNAL BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
sequencing project.
COMMENT This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. cDNA was prepared
from RNA extracted from limbs, normalised, and poly A-trimmed.
EcoRI-NotI cut cDNA was then ligated into the vector. Vector:
pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia
coli DH10B.

FEATURES
source Location/Qualifiers
1..979
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST966g24"
/dev_stage="stage 36"

ORIGIN
Alignment Scores:
Pred. No.: 2.42e+03 Length: 979
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-12 (1-5) x CR523245 (1-979)

Qy 1 HisAenLaHisH1s 5
|||||
Db 334 CACAATGCCATCATC 348

RESULT 94
CR541849/c 990 bp mRNA linear PRI 29-JUN-2004
LOCUS Homo sapiens full open reading frame cDNA clone RZP0834H0232D for
gene GRAP2, GRB2-related adaptor protein 2; complete cds, without
stopcodon.
ACCESSION CR541849
VERSION CR541849.1 GI:49456652
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 990)
REFERENCE Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Katrang,K., Schattner,R., Shen,B., Henze,S., Mar,W.,
```

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

Korn, B., Zuo, D., Hu, Y. and LaBaer, J.  
 Cloning of human full open reading frames in Gateway(TM) system  
 entry vector (pDONR201)  
 2 (bases 1 to 990)  
 Halleck, A., Ebert, L., Mkoondinya, M., Schick, M., Eisenstein, S.,  
 Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,  
 Korn, B., Zuo, D., Hu, Y. and LaBaer, J.  
 Direct Submission  
 Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer  
 Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,  
 Germany  
 RZPD: RZPD0834H0232D, ORFNo 3794  
 www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0232D RZPDLIB;  
 Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.  
 834  
 www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834  
 www.rzpd.de/products/orfclones/  
 Contact: Inge Arlt  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 100  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available from RZPD;  
 Contact RZPD (customer.service@rzpd.de) for further information.  
 Clone name at Harvard Institute of Proteomics  
 (www.hip.harvard.edu): FLH30889.01L  
 This CDS clone is part of a collection of human full ORF clones  
 jointly established and verified by the Harvard Institute of  
 Proteomics (HIP) and RZPD.  
 This CDS has been cloned without stopcodon.  
 The CDS has been inserted into pDONR201 via a BP Clonase(TM)  
 reaction. Additional sequence has been added in front of the start  
 codon: att. .AAAAA GCA GGC TCC ACC (ATG).  
 The last codon is followed by the 3' att site: GACCCAGCTTCTT. .att  
 The clone is validated by full sequence check.  
 Compared to the reference sequence NM\_004810 (GI:19913386) we found  
 AA exchange(s) at position (first base of changed triplet):  
 586 (gln->arg)  
 Clone distribution: http://www.rzpd.de/products/orfclones/.  
**FEATURES**  
 source  
 1. .990  
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 /db\_xref="taxon:9606"  
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 /clone\_lib="Human Full ORF Clones Gateway(TM) - RZPD"  
 /lab\_host="DH5alpha"  
 /note="Vector: pDONR201, Site\_1: attP1; Site\_2: attP2"  
 1. .990  
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 1. .>990  
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 /db\_xref="GI:49456653"  
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 YVKNFIDIQPKWFGHGLRQHAENLGMKEVGFITIRASQSPGDFISVRHEDDV  
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 QHRSQGGPHLSGAVGEIRPSMRNKLSDHPPTLPLRQHQPOPPQVAPAPQOLQPP  
 QQRYLQHHFHQERGGSLDNDGCHCTGLGSENNALMHRHTDPVQLQAGVRWA  
 RALYDFEALEDDELGFHSGEVVEVLDSSNFSNWTGRLNKLGLFPANYVAPMTR"

**ORIGIN**

Alignment Scores:  
 Pred. No.: 2.45e+03 Length: 990  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x CR541849 (1-990)

**Qy** 1 HisAsnAlaHisHis 5  
**Db** 733 CACAATGCCCATCAT 719

RESULT 95  
 BD235644/c  
 LOCUS BD235644 993 bp DNA linear PAT 17-JUL-2003  
 DEFINITION GRIP and GRB2 family member-associated human adaptor proteins.  
 ACCESSION BD235644  
 VERSION BD235644.1 GI:33045414  
 KEYWORDS JP 2002523429-A/3.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 993)  
 AUTHORS Ellis, J.H.  
 TITLE GRIP and GRB2 family member-associated human adaptor proteins  
 JOURNAL Patent: JP 2002523429-A 3 30-JUL-2002;  
 COMMENT GLAXO GROUP LTD  
 OS Homo sapiens (human)  
 PN JP 2002523429-A/3  
 PD 30-JUL-2002  
 PR 18-AUG-1999 JP 2000566414  
 PR 19-AUG-1998 GB 9818124.1  
 PI JONATHAN HENRY ELLIS  
 PC C07K14/47,A61K45/00,A61P35/00,A61P37/06,C12N15/09,G01N33/15,  
 PC G01N33/50,  
 CC G01N33/566,C12N15/00  
 CC GRIP and GRB2 family member-associated human adaptor proteins  
 FH Key Location/Qualifiers  
 FT CDS (1)..(993).  
**FEATURES**  
 source  
 1. .993  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
**ORIGIN**

Alignment Scores:  
 Pred. No.: 2.45e+03 Length: 993  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD235644 (1-993)

**Qy** 1 HisAsnAlaHisHis 5  
**Db** 733 CACAATGCCCATCAT 719

RESULT 96  
 BD235645  
 LOCUS BD235645 993 bp DNA linear PAT 17-JUL-2003  
 DEFINITION GRIP and GRB2 family member-associated human adaptor proteins.  
 ACCESSION BD235645  
 VERSION BD235645.1 GI:33045415  
 KEYWORDS JP 2002523429-A/4.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 993)  
 AUTHORS Ellis, J.H.  
 TITLE GRIP and GRB2 family member-associated human adaptor proteins  
 JOURNAL Patent: JP 2002523429-A 4 30-JUL-2002;  
 COMMENT GLAXO GROUP LTD  
 OS Homo sapiens (human)  
 PN JP 2002523429-A/4

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PD 30-JUL-2002
PF 18-AUG-1999 JP 2000566414
PI 19-AUG-1998 GB 9818124.1
PI JONATHAN HENRY ELLIS
PC C07K14/47, A61K45/00, A61P35/00, A61P37/06, C12N15/09, G01N33/15,
G01N33/50, A61K45/00, A61P35/00, A61P37/06, C12N15/09, G01N33/15,
PC G01N33/566, C12N15/00
CC GRIP and GRB2 family member-associated human adaptor proteins
FH Key Location/Qualifiers
FT source 1..993
FT /organism='Homo sapiens (human)'.

FEATURES
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        Location/Qualifiers
            1..993
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2.46e+03 Length: 993
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD235645 (1-993)

QY 1 HisAenAlaHis 5
DB 261 CACAAATGCCCATCAT 275

RESULT 97
AF236120/c
LOCUS AF236120 993 bp mRNA linear PRI 30-JUN-2000
DEFINITION Homo sapiens cell-line Jurkat J6 T cell lymphoma adaptor protein
GRID (GRID) mRNA, complete cds.
ACCESSION AF236120
VERSION AF236120.1 GI:7331202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 993)
AUTHORS Ellis J.H., Ashman, C., Burden, M.N., Kilpatrick, K.E., Morse, M.A. and Hamblin, P.A.
TITLE GRID: a novel Grb-2-related adaptor protein that interacts with the activated T cell costimulatory receptor CD28
J. Immunol. 164 (11), 5805-5814 (2000)
JOURNAL MEDLINE
PUBMED 10820259
REFERENCE
2 (bases 1 to 993)
AUTHORS Ellis, J.H., Ashman, C., Burden, M.N., Kilpatrick, K.E., Morse, M.A. and Hamblin, P.A.
Direct Submission
Submitted (18-FEB-2000) Immunopathology Unit, GlaxoWellcome
Medicine Research Centre, Gunnels Wood Road, Stevenage,
Hertfordshire SG1 2NY, UK
FEATURES
    source
        Location/Qualifiers
            1..993
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DRRSGGPHLSGAVGEEIRPSPNKRKLSDPPTLPQQHQHQFQPPYAPAPQQLQPP
QQRYLQHHFHQRRGSLDINDGCGTGLGSENNALMHRHTDPVQLQAGRVRA
RALYDFEALEDDELGFHSGVEVLDSSNPSNMTGRLHNLKGLFPANTVAPMTR"

ORIGIN
Alignment Scores:
Pred. No.: 2.46e+03 Length: 993
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x AF236120 (1-993)

QY 1 HisAenAlaHis 5
DB 733 CACAAATGCCCATCAT 719

RESULT 98
CR536524/c
LOCUS CR536524 993 bp mRNA linear PRI 23-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834F0120D for gene GRAP2, GRB2-related adaptor protein 2; complete cds, incl. stopcodon.
ACCESSION CR536524
VERSION CR536524.1 GI:49168531
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 993)
AUTHORS Halleck, A., Ebert, L., Mkundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and Labaer, J.
Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
Unpublished
2 (bases 1 to 993)
AUTHORS Halleck, A., Ebert, L., Mkundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and Labaer, J.
Direct Submission
Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; RZPD0834F0120D, ORFNo 3096
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834F0120D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel.: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics and RZPD.
This CDS has been inserted into pDONR201 via a BP Clonase(TM)

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reaction. Additional sequence has been added in front of the start codon: att. AAAAAA GCA GGC TCC ACC (ATG).  
The stopcodon is followed by the 3', att site:  
(scop)GACCACTTCTT. att compared to the reference sequence  
NM\_004810 (gi19913386) we did not find any amino acid exchanges.  
Clone distribution: <http://www.rzpd.de/products/orfclones/>.

## FEATURES

Location/Qualifiers

1..993

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="RZPD0834F0120D"

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1..993

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1..993

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QORYLQHHFHQERRGSLINDCHGCTGLGSENNALMRHRHTDFVLQAGRVRA  
RALYDFEALEDDELGFHSGEVVEVLDSNFSWMTGRHLNKLGLFPFANYVAPMTK"

## ORIGIN

## Alignment Scores:

Pred. No.: 2.46e+03 Length: 993  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservat: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x CR536524 (1-993)

## Qy

1 HisAenAlaHisHis 5

|||||

733 CACAATGCCCATCAT 719

## RESULT 99

AX925633

LOCUS

AX925633 Sequence 12 from Patent WO03083098. 1026 bp DNA linear PAT 19-DEC-2003

DEFINITION

AX925633

ACCESSION

AX925633.1

VERSION

AX925633.1

KEYWORDS

Alternaria alternata

SOURCE

ORGANISM

Alternaria alternata

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;

Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria;

Alternaria alternata group.

REFERENCE

1

AUTHORS

Simon-Nobbe, B., Schneider, P., Denk, U., Wally, V., Richter, K.,

Radauer, C., Teige, M., Ebner, C. and Breitenbach, M.

Nucleic acid sequence and protein in addition to polypeptides

coding for mannitol-dehydrogenases or parts thereof and the

production and use thereof in diagnosis and therapy

Patent: WO 03083098-A 12.09-OCT-2003;

BIOMAY Produktions- und Handels- Aktiengesellschaft (AT)

LOCATION/Qualifiers

1..1026

/organism="Alternaria alternata"

/mol\_type="unassigned DNA"

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## ORIGIN

## Alignment Scores:

Pred. No.: 2.53e+03 Length: 1026

Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservat: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX925633 (1-1026)

## Qy

1 HisAenAlaHisHis 5

|||||

83 CACAATGCCCATCAC 97

## RESULT 100

AF034693

LOCUS

AF034693

DEFINITION

Coturnix coturnix japonica

gene, complete cds.

ACCESSION

AF034693

VERSION

AF034693.1

KEYWORDS

Coturnix japonica

ORGANISM

Coturnix japonica

Eukaryota; Metazoa;

Archosauria; Aves;

Neognathae; Galliformes; Phasianidae;

Phasianinae; Coturnix.

REFERENCE

1

AUTHORS

Benkheifia, S., Provot, S.,

Felder-Schmittbuhl, M.F.

mafa, a novel member of the maf proto-oncogene family, displays

developmental regulation and mitogenic capacity in avian

neuroretina cells

TITLE

Oncogene 17 (2), 247-254 (1998)

JOURNAL

MEDLINE

98337467

PUBMED

9674710

REFERENCE

2

AUTHORS

Benkheifia, S., Felder-Schmittbuhl, M.P. and Calothy, G.

Direct Submission

TITLE

Submitted (17-NOV-1997)

JOURNAL

Centre universitaire, Orsay 91405, France

FEATURES

Location/Qualifiers

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&lt;161..&gt;1021

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161..1021

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KRVQQRHILENEKQLQSQVQLKQEVSRLEKRDLYKEKYEKLAARGFPRETSPPA

PKTTAADFFW"

## ORIGIN

## Alignment Scores:

Pred. No.: 2.53e+03 Length: 1027  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservat: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-029-756-12 (1-5) x AF034693 (1-1027)

## Qy

1 HisAenAlaHisHis 5

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Db 623 CACACGCTCATCAT 637

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Job time : 1104.6 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein. - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 11:36:25 ; Search time 76.3158 Seconds  
(without alignments)  
107.204 Million cell updates/sec

Title: US-10-029-756-12  
Perfect score: 34  
Sequence: 1 HNAH 5

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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5	34	100.0	316	4	US-08-956-171E-4362
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66	34	100.0	4051	3	US-08-549-515-1
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89	34	100.0	5188	4	US-09-628-730-59	Sequence 59, Appl	c 162	31	91.2	908	3	US-08-991-789A-46	Sequence 46, Appl
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95	34	100.0	7015	3	US-09-770-315-1	Sequence 1, Appli	c 168	31	91.2	927	4	US-09-248-796A-7190	Sequence 7190, Ap
96	34	100.0	9600	3	US-08-910-647-1	Sequence 1, Appli	c 169	31	91.2	970	3	US-09-735-935-1	Sequence 1, Appli
97	34	100.0	15538	4	US-09-554-337-1	Sequence 1, Appli	c 170	31	91.2	970	4	US-10-162-639-1	Sequence 5029, Ap
98	34	100.0	21893	4	US-09-949-016-16407	Sequence 16407, A	c 171	31	91.2	1002	4	US-09-248-796A-5029	Sequence 120, App
99	34	100.0	22406	4	US-09-949-016-14958	Sequence 14958, A	c 172	31	91.2	1089	4	US-09-543-681A-120	Sequence 43, Appl
100	34	100.0	24056	4	US-09-949-016-14320	Sequence 14320, A	c 173	31	91.2	1197	4	US-09-710-279-43	Sequence 1497, Ap
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102	34	100.0	28063	4	US-09-949-016-16795	Sequence 16795, A	c 175	31	91.2	1254	3	US-09-134-001C-973	Sequence 973, App
103	34	100.0	31214	4	US-09-949-016-17097	Sequence 17097, A	c 176	31	91.2	1254	3	US-09-614-912-177	Sequence 177, App
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105	34	100.0	41180	4	US-09-949-016-12088	Sequence 12088, A	c 178	31	91.2	1315	3	US-09-234-186-2	Sequence 2, Appli
106	34	100.0	60304	4	US-09-949-016-11995	Sequence 11995, A	c 179	31	91.2	1315	3	US-09-234-186-4	Sequence 4, Appli
107	34	100.0	60304	4	US-09-949-016-17264	Sequence 17264, A	c 180	31	91.2	1315	3	US-09-234-186-5	Sequence 5, Appli
108	34	100.0	60465	4	US-09-949-016-15995	Sequence 15995, A	c 181	31	91.2	1315	3	US-09-234-186-6	Sequence 6, Appli
109	34	100.0	87562	4	US-09-949-016-13685	Sequence 13685, A	c 182	31	91.2	1315	3	US-09-233-527-2	Sequence 2, Appli
110	34	100.0	90618	4	US-09-949-016-15964	Sequence 15964, A	c 183	31	91.2	1315	3	US-09-233-527-4	Sequence 4, Appli
111	34	100.0	91933	4	US-09-949-016-11855	Sequence 11855, A	c 184	31	91.2	1315	3	US-09-233-527-5	Sequence 5, Appli
112	34	100.0	91933	4	US-09-949-016-11855	Sequence 11855, A	c 185	31	91.2	1315	3	US-09-233-527-6	Sequence 6, Appli
113	34	100.0	99629	4	US-09-596-002-37	Sequence 37, Appl	c 186	31	91.2	1315	5	PCT-US93-05651-2	Sequence 2, Appli
114	34	100.0	152393	4	US-09-949-016-14514	Sequence 14514, A	c 187	31	91.2	1410	4	US-09-543-681A-2896	Sequence 2896, App
115	34	100.0	152393	4	US-09-949-016-14515	Sequence 14515, A	c 188	31	91.2	1546	4	US-09-799-451-323	Sequence 323, App
116	34	100.0	156894	4	US-09-949-016-12765	Sequence 12765, A	c 189	31	91.2	1548	3	US-08-600-656-6	Sequence 6, Appli
117	34	100.0	156894	4	US-09-949-016-12765	Sequence 12765, A	c 190	31	91.2	1548	3	US-09-170-670-11	Sequence 11, Appl
118	34	100.0	156895	4	US-09-949-016-16957	Sequence 16957, A	c 191	31	91.2	1548	3	US-09-193-068-11	Sequence 11, Appl
119	34	100.0	156895	4	US-09-949-016-16958	Sequence 16958, A	c 192	31	91.2	1548	3	US-09-183-412-11	Sequence 11, Appl
120	34	100.0	156895	4	US-09-949-016-16958	Sequence 16958, A	c 193	31	91.2	1548	3	US-09-354-191A-6	Sequence 6, Appli
121	34	100.0	166698	4	US-09-949-016-16038	Sequence 16038, A	c 194	31	91.2	1548	3	US-09-290-734-11	Sequence 11, Appl
122	34	100.0	183202	4	US-09-949-016-13614	Sequence 13614, A	c 195	31	91.2	1548	3	US-09-537-168-7	Sequence 7, Appli
123	34	100.0	199945	4	US-09-949-016-15436	Sequence 15436, A	c 196	31	91.2	1548	4	US-09-545-586-11	Sequence 11, Appl
124	34	100.0	269223	4	US-09-596-002-41	Sequence 41, Appl	c 197	31	91.2	1548	4	US-09-749-864-11	Sequence 11, Appl
125	34	100.0	580073	4	US-08-545-528D-1	Sequence 1, Appli	c 198	31	91.2	1739	4	US-09-949-016-4226	Sequence 4226, Ap
126	34	100.0	1830121	4	US-09-557-884-1	Sequence 1, Appli	c 199	31	91.2	1814	1	US-08-720-899-5	Sequence 5, Appli
127	34	100.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli	c 200	31	91.2	1814	1	US-08-459-610-5	Sequence 5, Appli
128	34	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli	c 201	31	91.2	1814	2	US-08-343-804-5	Sequence 5, Appli
129	34	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli	c 202	31	91.2	1814	2	US-08-687-399-5	Sequence 5, Appli
130	31	91.2	25	4	US-09-396-136C-44377	Sequence 44377, A	c 203	31	91.2	1814	2	US-08-600-908A-5	Sequence 5, Appli
131	31	91.2	45	4	US-09-069-827A-65	Sequence 65, Appl	c 204	31	91.2	1814	3	US-08-683-838A-5	Sequence 5, Appli
132	31	91.2	50	4	US-09-554-929-43	Sequence 43, Appl	c 205	31	91.2	1814	3	US-09-182-859-5	Sequence 5, Appli
133	31	91.2	50	4	US-09-513-999C-32775	Sequence 32775, A	c 206	31	91.2	1814	3	US-09-672-459-5	Sequence 5, Appli
134	31	91.2	99	4	US-09-513-999C-32775	Sequence 32775, A	c 207	31	91.2	1814	3	US-09-636-252A-5	Sequence 5, Appli
135	31	91.2	137	4	US-09-513-999C-9545	Sequence 9545, Ap	c 208	31	91.2	1814	4	US-10-186-042-5	Sequence 5, Appli
136	31	91.2	210	4	US-09-248-796A-9553	Sequence 9553, Ap	c 209	31	91.2	1845	1	US-08-652-207A-1	Sequence 1, Appli
137	31	91.2	411	4	US-09-248-796A-6520	Sequence 6520, Ap	c 210	31	91.2	1845	3	US-09-488-857B-3	Sequence 3, Appli
138	31	91.2	413	4	US-09-513-999C-23181	Sequence 23181, A	c 211	31	91.2	1978	4	US-09-949-016-1358	Sequence 1358, Ap
139	31	91.2	453	4	US-09-621-976-19159	Sequence 19159, A	c 212	31	91.2	2225	4	US-09-799-451-318	Sequence 318, App
140	31	91.2	482	4	US-09-621-976-15665	Sequence 15665, A	c 213	31	91.2	2271	4	US-09-248-796A-633	Sequence 633, App
141	31	91.2	601	4	US-09-949-016-42885	Sequence 42885, A	c 214	31	91.2	2766	4	US-09-543-681A-1562	Sequence 1562, Ap
142	31	91.2	601	4	US-09-949-016-42886	Sequence 42886, A	c 215	31	91.2	2830	1	US-07-882-292-1	Sequence 1, Appli
143	31	91.2	601	4	US-09-949-016-42886	Sequence 42886, A	c 216	31	91.2	2830	2	US-08-331-644-1	Sequence 1, Appli
144	31	91.2	601	4	US-09-949-016-42886	Sequence 42886, A	c 217	31	91.2	2830	5	PCT-US93-04102-1	Sequence 1, Appli
145	31	91.2	601	4	US-09-949-016-72936	Sequence 72936, A	c 218	31	91.2	3264	4	US-09-710-279-4053	Sequence 4053, Ap
146	31	91.2	601	4	US-09-949-016-72938	Sequence 72938, A	c 219	31	91.2	3288	4	US-08-851-567B-33	Sequence 33, Appl
147	31	91.2	601	4	US-09-949-016-72938	Sequence 72938, A	c 220	31	91.2	3314	4	US-09-710-279-3745	Sequence 3745, Ap
148	31	91.2	601	4	US-09-949-016-77647	Sequence 77647, A	c 221	31	91.2	3314	4	US-09-710-279-3746	Sequence 3746, Ap
149	31	91.2	601	4	US-09-949-016-80314	Sequence 80314, A	c 222	31	91.2	3436	3	US-09-488-857B-12	Sequence 12, Appl
150	31	91.2	601	4	US-09-949-016-156637	Sequence 156637, A	c 223	31	91.2	3771	4	US-09-248-796A-3954	Sequence 3954, Ap
151	31	91.2	601	4	US-09-949-016-156627	Sequence 156627, A	c 224	31	91.2	3841	3	US-08-811-682-13	Sequence 13, Appl
152	31	91.2	601	4	US-09-949-016-156628	Sequence 156628, A	c 225	31	91.2	3897	4	US-09-949-016-2718	Sequence 2718, Ap
153	31	91.2	601	4	US-09-949-016-176385	Sequence 176385, A	c 226	31	91.2	4800	4	US-09-554-929-1	Sequence 1, Appli
154	31	91.2	601	4	US-09-949-016-178140	Sequence 178140, A	c 227	31	91.2	4835	1	US-08-386-435-9	Sequence 9, Appli
155	31	91.2	601	4	US-09-949-016-178141	Sequence 178141, A	c 228	31	91.2	4835	5	PCT-US96-02331-9	Sequence 9, Appli
156	31	91.2	601	4	US-09-949-016-180793	Sequence 180793, A	c 229	31	91.2	5044	3	US-09-735-935-3	Sequence 3, Appli
157	31	91.2	601	4	US-09-949-016-180794	Sequence 180794, A	c 230	31	91.2	5044	4	US-10-162-639-3	Sequence 3, Appli
158	31	91.2	645	4	US-09-949-016-180795	Sequence 180795, A	c 231	31	91.2	5177	4	US-09-814-915A-79	Sequence 79, Appl

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c 235	31	91.2	6559	3	US-09-234-186-1	Sequence 1, Appli	Sequence 1, Appli	30	91.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 236	31	91.2	6559	3	US-09-233-527-1	Sequence 1, Appli	Sequence 1, Appli	31	91.2	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 237	31	91.2	6560	5	PCT-US93-05651-1	Sequence 1, Appli	Sequence 1, Appli	30	88.2	23	4	US-09-280-428A-1	Sequence 1, Appli
c 238	31	91.2	7838	4	US-09-761-466-4	Sequence 1, Appli	Sequence 1, Appli	30	88.2	25	4	US-09-396-186G-47969	Sequence 47969, A
c 239	31	91.2	7916	4	US-09-479-040-1	Sequence 1, Appli	Sequence 1, Appli	30	88.2	25	4	US-09-396-196G-74247	Sequence 74247, A
c 240	31	91.2	8763	4	US-09-593-580B-1	Sequence 1, Appli	Sequence 1, Appli	31	88.2	27	2	US-08-558-823-11	Sequence 11, Appli
c 241	31	91.2	9464	4	US-09-378-847-1	Sequence 1, Appli	Sequence 1, Appli	30	88.2	45	4	US-09-769-863-2	Sequence 2, Appli
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c 243	31	91.2	9471	3	US-08-811-682-1	Sequence 1, Appli	Sequence 1, Appli	31	88.2	169	4	US-09-401-064-145	Sequence 145, App
c 244	31	91.2	9471	3	US-08-811-682-1	Sequence 1, Appli	Sequence 1, Appli	30	88.2	205	4	US-09-513-999C-20710	Sequence 20710, A
c 245	31	91.2	9975	3	US-08-977-171-1	Sequence 2, Appli	Sequence 2, Appli	30	88.2	207	4	US-09-328-352-2816	Sequence 2816, Ap
c 246	31	91.2	9934	3	US-08-977-171-2	Sequence 2, Appli	Sequence 2, Appli	30	88.2	208	4	US-09-471-276-153	Sequence 153, App
c 247	31	91.2	16302	4	US-09-949-016-17212	Sequence 17212, A	Sequence 17212, A	30	88.2	233	4	US-08-956-171E-4577	Sequence 4577, Ap
c 248	31	91.2	17607	4	US-09-949-016-15968	Sequence 15968, A	Sequence 15968, A	30	88.2	233	4	US-08-781-986A-4577	Sequence 4577, Ap
c 249	31	91.2	22143	4	US-09-949-016-15983	Sequence 15983, A	Sequence 15983, A	30	88.2	279	4	US-09-313-294A-3402	Sequence 3402, Ap
c 250	31	91.2	22375	4	US-09-949-016-15987	Sequence 15987, A	Sequence 15987, A	30	88.2	281	4	US-09-313-294A-5256	Sequence 5256, Ap
c 251	31	91.2	24538	4	US-09-949-016-13100	Sequence 13100, A	Sequence 13100, A	30	88.2	285	4	US-09-313-294A-1903	Sequence 1903, Ap
c 252	31	91.2	26777	4	US-09-949-016-13015	Sequence 13015, A	Sequence 13015, A	30	88.2	288	4	US-09-313-294A-2785	Sequence 2785, Ap
c 253	31	91.2	28366	4	US-09-949-016-15763	Sequence 15763, A	Sequence 15763, A	30	88.2	301	4	US-09-313-294A-7039	Sequence 7039, Ap
c 254	31	91.2	29970	4	US-09-949-016-14460	Sequence 14460, A	Sequence 14460, A	30	88.2	316	3	US-08-905-223-92	Sequence 92, Appli
c 255	31	91.2	35881	4	US-08-311-731A-127	Sequence 127, App	Sequence 127, App	30	88.2	392	4	US-09-621-976-3686	Sequence 3686, Ap
c 256	31	91.2	37715	4	US-09-949-016-13846	Sequence 13846, A	Sequence 13846, A	30	88.2	411	3	US-09-134-001C-1518	Sequence 1518, Ap
c 257	31	91.2	38969	4	US-09-949-016-14051	Sequence 14051, A	Sequence 14051, A	30	88.2	453	4	US-09-513-999C-851	Sequence 851, App
c 258	31	91.2	41798	4	US-09-949-016-16058	Sequence 16058, A	Sequence 16058, A	30	88.2	454	4	US-09-513-999C-13119	Sequence 13119, A
c 259	31	91.2	43986	4	US-09-949-016-17155	Sequence 17155, A	Sequence 17155, A	30	88.2	480	4	US-09-513-999C-960	Sequence 960, App
c 260	31	91.2	51928	4	US-09-949-016-13184	Sequence 13184, A	Sequence 13184, A	30	88.2	493	4	US-09-621-976-2468	Sequence 2468, Ap
c 261	31	91.2	52202	4	US-09-949-016-17006	Sequence 17006, A	Sequence 17006, A	30	88.2	508	4	US-09-621-976-2834	Sequence 2834, Ap
c 262	31	91.2	52851	4	US-09-949-016-13732	Sequence 13732, A	Sequence 13732, A	30	88.2	522	4	US-09-270-767-5998	Sequence 5998, Ap
c 263	31	91.2	64319	4	US-09-949-016-13804	Sequence 13804, A	Sequence 13804, A	30	88.2	535	4	US-09-270-767-30953	Sequence 30953, A
c 264	31	91.2	74527	4	US-09-949-016-12339	Sequence 12339, A	Sequence 12339, A	30	88.2	541	3	US-08-642-274D-37	Sequence 37, Appli
c 265	31	91.2	74528	4	US-09-949-016-13275	Sequence 13275, A	Sequence 13275, A	30	88.2	541	3	US-08-952-014C-37	Sequence 37, Appli
c 266	31	91.2	82496	4	US-09-596-002-36	Sequence 36, Appli	Sequence 36, Appli	30	88.2	546	2	US-08-558-823-9	Sequence 9, Appli
c 267	31	91.2	84207	4	US-09-596-002-36	Sequence 36, Appli	Sequence 36, Appli	30	88.2	546	2	US-09-513-999C-12585	Sequence 12585, A
c 268	31	91.2	93510	4	US-09-949-016-115095	Sequence 115095, A	Sequence 115095, A	30	88.2	552	4	US-09-513-999C-850	Sequence 850, App
c 269	31	91.2	94755	4	US-09-949-016-11839	Sequence 11839, A	Sequence 11839, A	30	88.2	564	4	US-09-328-352-3792	Sequence 3792, Ap
c 270	31	91.2	96109	4	US-09-596-002-35	Sequence 35, Appli	Sequence 35, Appli	30	88.2	568	4	US-09-540-236-1898	Sequence 1898, Ap
c 271	31	91.2	98302	4	US-09-949-016-16847	Sequence 16847, A	Sequence 16847, A	30	88.2	598	3	US-09-385-982-380	Sequence 380, App
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c 274	31	91.2	100551	4	US-09-949-016-16207	Sequence 16207, A	Sequence 16207, A	30	88.2	601	4	US-09-949-016-42297	Sequence 42297, A
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c 276	31	91.2	100877	4	US-09-949-016-13276	Sequence 13276, A	Sequence 13276, A	30	88.2	601	4	US-09-949-016-44996	Sequence 44996, A
c 277	31	91.2	101300	4	US-09-949-016-16108	Sequence 16108, A	Sequence 16108, A	30	88.2	601	4	US-09-949-016-59721	Sequence 59721, A
c 278	31	91.2	105055	4	US-09-949-016-14001	Sequence 14001, A	Sequence 14001, A	30	88.2	601	4	US-09-949-016-61414	Sequence 61414, A
c 279	31	91.2	105679	4	US-09-949-016-12360	Sequence 12360, A	Sequence 12360, A	30	88.2	601	4	US-09-949-016-62959	Sequence 62959, A
c 280	31	91.2	110585	4	US-09-949-016-13427	Sequence 13427, A	Sequence 13427, A	30	88.2	601	4	US-09-949-016-63789	Sequence 63789, A
c 281	31	91.2	110585	4	US-09-949-016-13427	Sequence 13427, A	Sequence 13427, A	30	88.2	601	4	US-09-949-016-63790	Sequence 63790, A
c 282	31	91.2	149543	4	US-09-949-016-15947	Sequence 15947, A	Sequence 15947, A	30	88.2	601	4	US-09-949-016-74695	Sequence 74695, A
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c 285	31	91.2	174259	4	US-09-949-016-11968	Sequence 11968, A	Sequence 11968, A	30	88.2	601	4	US-09-949-016-75292	Sequence 75292, A
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c 288	31	91.2	183770	4	US-09-949-016-15494	Sequence 15494, A	Sequence 15494, A	30	88.2	601	4	US-09-949-016-82721	Sequence 82721, A
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c 303	31	91.2	269223	4	US-09-596-002-41	Sequence 41, Appli	Sequence 41, Appli	30	88.2	601	4	US-09-949-016-99302	Sequence 99302, A
c 304	31	91.2	331814	4	US-09-949-016-12008	Sequence 12008, A	Sequence 12008, A	30	88.2	601	4	US-09-949-016-99302	Sequence 99302, A

378	30	88.2	601	4	US-09-949-016-99568	Sequence 99568, A	451	30	88.2	1362	4	US-09-769-863-13	Sequence 13, Appl
379	30	88.2	601	4	US-09-949-016-99834	Sequence 99834, A	C 452	30	88.2	1368	4	US-09-328-352-949	Sequence 949, App
380	30	88.2	601	4	US-09-949-016-100100	Sequence 100100, A	C 453	30	88.2	1377	4	US-09-543-681A-2152	Sequence 2152, Ap
381	30	88.2	601	4	US-09-949-016-100366	Sequence 100366, A	C 454	30	88.2	1386	4	US-09-602-787A-359	Sequence 359, App
382	30	88.2	601	4	US-09-949-016-100632	Sequence 100632, A	C 455	30	88.2	1387	4	US-09-567-003C-19	Sequence 19, Appl
383	30	88.2	601	4	US-09-949-016-100936	Sequence 100936, A	C 456	30	88.2	1398	4	US-09-489-039A-3060	Sequence 3060, Ap
384	30	88.2	601	4	US-09-949-016-101202	Sequence 101202, A	C 457	30	88.2	1454	2	US-08-713-000-7	Sequence 7, Appl
385	30	88.2	601	4	US-09-949-016-101468	Sequence 101468, A	C 458	30	88.2	1454	2	US-08-975-316-7	Sequence 7, Appl
386	30	88.2	601	4	US-09-949-016-101734	Sequence 101734, A	C 459	30	88.2	1454	3	US-09-211-710-7	Sequence 7, Appl
387	30	88.2	601	4	US-09-949-016-106049	Sequence 106049, A	C 460	30	88.2	1454	3	US-09-615-192A-7	Sequence 7, Appl
388	30	88.2	601	4	US-09-949-016-106248	Sequence 106248, A	C 461	30	88.2	1454	3	US-09-169-789-7	Sequence 7, Appl
389	30	88.2	601	4	US-09-949-016-106248	Sequence 106248, A	C 462	30	88.2	1460	3	US-09-615-192A-95	Sequence 95, Appl
390	30	88.2	601	4	US-09-949-016-106447	Sequence 106447, A	C 463	30	88.2	1460	3	US-09-567-003C-20	Sequence 20, Appl
391	30	88.2	601	4	US-09-949-016-106646	Sequence 106646, A	C 464	30	88.2	1460	4	US-09-169-789-95	Sequence 95, Appl
392	30	88.2	601	4	US-09-949-016-106845	Sequence 106845, A	C 465	30	88.2	1461	4	US-09-857-583B-1	Sequence 1, Appl
393	30	88.2	601	4	US-09-949-016-117009	Sequence 117009, A	C 466	30	88.2	1473	4	US-09-543-681A-3766	Sequence 3766, Ap
394	30	88.2	601	4	US-09-949-016-117618	Sequence 117618, A	C 467	30	88.2	1474	2	US-08-975-316-71	Sequence 71, Appl
395	30	88.2	601	4	US-09-949-016-120023	Sequence 120023, A	C 468	30	88.2	1474	3	US-09-615-192A-71	Sequence 71, Appl
396	30	88.2	601	4	US-09-949-016-120034	Sequence 120034, A	C 469	30	88.2	1474	3	US-09-615-192A-402	Sequence 402, App
397	30	88.2	601	4	US-09-949-016-120936	Sequence 120936, A	C 470	30	88.2	1474	3	US-09-325-932A-202	Sequence 202, App
398	30	88.2	601	4	US-09-949-016-130886	Sequence 130886, A	C 471	30	88.2	1474	4	US-09-169-789-71	Sequence 71, Appl
399	30	88.2	601	4	US-09-949-016-140911	Sequence 140911, A	C 472	30	88.2	1474	4	US-09-169-789-184	Sequence 184, App
400	30	88.2	601	4	US-09-949-016-169045	Sequence 169045, A	C 473	30	88.2	1476	4	US-09-248-796A-8230	Sequence 8230, Ap
401	30	88.2	601	4	US-09-949-016-169046	Sequence 169046, A	C 474	30	88.2	1491	4	US-09-249-020A-3	Sequence 3, Appl
402	30	88.2	601	4	US-09-949-016-176848	Sequence 176848, A	C 475	30	88.2	1491	4	US-09-668-286-3	Sequence 3, Appl
403	30	88.2	601	4	US-09-949-016-180641	Sequence 180641, A	C 476	30	88.2	1491	4	US-09-668-283-3	Sequence 3, Appl
404	30	88.2	601	4	US-09-949-016-196671	Sequence 196671, A	C 477	30	88.2	1491	4	US-10-442-173-3	Sequence 3, Appl
405	30	88.2	601	4	US-09-949-016-203969	Sequence 203969, A	C 478	30	88.2	1503	4	US-09-543-681A-1943	Sequence 1943, Ap
406	30	88.2	624	4	US-09-252-991A-6954	Sequence 995, App	C 479	30	88.2	1617	2	US-08-834-655-1	Sequence 1, Appl
407	30	88.2	632	4	US-09-513-999C-12584	Sequence 12584, A	C 480	30	88.2	1617	3	US-08-834-655A-1	Sequence 1, Appl
408	30	88.2	654	3	US-09-385-982-336	Sequence 336, App	C 481	30	88.2	1617	3	US-09-363-574-1	Sequence 1, Appl
409	30	88.2	654	3	US-09-328-352-2942	Sequence 2942, App	C 482	30	88.2	1617	3	US-09-363-526-1	Sequence 1, Appl
410	30	88.2	665	3	US-09-385-982-348	Sequence 348, App	C 483	30	88.2	1617	3	US-09-330-325-17	Sequence 17, Appl
411	30	88.2	669	4	US-09-328-352-2741	Sequence 2741, App	C 484	30	88.2	1701	4	US-09-328-352-683	Sequence 683, App
412	30	88.2	673	4	US-09-640-211A-328	Sequence 328, App	C 485	30	88.2	1884	4	US-09-328-352-3421	Sequence 3421, Ap
413	30	88.2	678	4	US-09-540-236-292	Sequence 292, App	C 486	30	88.2	1987	4	US-09-774-528-158	Sequence 158, App
414	30	88.2	694	4	US-09-270-767-3952	Sequence 3952, App	C 487	30	88.2	2043	4	US-09-248-796A-2264	Sequence 2264, Ap
415	30	88.2	694	4	US-09-270-767-19234	Sequence 19234, A	C 488	30	88.2	2234	4	US-09-949-016-3362	Sequence 3362, Ap
416	30	88.2	702	4	US-09-252-991A-6780	Sequence 6780, Ap	C 489	30	88.2	2394	4	US-09-620-312D-592	Sequence 592, App
417	30	88.2	732	4	US-09-248-796A-3894	Sequence 3894, Ap	C 490	30	88.2	2421	1	US-08-063-552-1	Sequence 1, Appl
418	30	88.2	745	4	US-09-513-999C-3929	Sequence 3929, App	C 491	30	88.2	2421	5	PCT-US93-05704-1	Sequence 1, Appl
419	30	88.2	756	4	US-09-248-796A-4002	Sequence 4002, App	C 492	30	88.2	2430	4	US-09-620-312D-176	Sequence 176, App
420	30	88.2	840	4	US-09-489-039A-2990	Sequence 2990, App	C 493	30	88.2	2430	4	US-09-620-312D-591	Sequence 591, App
421	30	88.2	868	4	US-09-270-767-13287	Sequence 13287, A	C 494	30	88.2	2436	3	US-08-983-275-1	Sequence 1, Appl
422	30	88.2	879	4	US-09-107-532A-214	Sequence 214, App	C 495	30	88.2	2508	4	US-09-248-796A-971	Sequence 971, App
423	30	88.2	957	4	US-09-902-540-8470	Sequence 8470, App	C 496	30	88.2	2593	4	US-09-624-912-89	Sequence 89, Appl
424	30	88.2	960	4	US-09-949-016-5223	Sequence 5223, App	C 497	30	88.2	2743	3	US-09-060-482-3	Sequence 3, Appl
425	30	88.2	996	4	US-09-270-767-10797	Sequence 10797, A	C 498	30	88.2	2880	4	US-09-949-016-2952	Sequence 2952, Ap
426	30	88.2	1022	4	US-09-270-767-14723	Sequence 14723, A	C 499	30	88.2	2881	4	US-09-702-705-1794	Sequence 1794, Ap
427	30	88.2	1068	4	US-09-567-003C-21	Sequence 21, Appl	C 500	30	88.2	2881	4	US-09-736-457-1794	Sequence 1794, Ap
428	30	88.2	1093	4	US-09-023-655-1169	Sequence 1169, App	C 501	30	88.2	2895	3	US-09-671-325-1794	Sequence 1794, Ap
429	30	88.2	1095	4	US-09-540-236-712	Sequence 712, App	C 502	30	88.2	2895	3	US-09-556-877-171	Sequence 171, App
430	30	88.2	1111	4	US-09-016-434-1297	Sequence 1297, App	C 503	30	88.2	2895	3	US-09-620-412C-171	Sequence 171, App
431	30	88.2	1116	4	US-09-252-991A-6913	Sequence 6913, App	C 504	30	88.2	2895	4	US-09-598-419-171	Sequence 171, App
432	30	88.2	1122	4	US-09-543-681A-245	Sequence 245, App	C 505	30	88.2	2934	3	US-09-556-877-183	Sequence 183, App
433	30	88.2	1143	4	US-09-328-352-2115	Sequence 2115, App	C 506	30	88.2	2934	3	US-09-620-412C-183	Sequence 183, App
434	30	88.2	1203	4	US-09-828-509-430	Sequence 490, App	C 507	30	88.2	2934	4	US-09-598-419-183	Sequence 183, App
435	30	88.2	1208	4	US-09-721-870-7	Sequence 7, Appl	C 508	30	88.2	3159	3	US-09-437-054A-7	Sequence 7, Appl
436	30	88.2	1211	4	US-09-023-655-793	Sequence 793, App	C 509	30	88.2	3209	4	US-09-949-016-3688	Sequence 3688, Ap
437	30	88.2	1214	4	US-09-721-870-5	Sequence 5, Appl	C 510	30	88.2	3237	2	US-08-419-075-26	Sequence 26, Appl
438	30	88.2	1220	4	US-09-721-870-9	Sequence 9, Appl	C 511	30	88.2	3348	4	US-09-312-762A-2	Sequence 2, Appl
439	30	88.2	1251	4	US-09-252-991A-6829	Sequence 6829, App	C 512	30	88.2	3356	4	US-09-634-238-8	Sequence 8, Appl
440	30	88.2	1251	4	US-09-540-236-645	Sequence 645, App	C 513	30	88.2	3442	3	US-09-438-906-1	Sequence 1, Appl
441	30	88.2	1254	4	US-09-248-796A-3831	Sequence 3831, App	C 514	30	88.2	3486	3	US-09-438-906-3	Sequence 3, Appl
442	30	88.2	1261	3	US-08-475-742-16	Sequence 16, Appl	C 515	30	88.2	3492	4	US-09-949-016-1688	Sequence 1688, Ap
443	30	88.2	1261	4	US-08-261-293-16	Sequence 16, Appl	C 516	30	88.2	3539	4	US-09-949-016-2396	Sequence 2396, Ap
444	30	88.2	1263	4	US-09-543-681A-3749	Sequence 3749, App	C 517	30	88.2	3556	1	US-07-971-624E-1	Sequence 1, Appl
445	30	88.2	1308	4	US-09-489-039A-2917	Sequence 2917, App	C 518	30	88.2	3572	1	US-07-971-624E-2	Sequence 2, Appl
446	30	88.2	1318	4	US-09-721-870-11	Sequence 11, Appl	C 519	30	88.2	3601	3	US-09-668-680-2	Sequence 2, Appl
447	30	88.2	1335	4	US-09-249-020A-1	Sequence 1, Appl	C 520	30	88.2	3616	4	US-09-976-594-265	Sequence 265, App
448	30	88.2	1335	4	US-09-668-286-1	Sequence 1, Appl	C 521	30	88.2	3616	4	US-09-976-594-265	Sequence 265, App
449	30	88.2	1335	4	US-09-668-283-1	Sequence 1, Appl	C 522	30	88.2	3934	4	US-09-023-748-3	Sequence 1066, Ap
450	30	88.2	1335	4	US-10-442-173-1	Sequence 1, Appl	C 523	30	88.2	4032	1	US-08-107-745-3	Sequence 3, Appl

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525	30	88.2	4032	5	PCT-US92-01385-3	Sequence 3, Appl1	598	30	88.2	46885	4	US-09-949-016-13848	Sequence 13848, A
526	30	88.2	4071	3	US-09-513-057C-5	Sequence 5, Appl1	c 599	30	88.2	47858	4	US-09-949-016-14965	Sequence 14965, A
527	30	88.2	4071	4	US-09-746-801A-5	Sequence 5, Appl1	c 600	30	88.2	47968	4	US-09-949-016-15240	Sequence 15240, A
528	30	88.2	4087	4	US-09-799-451-262	Sequence 262, Appl	c 601	30	88.2	48328	4	US-09-596-002-27	Sequence 27, Appl
529	30	88.2	4771	4	US-09-620-314D-121	Sequence 121, Appl	c 602	30	88.2	47995	3	US-09-453-702B-60	Sequence 60, Appl
c 530	30	88.2	5325	4	US-10-164-595-17	Sequence 17, Appl	c 603	30	88.2	49971	4	US-09-949-016-16888	Sequence 16888, A
c 531	30	88.2	5334	4	US-10-164-595-21	Sequence 21, Appl	c 604	30	88.2	55195	4	US-09-949-016-15854	Sequence 15854, A
c 532	30	88.2	5455	1	US-08-342-930-1	Sequence 1, Appl1	c 605	30	88.2	58829	4	US-09-949-016-13146	Sequence 13146, A
c 533	30	88.2	5581	4	US-10-164-595-19	Sequence 19, Appl	c 606	30	88.2	60788	4	US-09-949-016-16789	Sequence 16789, A
c 534	30	88.2	5512	2	US-08-629-001A-1	Sequence 1, Appl1	c 607	30	88.2	60990	4	US-09-949-016-14080	Sequence 14080, A
c 535	30	88.2	5512	3	US-08-642-274D-1	Sequence 1, Appl1	c 608	30	88.2	61663	4	US-09-453-702B-62	Sequence 62, Appl
c 536	30	88.2	5912	3	US-08-952-127-1	Sequence 1, Appl1	c 609	30	88.2	72128	4	US-09-949-016-16018	Sequence 16018, A
c 537	30	88.2	5912	3	US-08-952-014C-1	Sequence 1, Appl1	c 610	30	88.2	83617	4	US-09-949-016-12254	Sequence 12254, A
c 538	30	88.2	6298	4	US-09-830-123-20	Sequence 20, Appl	c 611	30	88.2	87205	4	US-09-949-016-13430	Sequence 13430, A
c 539	30	88.2	6380	4	US-09-902-540-891	Sequence 891, Appl	c 612	30	88.2	90150	4	US-09-949-016-17383	Sequence 17383, A
c 540	30	88.2	6525	1	US-08-493-092-3	Sequence 3, Appl1	c 613	30	88.2	94879	4	US-09-949-016-12101	Sequence 12101, A
c 541	30	88.2	6525	1	US-08-508-836A-3	Sequence 3, Appl1	c 614	30	88.2	94884	4	US-09-949-016-13393	Sequence 13393, A
c 542	30	88.2	7408	1	US-08-441-822-1	Sequence 1, Appl1	c 615	30	88.2	95122	4	US-09-949-016-17235	Sequence 17235, A
c 543	30	88.2	7410	1	US-08-493-092-1	Sequence 1, Appl1	c 616	30	88.2	95255	4	US-09-949-016-17067	Sequence 17067, A
c 544	30	88.2	7410	1	US-08-508-836A-1	Sequence 1, Appl1	c 617	30	88.2	95890	4	US-09-949-016-16412	Sequence 16412, A
c 545	30	88.2	7786	4	US-09-790-988-2	Sequence 2, Appl1	c 618	30	88.2	96109	4	US-09-596-002-35	Sequence 35, Appl
c 546	30	88.2	8230	4	US-09-949-016-14183	Sequence 14183, A	c 619	30	88.2	99797	4	US-09-949-016-15255	Sequence 15255, A
c 547	30	88.2	8502	3	US-09-234-827B-1	Sequence 1, Appl1	c 620	30	88.2	112132	3	US-09-741-150-3	Sequence 3, Appl1
c 548	30	88.2	9171	2	US-08-629-001A-2	Sequence 2, Appl1	c 621	30	88.2	112132	4	US-10-160-187-3	Sequence 3, Appl1
c 549	30	88.2	9171	3	US-08-642-274D-2	Sequence 2, Appl1	c 622	30	88.2	112623	4	US-09-949-016-17374	Sequence 17374, A
c 550	30	88.2	9171	3	US-08-952-127-2	Sequence 2, Appl1	c 623	30	88.2	119762	4	US-09-949-016-17313	Sequence 17313, A
c 551	30	88.2	9171	3	US-08-952-014C-2	Sequence 2, Appl1	c 624	30	88.2	121068	4	US-09-949-016-14138	Sequence 14138, A
c 552	30	88.2	9196	4	US-08-984-090-1	Sequence 1, Appl1	c 625	30	88.2	121970	4	US-09-949-016-17216	Sequence 17216, A
c 553	30	88.2	9385	2	US-08-874-266-1	Sequence 1, Appl1	c 626	30	88.2	123863	4	US-09-949-016-14202	Sequence 14202, A
c 554	30	88.2	9385	3	US-09-360-416-1	Sequence 1, Appl1	c 627	30	88.2	125188	4	US-09-949-016-11980	Sequence 11980, A
c 555	30	88.2	9385	4	US-09-949-016-14409	Sequence 4409, Ap	c 628	30	88.2	129778	4	US-09-949-016-12191	Sequence 12191, A
c 556	30	88.2	9558	4	US-09-949-016-13026	Sequence 13026, A	c 629	30	88.2	132978	4	US-09-949-016-17075	Sequence 17075, A
c 557	30	88.2	9870	1	US-08-508-836A-9	Sequence 9, Appl1	c 630	30	88.2	131631	4	US-09-949-016-11757	Sequence 11757, A
c 558	30	88.2	10451	4	US-09-949-016-12192	Sequence 12192, A	c 631	30	88.2	131978	4	US-09-949-016-13117	Sequence 13117, A
c 559	30	88.2	11928	4	US-09-919-039-288	Sequence 288, Appl	c 632	30	88.2	143612	4	US-09-949-016-16598	Sequence 16598, A
c 560	30	88.2	12032	4	US-09-949-016-15080	Sequence 15080, A	c 633	30	88.2	145801	4	US-09-949-016-16151	Sequence 16151, A
c 561	30	88.2	12032	4	US-09-949-016-15081	Sequence 15081, A	c 634	30	88.2	148783	4	US-09-949-016-15729	Sequence 15729, A
c 562	30	88.2	14600	4	US-09-949-016-16450	Sequence 16450, A	c 635	30	88.2	160759	4	US-09-949-016-16514	Sequence 16514, A
c 563	30	88.2	14635	4	US-09-949-016-13927	Sequence 13927, A	c 636	30	88.2	165651	4	US-09-949-016-13032	Sequence 13032, A
c 564	30	88.2	15164	4	US-09-919-497-20	Sequence 20, Appl	c 637	30	88.2	167708	4	US-09-949-016-16423	Sequence 16423, A
c 565	30	88.2	16883	4	US-09-949-016-14694	Sequence 14694, A	c 638	30	88.2	174639	4	US-09-949-016-16509	Sequence 16509, A
c 566	30	88.2	18157	4	US-09-949-016-16193	Sequence 16193, A	c 639	30	88.2	187595	4	US-09-949-016-15546	Sequence 15546, A
c 567	30	88.2	18620	4	US-09-949-016-13010	Sequence 13010, A	c 640	30	88.2	191433	4	US-09-949-016-16144	Sequence 16144, A
c 568	30	88.2	18994	2	US-08-459-586-4	Sequence 4, Appl1	c 641	30	88.2	192956	4	US-09-949-016-14382	Sequence 14382, A
c 569	30	88.2	18994	2	US-08-282-696-4	Sequence 4, Appl1	c 642	30	88.2	192956	4	US-09-949-016-14382	Sequence 14382, A
c 570	30	88.2	19566	4	US-09-949-016-12096	Sequence 12096, A	c 643	30	88.2	208433	4	US-09-949-016-13527	Sequence 13527, A
c 571	30	88.2	19567	4	US-09-949-016-14114	Sequence 14114, A	c 644	30	88.2	213456	4	US-09-820-007-3	Sequence 3, Appl1
c 572	30	88.2	22294	4	US-09-949-016-14020	Sequence 14020, A	c 645	30	88.2	229354	4	US-09-705-400-64	Sequence 64, Appl
c 573	30	88.2	23219	4	US-09-949-016-13556	Sequence 13556, A	c 646	30	88.2	236341	4	US-09-949-016-13978	Sequence 13978, A
c 574	30	88.2	24339	4	US-09-949-016-14068	Sequence 14068, A	c 647	30	88.2	254778	4	US-09-949-016-13417	Sequence 12417, A
c 575	30	88.2	24645	4	US-09-949-016-14062	Sequence 14062, A	c 648	30	88.2	276237	4	US-09-949-016-17504	Sequence 17504, A
c 576	30	88.2	25333	4	US-09-949-016-14069	Sequence 14069, A	c 649	30	88.2	278866	4	US-09-949-016-13922	Sequence 13922, A
c 577	30	88.2	26173	3	US-09-453-702B-69	Sequence 69, Appl	c 650	30	88.2	278866	4	US-09-949-016-13924	Sequence 13924, A
c 578	30	88.2	26664	3	US-09-564-805-28	Sequence 28, Appl	c 651	30	88.2	278866	4	US-09-949-016-13924	Sequence 13924, A
c 579	30	88.2	28585	4	US-09-949-016-17311	Sequence 17311, A	c 652	30	88.2	278866	4	US-09-949-016-13926	Sequence 13926, A
c 580	30	88.2	28720	3	US-09-341-587-7	Sequence 7, Appl1	c 653	30	88.2	278866	4	US-09-949-016-13926	Sequence 13926, A
c 581	30	88.2	29133	4	US-09-949-016-12694	Sequence 12694, A	c 654	30	88.2	278866	4	US-09-949-016-14699	Sequence 14699, A
c 582	30	88.2	29558	4	US-09-949-016-15607	Sequence 15607, A	c 655	30	88.2	278866	4	US-09-949-016-14700	Sequence 14700, A
c 583	30	88.2	30444	4	US-09-949-016-14997	Sequence 14997, A	c 656	30	88.2	278866	4	US-09-949-016-14701	Sequence 14701, A
c 584	30	88.2	33908	4	US-09-949-016-15104	Sequence 15104, A	c 657	30	88.2	278866	4	US-09-949-016-14702	Sequence 14702, A
c 585	30	88.2	35913	4	US-09-949-016-15586	Sequence 15586, A	c 658	30	88.2	278866	4	US-09-949-016-14703	Sequence 14703, A
c 586	30	88.2	36203	4	US-09-949-016-15430	Sequence 15430, A	c 659	30	88.2	323820	4	US-09-949-016-14139	Sequence 14139, A
c 587	30	88.2	36618	4	US-09-949-016-15935	Sequence 15935, A	c 660	30	88.2	325034	4	US-09-949-016-14957	Sequence 14957, A
c 588	30	88.2	36820	4	US-09-949-016-16665	Sequence 16665, A	c 661	30	88.2	340380	4	US-09-949-016-11179	Sequence 14179, A
c 589	30	88.2	36938	4	US-09-949-016-13484	Sequence 13484, A	c 662	30	88.2	346112	4	US-09-949-016-13165	Sequence 13165, A
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c 591	30	88.2	38479	4	US-09-949-016-16730	Sequence 16730, A	c 664	30	88.2	390890	4	US-09-949-016-14720	Sequence 14720, A
c 592	30	88.2	40586	4	US-09-949-016-16965	Sequence 16965, A	c 665	30	88.2	767677	4	US-09-949-016-12147	Sequence 12147, A
c 593	30	88.2	42894	4	US-09-949-016-13201	Sequence 12301, A	c 666	30	88.2	767677	4	US-09-949-016-17361	Sequence 17361, A
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c 595	30	88.2	42917	4	US-09-949-016-13795	Sequence 13795, A	c 668	30	88.2	818128	4	US-09-949-016-14547	Sequence 14547, A
c 596	30	88.2	46492	4	US-09-949-016-12953	Sequence 12953, A	c 669	30	88.2	818128	4	US-09-949-016-14548	Sequence 14548, A

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C 671	30	88.2	818128	4	US-09-949-016-14550	Sequence 14550, A	C 744	29	85.3	313	4	US-09-270-767-7295	Sequence 7295, Ap
C 672	30	88.2	818128	4	US-09-949-016-14551	Sequence 14551, A	C 745	29	85.3	313	4	US-09-270-767-22577	Sequence 22577, A
C 673	30	88.2	818128	4	US-09-949-016-14552	Sequence 14552, A	C 746	29	85.3	314	3	US-08-905-223-91	Sequence 91, Appl
C 674	30	88.2	818128	4	US-09-949-016-14553	Sequence 14553, A	C 747	29	85.3	315	4	US-09-902-540-8453	Sequence 8453, Ap
C 675	30	88.2	818128	4	US-09-949-016-14554	Sequence 14554, A	C 748	29	85.3	316	2	US-08-799-173A-16	Sequence 16, Appl
C 676	30	88.2	818128	4	US-09-949-016-14555	Sequence 14555, A	C 749	29	85.3	316	2	US-08-799-173A-17	Sequence 17, Appl
C 677	30	88.2	818128	4	US-09-949-016-14556	Sequence 14556, A	C 750	29	85.3	316	4	US-09-170-042A-17	Sequence 17, Appl
C 678	30	88.2	818128	4	US-09-949-016-14557	Sequence 14557, A	C 751	29	85.3	316	4	US-09-170-042A-18	Sequence 18, Appl
C 679	30	88.2	818128	4	US-09-949-016-14558	Sequence 14558, A	C 752	29	85.3	318	4	US-09-902-540-9225	Sequence 9225, Ap
C 680	30	88.2	818128	4	US-09-949-016-14559	Sequence 14559, A	C 753	29	85.3	321	4	US-09-248-796A-11993	Sequence 11993, A
C 681	30	88.2	818128	4	US-09-949-016-14560	Sequence 14560, A	C 754	29	85.3	322	1	US-08-421-356-2	Sequence 2, Appl1
C 682	30	88.2	818128	4	US-09-949-016-14561	Sequence 14561, A	C 755	29	85.3	322	3	US-09-046-783-2	Sequence 2, Appl1
C 683	30	88.2	818128	4	US-09-949-016-14562	Sequence 14562, A	C 756	29	85.3	324	3	US-09-134-001C-151	Sequence 151, App
C 684	30	88.2	818128	4	US-09-949-016-14563	Sequence 14563, A	C 757	29	85.3	334	4	US-09-270-767-28697	Sequence 28697, A
C 685	30	88.2	818128	4	US-09-949-016-14564	Sequence 14564, A	C 758	29	85.3	338	4	US-09-640-211A-1443	Sequence 1443, Ap
C 686	30	88.2	818128	4	US-09-949-016-14565	Sequence 14565, A	C 759	29	85.3	342	4	US-09-107-433-1625	Sequence 1625, Ap
C 687	30	88.2	818128	4	US-09-949-016-14566	Sequence 14566, A	C 760	29	85.3	348	2	US-08-853-659A-33	Sequence 33, Appl
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C 689	30	88.2	1230025	4	US-09-438-185A-1	Sequence 1, Appl1	C 762	29	85.3	357	4	US-09-775-932-23	Sequence 23, Appl
C 690	30	88.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl1	C 763	29	85.3	357	4	US-09-513-999C-3187	Sequence 3187, Ap
C 691	30	88.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl1	C 764	29	85.3	366	3	US-09-020-956-115	Sequence 115, App
C 692	29	85.3	25	2	US-08-859-998-105	Sequence 105, App	C 765	29	85.3	366	3	US-09-030-607-115	Sequence 115, App
C 693	29	85.3	25	3	US-09-225-928-105	Sequence 105, App	C 766	29	85.3	366	3	US-09-439-313-115	Sequence 115, App
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C 699	29	85.3	105	4	US-09-513-999C-19529	Sequence 19529, Ap	C 772	29	85.3	366	4	US-09-115-453-115	Sequence 115, App
C 700	29	85.3	114	4	US-09-902-540-5774	Sequence 5774, Ap	C 773	29	85.3	366	4	US-09-688-489-115	Sequence 115, App
C 701	29	85.3	140	4	US-09-270-767-25601	Sequence 25601, A	C 774	29	85.3	366	4	US-09-679-426-115	Sequence 115, App
C 702	29	85.3	140	4	US-09-513-999C-21615	Sequence 21615, A	C 775	29	85.3	366	4	US-09-759-143-115	Sequence 115, App
C 703	29	85.3	178	3	US-08-991-789A-188	Sequence 188, App	C 776	29	85.3	366	4	US-09-651-236-115	Sequence 115, App
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C 706	29	85.3	178	4	US-09-289-198-188	Sequence 188, App	C 779	29	85.3	375	4	US-09-621-976-17190	Sequence 17190, A
C 707	29	85.3	178	4	US-09-429-755-188	Sequence 188, App	C 780	29	85.3	375	4	US-09-640-211A-1413	Sequence 1413, Ap
C 708	29	85.3	178	4	US-09-699-295-188	Sequence 188, App	C 781	29	85.3	381	4	US-09-134-000C-593	Sequence 593, App
C 709	29	85.3	186	4	US-09-270-767-26311	Sequence 26311, A	C 782	29	85.3	384	4	US-09-902-540-1711	Sequence 1711, Ap
C 710	29	85.3	186	4	US-09-270-767-27947	Sequence 27947, A	C 783	29	85.3	390	1	US-08-482-889-79	Sequence 79, Appl
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C 712	29	85.3	189	4	US-09-248-796A-13566	Sequence 13566, A	C 785	29	85.3	390	2	US-08-487-113D-79	Sequence 79, Appl
C 713	29	85.3	201	4	US-09-248-796A-9277	Sequence 9277, Ap	C 786	29	85.3	390	2	US-08-473-503-79	Sequence 79, Appl
C 714	29	85.3	201	4	US-09-248-796A-10910	Sequence 10910, A	C 787	29	85.3	390	2	US-08-483-932-79	Sequence 79, Appl
C 715	29	85.3	215	4	US-09-513-999C-26837	Sequence 26837, A	C 788	29	85.3	390	2	US-08-720-420A-79	Sequence 79, Appl
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C 717	29	85.3	222	4	US-09-513-999C-13712	Sequence 13712, A	C 790	29	85.3	390	3	US-08-475-680-79	Sequence 79, Appl
C 718	29	85.3	227	4	US-09-621-976-14248	Sequence 14248, A	C 791	29	85.3	390	4	US-09-902-540-2819	Sequence 2819, Ap
C 719	29	85.3	231	4	US-09-107-532A-3197	Sequence 3197, Ap	C 792	29	85.3	391	4	US-09-270-767-3793	Sequence 3793, Ap
C 720	29	85.3	237	4	US-09-270-767-28845	Sequence 28845, A	C 793	29	85.3	391	4	US-09-270-767-19075	Sequence 19075, A
C 721	29	85.3	252	4	US-09-313-294A-2390	Sequence 2390, Ap	C 794	29	85.3	393	4	US-09-621-976-8394	Sequence 8394, Ap
C 722	29	85.3	255	4	US-09-902-540-8500	Sequence 8500, Ap	C 795	29	85.3	393	4	US-09-107-433-943	Sequence 943, App
C 723	29	85.3	258	4	US-09-513-999C-35366	Sequence 35366, A	C 796	29	85.3	399	4	US-09-902-540-2937	Sequence 2937, Ap
C 724	29	85.3	262	4	US-09-313-294A-2014	Sequence 2014, Ap	C 797	29	85.3	400	4	US-08-956-171E-3726	Sequence 3726, Ap
C 725	29	85.3	267	4	US-09-313-294A-117	Sequence 117, App	C 798	29	85.3	400	4	US-08-781-986A-3726	Sequence 3726, Ap
C 726	29	85.3	288	4	US-09-270-767-10837	Sequence 10837, A	C 799	29	85.3	402	4	US-09-621-976-13154	Sequence 13154, A
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C 728	29	85.3	300	2	US-08-637-759B-32	Sequence 32, Appl	C 801	29	85.3	405	4	US-09-248-796A-7651	Sequence 7651, Ap
C 729	29	85.3	300	3	US-08-871-355A-32	Sequence 32, Appl	C 802	29	85.3	408	4	US-09-248-796A-8543	Sequence 8543, Ap
C 730	29	85.3	300	3	US-09-201-945-32	Sequence 32, Appl	C 803	29	85.3	409	4	US-08-956-171E-2941	Sequence 2941, Ap
C 731	29	85.3	300	4	US-09-270-767-30861	Sequence 30861, A	C 804	29	85.3	409	4	US-08-781-986A-2941	Sequence 2941, Ap
C 732	29	85.3	305	3	US-09-439-313-295	Sequence 295, App	C 805	29	85.3	411	4	US-09-902-540-8481	Sequence 8481, Ap
C 733	29	85.3	305	3	US-09-352-616A-295	Sequence 295, App	C 806	29	85.3	412	4	US-09-621-976-623	Sequence 623, App
C 734	29	85.3	305	3	US-09-232-149A-295	Sequence 295, App	C 807	29	85.3	429	4	US-09-543-681A-3274	Sequence 3274, Ap
C 735	29	85.3	305	4	US-09-159-812-295	Sequence 295, App	C 808	29	85.3	429	4	US-09-621-976-14106	Sequence 14106, A
C 736	29	85.3	305	4	US-09-636-215-295	Sequence 295, App	C 809	29	85.3	437	4	US-09-270-767-31041	Sequence 31041, A
C 737	29	85.3	305	4	US-09-685-166A-295	Sequence 295, App	C 810	29	85.3	441	3	US-09-328-111-77	Sequence 77, Appl
C 738	29	85.3	305	4	US-09-688-489-295	Sequence 295, App	C 811	29	85.3	441	4	US-09-248-796A-7067	Sequence 7067, Ap
C 739	29	85.3	305	4	US-09-679-426-295	Sequence 295, App	C 812	29	85.3	443	4	US-09-513-999C-3784	Sequence 3784, Ap
C 740	29	85.3	305	4	US-09-759-143-295	Sequence 295, App	C 813	29	85.3	446	4	US-09-270-767-12225	Sequence 12225, A
C 741	29	85.3	305	4	US-09-651-236-295	Sequence 295, App	C 814	29	85.3	447	4	US-09-501-115-17	Sequence 17, Appl
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C 817	29	85.3	453	4	US-09-902-540-5781	Sequence 5781, Ap	890	29	85.3	601	4	US-09-949-016-25579	Sequence 25579, A
C 818	29	85.3	456	1	US-08-450-945-70	Sequence 70, Appl	891	29	85.3	601	4	US-09-949-016-25580	Sequence 25580, A
C 819	29	85.3	456	3	US-08-976-161-70	Sequence 170, Appl	C 892	29	85.3	601	4	US-09-949-016-26974	Sequence 26974, A
C 820	29	85.3	456	4	US-09-328-352-1362	Sequence 1362, Ap	C 893	29	85.3	601	4	US-09-949-016-28832	Sequence 28832, A
C 821	29	85.3	456	4	US-09-328-352-1787	Sequence 1787, Ap	C 894	29	85.3	601	4	US-09-949-016-28833	Sequence 28833, A
C 822	29	85.3	462	4	US-09-134-000C-2336	Sequence 2336, Ap	C 895	29	85.3	601	4	US-09-949-016-28834	Sequence 28834, A
C 823	29	85.3	464	4	US-09-270-767-10019	Sequence 10019, A	C 896	29	85.3	601	4	US-09-949-016-28835	Sequence 28835, A
C 824	29	85.3	464	4	US-09-513-999C-32614	Sequence 32614, A	C 897	29	85.3	601	4	US-09-949-016-32083	Sequence 32083, A
C 825	29	85.3	464	4	US-09-248-796A-4086	Sequence 4086, Ap	C 898	29	85.3	601	4	US-09-949-016-37394	Sequence 37394, A
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C 828	29	85.3	478	4	US-09-513-999C-19248	Sequence 19248, A	C 901	29	85.3	601	4	US-09-949-016-40199	Sequence 40199, A
C 829	29	85.3	480	4	US-09-489-039A-3486	Sequence 3486, Ap	C 902	29	85.3	601	4	US-09-949-016-41191	Sequence 41191, A
C 830	29	85.3	481	4	US-09-621-976-1469	Sequence 1469, Ap	C 903	29	85.3	601	4	US-09-949-016-41766	Sequence 41766, A
C 831	29	85.3	484	4	US-09-439-313-434	Sequence 434, Appl	C 904	29	85.3	601	4	US-09-949-016-48711	Sequence 48711, A
C 832	29	85.3	484	3	US-09-352-616A-434	Sequence 434, Appl	C 905	29	85.3	601	4	US-09-949-016-55344	Sequence 55344, A
C 833	29	85.3	484	4	US-09-636-215-434	Sequence 434, Appl	C 906	29	85.3	601	4	US-09-949-016-56300	Sequence 56300, A
C 834	29	85.3	484	4	US-09-685-166A-434	Sequence 434, Appl	C 907	29	85.3	601	4	US-09-949-016-56619	Sequence 56619, A
C 835	29	85.3	484	4	US-09-679-426-434	Sequence 434, Appl	C 908	29	85.3	601	4	US-09-949-016-56620	Sequence 56620, A
C 836	29	85.3	484	4	US-09-759-143-434	Sequence 434, Appl	C 909	29	85.3	601	4	US-09-949-016-56621	Sequence 56621, A
C 837	29	85.3	484	4	US-09-651-236-434	Sequence 434, Appl	C 910	29	85.3	601	4	US-09-949-016-57166	Sequence 57166, A
C 838	29	85.3	485	4	US-09-489-039A-2102	Sequence 2102, Ap	C 911	29	85.3	601	4	US-09-949-016-57884	Sequence 57884, A
C 839	29	85.3	489	4	US-09-270-767-9705	Sequence 9705, Ap	C 912	29	85.3	601	4	US-09-949-016-62158	Sequence 62158, A
C 840	29	85.3	489	4	US-09-270-767-24987	Sequence 24987, A	C 913	29	85.3	601	4	US-09-949-016-62159	Sequence 62159, A
C 841	29	85.3	492	4	US-09-328-352-1653	Sequence 1653, Ap	C 914	29	85.3	601	4	US-09-949-016-62728	Sequence 62728, A
C 842	29	85.3	495	4	US-09-248-796A-7994	Sequence 7994, Ap	C 915	29	85.3	601	4	US-09-949-016-62526	Sequence 62526, A
C 843	29	85.3	495	5	PCT-US94-07091-3	Sequence 3, Appl	C 916	29	85.3	601	4	US-09-949-016-65303	Sequence 65303, A
C 844	29	85.3	497	4	US-09-328-475C-222	Sequence 222, Appl	C 917	29	85.3	601	4	US-09-949-016-67176	Sequence 67176, A
C 845	29	85.3	498	4	US-09-248-796A-7677	Sequence 7677, Ap	C 918	29	85.3	601	4	US-09-949-016-67177	Sequence 67177, A
C 846	29	85.3	498	5	PCT-US94-07091-4	Sequence 4, Appl	C 919	29	85.3	601	4	US-09-949-016-67178	Sequence 67178, A
C 847	29	85.3	499	4	US-09-621-976-13988	Sequence 13988, A	C 920	29	85.3	601	4	US-09-949-016-70204	Sequence 70204, A
C 848	29	85.3	501	4	US-09-328-352-2383	Sequence 2383, Ap	C 921	29	85.3	601	4	US-09-949-016-71253	Sequence 71253, A
C 849	29	85.3	504	4	US-09-252-991A-5289	Sequence 5289, Ap	C 922	29	85.3	601	4	US-09-949-016-73630	Sequence 73630, A
C 850	29	85.3	508	3	US-09-221-017B-535	Sequence 535, Appl	C 923	29	85.3	601	4	US-09-949-016-73631	Sequence 73631, A
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Sequence 205970,

ALIGNMENTS

RESULT 1  
US-09-396-196G-33466  
; Sequence 33466, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33466  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-33466  
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Score: 34.00 Matches: 5  
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Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

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Db 6 CACAATGCACATCAC 20  
RESULT 2  
US-09-270-767-8295  
; Sequence 8295, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8295  
; LENGTH: 82  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-8295  
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Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
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DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-8295 (1-82)  
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Db 2 CACAACGCCACCCAC 16  
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US-09-270-767-23577  
; Sequence 23577, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
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; LENGTH: 82  
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; ORGANISM: Drosophila melanogaster  
US-09-270-767-23577  
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Percent Similarity: 100.00% Conservatives: 0  
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Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-23577 (1-82)  
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Db 2 CACAACGCCACCCAC 16  
RESULT 4  
US-09-270-767-28874

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; Sequence 28874, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28874

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DB:                4      Gaps:      0

US-10-029-756-12 (1-5) x US-09-270-767-28874 (1-206)

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Db      183 CACAAATGCCCAACAT 197
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RESULT 5
US-08-956-171E-4362/c
; Sequence 4362, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4362:
; SEQUENCE CHARACTERISTICS:

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Oy 1 HisaenAlaHisHis 5
Db 205 CATACGGCACATCAT 191

RESULT 7
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; Sequence 3814, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3814
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3814

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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-543-681A-3814 (1-333)

Oy 1 HisaenAlaHisHis 5
Db 205 CATACGGCACCAT 191

RESULT 8
US-08-956-171E-4136
; Sequence 4136, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
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; APPLICATION NUMBER: US/08/956,171E
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4136

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US-10-029-756-12 (1-5) x US-08-956-171E-4136 (1-348)

Oy 1 HisaenAlaHisHis 5
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RESULT 9
US-08-781-986A-4136
; Sequence 4136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
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; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4136

Alignment Scores:
Pred. No.: 358 Length: 348
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4136:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4136:
US-08-956-171E-4136

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US-10-029-756-12 (1-5) x US-08-956-171E-4136 (1-348)

Oy 1 HisaenAlaHisHis 5
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RESULT 9
US-08-781-986A-4136
; Sequence 4136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4136

Alignment Scores:
Pred. No.: 358 Length: 348
Score: 34.00 Matches: 5
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Query Match: 100.00% Indels: 0
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Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-4136 (1-348)

Qy 1 HisAenAlaHisHis 5  
Db 144 CATAACGCACCAT 158

RESULT 10  
US-08-975-316-33/c  
; Sequence 33, Application US/08975316  
; Patent No. 5952486  
; GENERAL INFORMATION:  
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-SEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/975,316  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/713,000  
; FILING DATE: September 11, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SLEATH, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000/1003C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 380 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-975-316-33

Alignment Scores:  
Pred. No.: 395 Length: 380  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-975-316-33 (1-380)

Qy 1 HisAenAlaHisHis 5  
Db 50 CACAACGCTCCCAT 36

RESULT 11  
US-09-615-192A-33/c

; Sequence 33, Application US/09615192A  
; Patent No. 6410718  
; GENERAL INFORMATION:  
; APPLICANT: BLOKSBERG, Leonard N.  
; APPLICANT: Havukkala, Ilkka  
; TITLE OF INVENTION: Materials and Methods for the  
; TITLE OF INVENTION: Modification of Plant Lignin Content  
; FILE REFERENCE: 11000.1003C4U  
; CURRENT APPLICATION NUMBER: US/09/615,192A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 08/975,316  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: US 08/713,000  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: US 09/169,789  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-615-192A-33

Alignment Scores:  
Pred. No.: 395 Length: 380  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-615-192A-33 (1-380)

Qy 1 HisAenAlaHisHis 5  
Db 50 CACAACGCTCCCAT 36

RESULT 12  
US-09-169-789-33/c  
; Sequence 33, Application US/09169789  
; Patent No. 6653528  
; GENERAL INFORMATION:  
; APPLICANT: BLOKSBERG, Leonard N.  
; APPLICANT: Havukkala, Ilkka  
; TITLE OF INVENTION: Materials and Methods for the  
; TITLE OF INVENTION: Modification of Plant Lignin Content  
; FILE REFERENCE: 11000.1003C2  
; CURRENT APPLICATION NUMBER: US/09/169,789  
; CURRENT FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 08/975,316  
; EARLIER FILING DATE: 1997-11-21  
; EARLIER APPLICATION NUMBER: US 08/713,000  
; EARLIER FILING DATE: 1996-09-11  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-169-789-33

Alignment Scores:  
Pred. No.: 395 Length: 380  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-169-789-33 (1-380)

Qy 1 HisAenAlaHisHis 5

```
Db      50 CACAACGCTCACCAT 36
|||||
RESULT 13
US-08-956-171E-3743
; Sequence 3743, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956.171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 3743:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3743:
US-08-956-171E-3743
Alignment Scores:
Pred. No.: 418 Length: 400
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-08-956-171E-3743 (1-400)
Qy      1 HisAenAlaHisHis 5
Db      79 CATAACGCACATCAT 93
|||||
RESULT 15
US-09-615-192A-115/c
; Sequence 115, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Blokeberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C4U
; CURRENT APPLICATION NUMBER: US/09/615.192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 420
; TYPE: DNA
; APPLICANT: Charles Kunsch
```

```
; ORGANISM: Eucalyptus grandis
US-09-615-192A-115

Alignment Scores:
Pred. No.: 441          Length: 420
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-615-192A-115 (1-420)

Qy 1 HisAenAlaHisHis 5
Db 80 CACAACGCTCACCAT 66

RESULT 16
US-09-169-789-115/c
; Sequence 115, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; EARLIER FILING DATE: 1998-10-09
; EARLIER FILING DATE: 1997-11-21
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-115

Alignment Scores:
Pred. No.: 441          Length: 420
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-169-789-115 (1-420)

Qy 1 HisAenAlaHisHis 5
Db 80 CACAACGCTCACCAT 66

RESULT 17
US-09-513-999C-12497
; Sequence 12497, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; EARLIER FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 12497

; LENGTH: 428
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 337_feature
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: 353_feature
; OTHER INFORMATION: r=a or g
; NAME/KEY: misc_feature
; LOCATION: 354
; OTHER INFORMATION: r=a or g
US-09-513-999C-12497

Alignment Scores:
Pred. No.: 451          Length: 428
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-513-999C-12497 (1-428)

Qy 1 HisAenAlaHisHis 5
Db 109 CACAATGCCACCAC 123

RESULT 18
US-09-593-887-7/c
; Sequence 7, Application US/09593887
; Patent No. 6607914
; GENERAL INFORMATION:
; APPLICANT: Belyavsky, Alexander
; APPLICANT: Popsueva, Anna
; APPLICANT: Luchinskaya, Natalia
; TITLE OF INVENTION: CAMELLO GENE FAMILY AND USES THEREOF
; FILE REFERENCE: 63475/258
; CURRENT APPLICATION NUMBER: US/09/593,887
; EARLIER FILING DATE: 2000-06-14
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-593-887-7

Alignment Scores:
Pred. No.: 455          Length: 432
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-593-887-7 (1-432)

Qy 1 HisAenAlaHisHis 5
Db 216 CACAATGCCACCAC 202

RESULT 19
US-09-270-767-4421
; Sequence 4421, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

```
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4421
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-4421

Alignment Scores:
Pred. No.: 610 Length: 562
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-4421 (1-562)

Qy 1 HisAenAlahisHis 5
Db 346 CATAACGGCACCAC 360

RESULT 20
US-09-270-767-19703
; Sequence 19703, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19703
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-19703

Alignment Scores:
Pred. No.: 610 Length: 562
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-19703 (1-562)

Qy 1 HisAenAlahisHis 5
Db 346 CATAACGGCACCAC 360

RESULT 21
US-09-949-016-94983/c
; Sequence 94983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

```
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94983
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94983

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-94983 (1-601)

Qy 1 HisAenAlahisHis 5
Db 381 CACAATGCACATCAC 367

RESULT 22
US-09-949-016-95095/c
; Sequence 95095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95095
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-95095

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-95095 (1-601)

Qy 1 HisAenAlahisHis 5
Db 381 CACAATGCACATCAC 367

RESULT 23
US-09-949-016-150166
; Sequence 150166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```



; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 150166  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-150166

Alignment Scores:  
Pred. No.: 657 Length: 601  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-150166 (1-601)

Qy 1 HisAenAlaHisHis 5  
Db 318 CACAAGGCCACCAC 332

## RESULT 24

US-09-949-016-153056/c  
; Sequence 153056, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 153056

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-153056

## Alignment Scores:

Pred. No.: 657 Length: 601  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-153056 (1-601)

Qy 1 HisAenAlaHisHis 5  
Db 455 CACAATGCCACCAC 441

## RESULT 25

US-09-949-016-165560  
; Sequence 165560, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 165560  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-165560

Alignment Scores:  
Pred. No.: 657 Length: 601  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-165560 (1-601)

Qy 1 HisAenAlaHisHis 5  
Db 487 CATAATGCCACCAC 501

## RESULT 26

US-09-949-016-181710/c  
; Sequence 181710, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 181710

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-181710

## Alignment Scores:

Pred. No.: 657 Length: 601  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-181710 (1-601)

Qy 1 HisAenAlaHisHis 5  
Db 381 CACAATGCCACCAC 367

```
RESULT 27
US-09-949-016-181829/c
; Sequence 181829, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181829
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-181829

Alignment Scores:
Pred. No.:      657      Length:      601
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-12 (1-5) x US-09-949-016-181829 (1-601)

Qy      1 HisAsnAlaHisHis 5
      |||||
Db      381 CACAATGCACATCAC 367

RESULT 28
US-09-949-016-181948/c
; Sequence 181948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181948
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-181948

Alignment Scores:
Pred. No.:      657      Length:      601
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-12 (1-5) x US-09-949-016-181948 (1-601)

Qy      1 HisAsnAlaHisHis 5
      |||||
Db      381 CACAATGCACATCAC 367

RESULT 29
US-09-702-705-1397
; Sequence 1397, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1397

Alignment Scores:
Pred. No.:      721      Length:      653
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-12 (1-5) x US-09-702-705-1397 (1-653)

Qy      1 HisAsnAlaHisHis 5
      |||||
Db      448 CACAATGCCACACAC 462

RESULT 30
US-09-736-457-1397
; Sequence 1397, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1397
```

```
Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-736-457-1397 (1-653)

Qy 1 HisaenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 31
US-09-614-124B-1397
; Sequence 1397, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-1397

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-614-124B-1397 (1-653)

Qy 1 HisaenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 32
US-09-671-325-1397
; Sequence 1397, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
```

```
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-1397

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-671-325-1397 (1-653)

Qy 1 HisaenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 33
US-09-658-824-1397
; Sequence 1397, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-1397

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-658-824-1397 (1-653)

Qy 1 HisaenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 34
US-09-495-052-56
; Sequence 56, Application US/09495052
; Patent No. 6479258
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11
```

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; CURRENT APPLICATION NUMBER: US/09/495,052
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-495-052-56

Alignment Scores:
Pred. No.: 933 Length: 824
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-495-052-56 (1-824)

Qy 1 HisAenAlaHis 5
Db 523 CACAATGCCACCAC 537

RESULT 35
US-09-270-767-12993
; Sequence 12993, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12993
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12993

Alignment Scores:
Pred. No.: 1,01e+03 Length: 881
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-12993 (1-881)

Qy 1 HisAenAlaHis 5
Db 858 CACAATGCCACCAC 872

RESULT 36
US-09-991A-10187
; Sequence 10187, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10187
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10187

Alignment Scores:
Pred. No.: 1.25e+03 Length: 1068
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-252-991A-10187 (1-1068)

Qy 1 HisAenAlaHis 5
Db 832 CACAATGCCACCAC 846

RESULT 37
US-09-949-016-5053/c
; Sequence 5053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 5053
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5053

Alignment Scores:
Pred. No.: 1.26e+03 Length: 1081
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-5053 (1-1081)

Qy 1 HisAenAlaHis 5
Db 758 CACAATGCCACCAC 744

RESULT 38
US-09-328-352-1975/c
; Sequence 1975, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
```

```
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1975
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1975

Alignment Scores:
Pred. No.: 1.27e+03 Length: 1086
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-328-352-1975 (1-1086)

Qy 1 HisAenAlaHisHis 5
Db 937 CATAATGCCACCAT 923

RESULT 39
US-09-543-681A-1032/c
; Sequence 1032, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1032
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1032

Alignment Scores:
Pred. No.: 1.39e+03 Length: 1179
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-543-681A-1032 (1-1179)

Qy 1 HisAenAlaHisHis 5
Db 663 CATAATGCCACCAT 649

RESULT 40
US-09-857-583B-3
; Sequence 3, Application US/09857583B
; Patent No. 6825017
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browne, John A
; APPLICANT: Wallis, James G
; APPLICANT: Watts, Jennifer L
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 4630-58963
```

```
; CURRENT APPLICATION NUMBER: US/09/857,583B
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; CURRENT APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Euglena gracilis
US-09-857-583B-3

Alignment Scores:
Pred. No.: 1.52e+03 Length: 1281
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-857-583B-3 (1-1281)

Qy 1 HisAenAlaHisHis 5
Db 557 CACAATGCACATCAT 571

RESULT 41
US-09-540-236-1347/c
; Sequence 1347, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAT
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1347
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1347

Alignment Scores:
Pred. No.: 1.54e+03 Length: 1293
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-540-236-1347 (1-1293)

Qy 1 HisAenAlaHisHis 5
Db 757 CATAATGCCACATCAC 743

RESULT 42
US-09-248-796A-442
; Sequence 442, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
```

; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 442  
; LENGTH: 1323  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-442

Alignment Scores:  
Pred. No.: 1.58e+03 Length: 1323  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-248-796A-442 (1-1323)

Qy 1 HisAsnAlaHisHis 5  
Db 742 CATAATGCATCATC 756

## RESULT 43

; Sequence 1678, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 1678  
; LENGTH: 1425  
; TYPE: DNA  
; ORGANISM: M.catarrhalis  
US-09-540-236-1678

Alignment Scores:  
Pred. No.: 1.72e+03 Length: 1425  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-540-236-1678 (1-1425)

Qy 1 HisAsnAlaHisHis 5  
Db 730 CATAACGCTCATCAT 716

## RESULT 44

; Sequence 4667, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 4667  
; LENGTH: 1479  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-4667

Alignment Scores:  
Pred. No.: 1.79e+03 Length: 1479  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-489-039A-4667 (1-1479)

Qy 1 HisAsnAlaHisHis 5  
Db 1119 CATAATGCCACCAC 1105

## RESULT 45

; Sequence 4296, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4296  
; LENGTH: 1499  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-4296

Alignment Scores:  
Pred. No.: 1.82e+03 Length: 1499  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-4296 (1-1499)

Qy 1 HisAsnAlaHisHis 5  
Db 1241 CACAATGCCACCAC 1227

## RESULT 46

; Sequence 41, Application US/09814915A  
; Patent No. 6750015  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Kathryn  
; APPLICANT: Richer, Jennifer  
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat  
; TITLE OF INVENTION: Thiereto  
; FILE REFERENCE: 2848-39  
; CURRENT APPLICATION NUMBER: US/09/814,915A  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: 60/214,870  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 1517

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-41

Alignment Scores:
Pred. No.: 1.84e+03 Length: 1517
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-814-915A-41 (1-1517)

QY 1 HisAenAlaHisHis 5
Db 1259 CACAATGCCACCAC 1245

RESULT 47
US-08-815-176-2/c
; Sequence 2, Application US/08815176
; Patent No. 5874224
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Diegidio, Tony
; TITLE OF INVENTION: NOVEL EGF RECEPTOR BINDING PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,176
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,176
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0236 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGNNOT03
; CLONE: 1291904
US-08-815-176-2

Alignment Scores:
Pred. No.: 2.03e+03 Length: 1661
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-815-176-2 (1-1661)

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-41

Alignment Scores:
Pred. No.: 1.84e+03 Length: 1517
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-814-915A-41 (1-1517)

QY 1 HisAenAlaHisHis 5
Db 1259 CACAATGCCACCAC 1245

RESULT 47
US-08-815-176-2/c
; Sequence 2, Application US/08815176
; Patent No. 5874224
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Diegidio, Tony
; TITLE OF INVENTION: NOVEL EGF RECEPTOR BINDING PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,176
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0236 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGNNOT03
; CLONE: 1291904
US-08-815-176-2

Alignment Scores:
Pred. No.: 2.03e+03 Length: 1661
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-815-176-2 (1-1661)

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-41

Alignment Scores:
Pred. No.: 1.84e+03 Length: 1517
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-814-915A-41 (1-1517)

QY 1 HisAenAlaHisHis 5
Db 1259 CACAATGCCACCAC 1245

RESULT 47
US-08-815-176-2/c
; Sequence 2, Application US/08815176
; Patent No. 5874224
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Diegidio, Tony
; TITLE OF INVENTION: NOVEL EGF RECEPTOR BINDING PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,176
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,176
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0236 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGNNOT03
; CLONE: 1291904
US-08-815-176-2

Alignment Scores:
Pred. No.: 2.03e+03 Length: 1661
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-197-344-2 (1-1661)

QY 1 HisAenAlaHisHis 5
Db 1114 CACAATGCCCATCAT 1100

RESULT 48
US-09-197-344-2/c
; Sequence 2, Application US/09197344
; Patent No. 6417329
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Diegidio, Tony
; TITLE OF INVENTION: NOVEL EGF RECEPTOR BINDING PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,344
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,176
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0236 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGNNOT03
; CLONE: 1291904
US-09-197-344-2

Alignment Scores:
Pred. No.: 2.03e+03 Length: 1661
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-197-344-2 (1-1661)

QY 1 HisAenAlaHisHis 5
Db 1114 CACAATGCCCATCAT 1100

RESULT 49
US-08-831-570-1
; Sequence 1, Application US/08831570
; Patent No. 5959175
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Nunberg, Andrew N.
; APPLICANT: Beremand, Phillip D.
```

```
; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
; TITLE OF INVENTION: COMPOSITION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,570
; FILING DATE: 09-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10545
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
; US-08-831-570-1
;
Alignment Scores:
Pred. No.: 2.07e+03 Length: 1684
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
;
US-10-029-756-12 (1-5) x US-08-831-570-1 (1-1684)
;
Qy 1 HisaenAlaHisHis 5
Db 628 CATAATGCACATCAC 642
;
RESULT 50
US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongsen
; TITLE OF INVENTION: AN OLICOSIN 5'REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/831,575
; APPLICATION NUMBER: US/08/831,575
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
; US-08-831-575-1
;
Alignment Scores:
Pred. No.: 2.07e+03 Length: 1684
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
;
US-10-029-756-12 (1-5) x US-08-831-575-1 (1-1684)
;
Qy 1 HisaenAlaHisHis 5
Db 628 CATAATGCACATCAC 642
;
RESULT 51
US-08-366-779-4
; Sequence 4, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Nuccio, Avutu S.
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXW
; TELECOMMUNICATION INFORMATION:
```



```

; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-366-779-4

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-12 (1-5) x US-08-366-779-4 (1-1685)

Qy 1 HisaenAlaHisHis 5
Db 629 CATATGCATCAC 643

RESULT 52
US-08-789-936-4
; Sequence 4, Application US/08789936
; Patent No. 5789220
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyasinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-934-254-4 (1-1685)

Qy 1 HisaenAlaHisHis 5
Db 629 CATATGCATCAC 643

RESULT 54
US-08-789-936-4
; Sequence 4, Application US/08789936
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-934-254-4 (1-1685)

Qy 1 HisaenAlaHisHis 5
Db 629 CATATGCATCAC 643

RESULT 54
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```
US-09-685-775-4
; Sequence 4, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/685,775
; FILING DATE: 10-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-685-775-4
Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-09-685-775-4 (1-1685)
Qy 1 HisenAlaHisHis 5
Db 629 CATAATGCACATCAC 643
RESULT 55
US-08-934-254-26
; Sequence 26, Application US/08934254
; Patent No. 635861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
US-09-685-775-4
; Sequence 4, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
US-08-934-254-26
Alignment Scores:
Pred. No.: 2.09e+03 Length: 1702
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-08-934-254-26 (1-1702)
Qy 1 HisenAlaHisHis 5
Db 636 CACAACGCCACCAC 650
RESULT 56
US-09-685-775-26
; Sequence 26, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/685,775
; FILING DATE: 10-Oct-2000
; CLASSIFICATION: <Unknown>
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-685-775-26
Alignment Scores:
Pred. No.: 2,09e+03 Length: 1702
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-09-685-775-26 (1-1702)
QY 1 HisanAlaHisHis 5
|||||
DB 636 CACAAGCCACCAC 650
RESULT 57
US-09-489-039A-5879/c
; Sequence 5879, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5879
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5879
Alignment Scores:
Pred. No.: 2,22e+03 Length: 1800
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-09-489-039A-5879 (1-1800)
QY 1 HisanAlaHisHis 5
|||||
DB 574 CATAATGCTCATCAT 560
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/252,991A
; FILING DATE: 1999-02-18
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9887
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9887
Alignment Scores:
Pred. No.: 2,53e+03 Length: 2022
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-09-252-991A-9887 (1-2022)
QY 1 HisanAlaHisHis 5
|||||
DB 255 CACAAGCCACCAC 241
RESULT 59
US-09-614-221A-602/c
; Sequence 602, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulofini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 602
; LENGTH: 2373
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-602
Alignment Scores:
Pred. No.: 3,02e+03 Length: 2373
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-09-614-221A-602 (1-2373)
QY 1 HisanAlaHisHis 5
|||||
DB 574 CATAATGCTCATCAT 560
```

RESULT 60  
US-08-549-515-2  
; Sequence 2, Application US/08549515  
; Patent No. 6054123  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: Haemophilus Influenzae  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: Suite 701, 330 Unviersity Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/549,515  
; FILING DATE: 27-OCT-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-522  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2418 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-549-515-2

Alignment Scores:  
Pred. No.: 3.09e+03 Length: 2418  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-549-515-2 (1-2418)

Qy 1 HisaenAlaHisHis 5  
Db 2351 CACAAGGCCCATCAC 2365

RESULT 61  
US-09-023-655-1000/c  
; Sequence 1000, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA

; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1000:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2591 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g178083  
; US-09-023-655-1000

Alignment Scores:  
Pred. No.: 3.34e+03 Length: 2591  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-023-655-1000 (1-2591)

Qy 1 HisaenAlaHisHis 5  
Db 1206 CACAATGCCCATCAC 1192

RESULT 62  
US-09-540-236-217/c  
; Sequence 217, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 217  
; LENGTH: 2970  
; TYPE: DNA  
; ORGANISM: M.catarrhalis  
; US-09-540-236-217

Alignment Scores:  
Pred. No.: 3.88e+03 Length: 2970  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-540-236-217 (1-2970)

```
Qy      1 HisAenAlaHisHis 5
Db      796 CATACGCTCATCAT 782

RESULT 63
US-09-919-172-63/c
; Sequence 63, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 63
; LENGTH: 3304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1252415.1
; NAME/KEY: unsure
; LOCATION: 3267, 3276, 3289-3290, 3297, 3299
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-63

Alignment Scores:
Pred. No.:      4.37e+03      Length:      3304
Score:          34.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%     Indels:      0
DB:              4          Gaps:        0

US-10-029-756-12 (1-5) x US-09-919-172-63 (1-3304)

Qy      1 HisAenAlaHisHis 5
Db      1894 CACAATGCCACCAC 1870

RESULT 64
US-08-956-171E-816
; Sequence 816, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Gil H. Choi
; APPLICANT: Patrick S. Dillon
; APPLICANT: Craig A. Rosen
; APPLICANT: Steven C. Barash
; APPLICANT: Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB2488PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 816:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE DESCRIPTION: SEQ ID NO: 816:

```

```
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 816:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3989 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 816:
US-08-956-171E-816

Alignment Scores:
Pred. No.:      5.39e+03      Length:      3989
Score:          34.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%     Indels:      0
DB:              4          Gaps:        0

US-10-029-756-12 (1-5) x US-08-956-171E-816 (1-3989)

Qy      1 HisAenAlaHisHis 5
Db      2089 CATACGCTCATCAT 2103

RESULT 65
US-08-781-986A-816
; Sequence 816, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB2488PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 816:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE DESCRIPTION: SEQ ID NO: 816:

```

```

; LENGTH: 3989 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-816

Alignment Scores:
Pred. No.: 5.39e+03 Length: 3989
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-816 (1-3989)

Qy 1 HisAenAlaHisHis 5
Db 2089 CATAACGCACATCAT 2103

RESULT 66
US-08-549-515-1
; Sequence 1, Application US/08549515
; Patent No. 6054123
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Haemophilus Influenzae
; TITLE OF INVENTION: Dimethylsulphoxide Reductase Enzyme
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549.515
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-522
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4051 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(65..2482, 2496..3110, 3115..3951)
US-08-549-515-1

Alignment Scores:
Pred. No.: 5.48e+03 Length: 4051
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-549-515-1 (1-4051)

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```

Qy 1 HisAenAlaHisHis 5
Db 2415 CACAACGCCCATCAC 2429

RESULT 67
US-09-721-480-1
; Sequence 1, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721.480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4276
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pCMVII
US-09-721-480-1

Alignment Scores:
Pred. No.: 5.82e+03 Length: 4276
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-721-480-1 (1-4276)

Qy 1 HisAenAlaHisHis 5
Db 1662 CACAATGCCCATCAC 1676

RESULT 68
US-08-760-615-7
; Sequence 7, Application US/08760615
; Patent No. 6200959
; GENERAL INFORMATION:
; APPLICANT: Haynes, Joel R
; APPLICANT: Schmaljohn, Connie S
; APPLICANT: Fuller, Deborah L
; APPLICANT: Schmaljohn, Alan
; APPLICANT: Jahrling, Peter B
; TITLE OF INVENTION: GENETIC INDUCTION OF ANTI-VIRAL IMMUNE
; TITLE OF INVENTION: RESPONSE AND GENETIC VACCINE FOR FILOVIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/760.615
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094

```

REFERENCE/DOCKET NUMBER: 110229.91241  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4326 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Expression vector  
DESCRIPTION: Construct"  
CLONE: pWRG7077  
FEATURE:  
NAME/KEY: promoter  
LOCATION: 1250..2062  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2063..2887  
OTHER INFORMATION: /function= "Human Cytomegalovirus  
OTHER INFORMATION: Intron A"  
FEATURE:  
NAME/KEY: polyA site  
LOCATION: 2912..3314  
FEATURE:  
NAME/KEY: CDS  
LOCATION: complement (299..1114)

Alignment Scores:  
Pred. No.: 5.9e+03 Length: 4326  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-760-615-7 (1-4326)

Qy 1 HisaenAlaHisHis 5  
Db 2586 CACAATGCCACCAC 2600

RESULT 69

US-09-132-808-1  
Sequence 1, Application US/09132808  
Patent No. 6197332  
GENERAL INFORMATION:  
APPLICANT: Ronald Zuckermann et al.  
TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related  
TITLE OF INVENTION: Compositions and Methods Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/132,808  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459

REFERENCE/DOCKET NUMBER: 1387.002  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 923-2706  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-132-808-1  
Alignment Scores:  
Pred. No.: 5.9e+03 Length: 4328  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-132-808-1 (1-4328)

Qy 1 HisaenAlaHisHis 5  
Db 1333 CACAATGCCACCAC 1347

RESULT 70

US-08-910-647-2  
Sequence 2, Application US/08910647  
Patent No. 6251433  
GENERAL INFORMATION:  
APPLICANT: Zuckermann et al.  
TITLE OF INVENTION: Compositions and Methods for  
TITLE OF INVENTION: Polynucleotide Delivery  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,647  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459  
REFERENCE/DOCKET NUMBER: 1218.002  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-910-647-2  
Alignment Scores:  
Pred. No.: 5.9e+03 Length: 4328  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-910-647-2 (1-4328)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 1333 CACAATGCCACCAC 1347

RESULT 71

US-09-620-925-2  
; Sequence 2, Application US/09620925  
; Patent No. 6468986  
; GENERAL INFORMATION:  
; APPLICANT: Zuckermann et al.  
; TITLE OF INVENTION: Compositions and Methods for Polynucleotide Delivery

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/620,925  
FILING DATE: 21-Jul-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/910,647  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459  
REFERENCE/DOCKET NUMBER: 1218.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-620-925-2

Alignment Scores:  
Pred. No.: 5.9e+03 Length: 4328  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-925-2 (1-4328)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 1333 CACAATGCCACCAC 1347

RESULT 72

US-09-620-260-1  
; Sequence 1, Application US/09620260  
; Patent No. 6569450  
; GENERAL INFORMATION:  
; APPLICANT: Ronald Zuckermann et al.  
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related Compositions and Methods Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICANT: Ronald Zuckermann et al.  
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related Compositions and Methods Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/620,260  
FILING DATE: 09-Oct-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459  
REFERENCE/DOCKET NUMBER: 1387.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-620-260-1

Alignment Scores:  
Pred. No.: 5.9e+03 Length: 4328  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-260-1 (1-4328)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 1333 CACAATGCCACCAC 1347

RESULT 73

US-09-620-259-1  
; Sequence 1, Application US/09620259  
; Patent No. 6572881  
; GENERAL INFORMATION:  
; APPLICANT: Ronald Zuckermann et al.  
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related Compositions and Methods Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/09/620,259  
FILING DATE: 03-Oct-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459  
REFERENCE/DOCKET NUMBER: 1387,002  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-620-259-1

Alignment Scores:  
Pred. No.: 5.9e+03 Length: 4328  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-259-1 (1-4328)

Qy 1 HisAenAlaHis 5  
Db 1333 CACAATGCCACCAC 1347

## RESULT 74

US-08-956-171E-546/c  
; Sequence 546, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:

APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 546:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4336 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 546:  
US-08-956-171E-546

Alignment Scores:  
Pred. No.: 5.91e+03 Length: 4336  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-956-171E-546 (1-4336)

Qy 1 HisAenAlaHis 5  
Db 2081 CATACGCACATCAT 2067

## RESULT 75

US-08-781-986A-546/c  
; Sequence 546, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:

APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A

FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PPP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 546:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4336 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-546

Alignment Scores:  
Pred. No.: 5.91e+03 Length: 4336  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-546 (1-4336)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 2081 CATAACGCACATCAT 2067

RESULT 76

US-09-949-016-1943/c  
; Sequence 1943, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1943  
; LENGTH: 4531  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1943

Alignment Scores:

Pred. No.:	6.21e+03	Length:	4531
Score:	34.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-029-756-12 (1-5) x US-09-949-016-1943 (1-4531)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 3947 CACAATGCCACCAC 3933

RESULT 77

US-08-910-647-4  
; Sequence 4, Application US/08910647  
; Patent No. 6251433  
; GENERAL INFORMATION:  
; APPLICANT: Zuckermann et al.  
; TITLE OF INVENTION: Compositions and Methods for  
; Polynucleotide Delivery  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,647  
; FILING DATE: 21-Jul-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/910,647  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fujita, Sharon M.  
; REGISTRATION NUMBER: 38,459  
; REFERENCE/DOCKET NUMBER: 1218.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 923-2706  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-620-925-4

NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459  
REFERENCE/DOCKET NUMBER: 1218.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4818 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-620-925-4

Alignment Scores:

Pred. No.:	6.55e+03	Length:	4818
Score:	34.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-029-756-12 (1-5) x US-08-910-647-4 (1-4818)

Qy 1 HisAsnAlaHisHis 5  
|||||

Db 1336 CACAATGCCACCAC 1350

RESULT 78

US-09-620-925-4  
; Sequence 4, Application US/09620925  
; Patent No. 6468986  
; GENERAL INFORMATION:  
; APPLICANT: Zuckermann et al.  
; TITLE OF INVENTION: Compositions and Methods for  
; Polynucleotide Delivery  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/620,925  
; FILING DATE: 21-Jul-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/910,647  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fujita, Sharon M.  
; REGISTRATION NUMBER: 38,459  
; REFERENCE/DOCKET NUMBER: 1218.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 923-2706  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-620-925-4

Alignment Scores:  
 Pred. No.: 6.65e+03 Length: 4818  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-925-4 (1-4818)

Qy 1 HisaenAlaHisHis 5  
 Db 1336 CACAATGCCACCAC 1350

RESULT 79  
 ; Sequence 1, Application US/08345913  
 ; Patent No. 5641665  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hobart, Peter  
 ; APPLICANT: Parker, Suzanne  
 ; APPLICANT: Margalith, Michal  
 ; APPLICANT: Khatibi, Shirin  
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR IL-2 EXPRESSION  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear  
 ; STREET: 620 Newport Center Drive 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/345,913  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ways Vensko, Nancy  
 ; REGISTRATION NUMBER: 36,298  
 ; REFERENCE/DOCKET NUMBER: VICAL.043A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4928 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE:  
 ; ORIGINAL SOURCE:  
 ; FEATURE:  
 ; NAME/KEY: Coding Sequence  
 ; LOCATION: 1689...2159  
 ; OTHER INFORMATION:  
 ; US-08-345-913-1

Alignment Scores:  
 Pred. No.: 6.81e+03 Length: 4928  
 Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-12 (1-5) x US-08-345-913-1 (1-4928)

Qy 1 HisaenAlaHisHis 5  
 Db 1316 CACAATGCCACCAC 1330

RESULT 80  
 ; Sequence 1, Application US/08818562  
 ; Patent No. 6147055  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hobart, Peter M.  
 ; APPLICANT: Margalith, Michal  
 ; APPLICANT: Parker, Suzanne E.  
 ; APPLICANT: Khatibi, Shirin  
 ; TITLE OF INVENTION: Plasmids Suitable for IL-2 Expression  
 ; FILE REFERENCE: 1530.0080001  
 ; CURRENT APPLICATION NUMBER: US/08/818,562  
 ; CURRENT FILING DATE: 1997-03-14  
 ; EARLIER APPLICATION NUMBER: US 08/345,913  
 ; EARLIER FILING DATE: 1994-11-28  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4928  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1689)..(2159)  
 ; US-08-818-562-1

Alignment Scores:  
 Pred. No.: 6.81e+03 Length: 4928  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-818-562-1 (1-4928)

Qy 1 HisaenAlaHisHis 5  
 Db 1316 CACAATGCCACCAC 1330

RESULT 81  
 ; Sequence 1, Application US/09628445  
 ; Patent No. 6399588  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hobart, Peter M.  
 ; APPLICANT: Margalith, Michal  
 ; APPLICANT: Parker, Suzanne E.  
 ; APPLICANT: Khatibi, Shirin  
 ; TITLE OF INVENTION: Cancer Treatment Utilizing Plasmids Suitable for IL-2 Expression  
 ; FILE REFERENCE: 1530.0080002  
 ; CURRENT APPLICATION NUMBER: US/09/628,445  
 ; CURRENT FILING DATE: 2000-07-28  
 ; PRIOR APPLICATION NUMBER: US 08/818,562  
 ; PRIOR FILING DATE: 1997-03-14  
 ; PRIOR APPLICATION NUMBER: US 08/345,913  
 ; PRIOR FILING DATE: 1994-11-28  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4928  
 ; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1689)..(2159)
US-09-628-445-1
Alignment Scores:
Pred. No.: 6.81e+03 Length: 4928
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-09-628-445-1 (1-4928)
Qy 1 HisAenAlaHisHis 5
Db 1316 CACAATGCCACCAC 1330
RESULT 82
US-08-910-647-3
; Sequence 3, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,647
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5107 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-910-647-3
Alignment Scores:
Pred. No.: 7.09e+03 Length: 5107
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-08-910-647-3 (1-5107)
Qy 1 HisAenAlaHisHis 5
Db 1316 CACAATGCCACCAC 1330
```

```
Db 1336 CACAATGCCACCAC 1350
RESULT 83
US-09-620-925-3
; Sequence 3, Application US/09620925
; Patent No. 6468986
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/620,925
; FILING DATE: 21-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,647
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5107 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-620-925-3
Alignment Scores:
Pred. No.: 7.09e+03 Length: 5107
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-09-620-925-3 (1-5107)
Qy 1 HisAenAlaHisHis 5
Db 1336 CACAATGCCACCAC 1350
RESULT 84
US-09-628-730-51
; Sequence 51, Application US/09628730
; Patent No. 6759393
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; COMPOSITIONS
; FILE REFERENCE: FC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 5108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29WTCMV construct
US-09-628-730-51

Alignment Scores:
Pred. No.:      7,09e+03      Length:      5108
Score:          34.00        Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%      Indels:       0
DB:             4           Gaps:         0

US-10-029-756-12 (1-5) x US-09-628-730-51 (1-5108)

QY      1 HisAsnAlaHisHis 5
Db      4544 CACAATGCCACCAC 4558

RESULT 85
US-09-628-730-52
; Sequence 52, Application US/09628730
; Patent No. 6759393
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 5108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29WTCMV construct
US-09-628-730-52

Alignment Scores:
Pred. No.:      7,09e+03      Length:      5108
Score:          34.00        Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%      Indels:       0
DB:             4           Gaps:         0

US-10-029-756-12 (1-5) x US-09-628-730-52 (1-5108)

QY      1 HisAsnAlaHisHis 5
Db      4544 CACAATGCCACCAC 4558

RESULT 86
US-09-628-730-55
; Sequence 55, Application US/09628730
; Patent No. 6759393
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 55
; LENGTH: 5111
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29fa1a1522CMV construct
US-09-628-730-55

Alignment Scores:
Pred. No.:      7,1e+03      Length:      5111
Score:          34.00        Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%      Indels:       0
DB:             4           Gaps:         0

US-10-029-756-12 (1-5) x US-09-628-730-55 (1-5111)

QY      1 HisAsnAlaHisHis 5
Db      4544 CACAATGCCACCAC 4558

RESULT 87
US-09-721-480-2
; Sequence 2, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: CDS
; LOCATION: (1988) ..(2830)
US-09-721-480-2

Alignment Scores:
Pred. No.:      7,12e+03     Length:      5128
Score:          34.00        Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%      Indels:       0
DB:             4           Gaps:         0

US-10-029-756-12 (1-5) x US-09-721-480-2 (1-5128)

QY      1 HisAsnAlaHisHis 5
Db      1662 CACAATGCCACCAC 1676

RESULT 88
US-09-628-730-47
; Sequence 47, Application US/09628730
; Patent No. 6759393
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
; SOFTWARE: PatentIn Ver. 2.1
```

; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 5185  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pGHRH-4  
; OTHER INFORMATION: construct  
US-09-628-730-47

Alignment Scores:  
Pred. No.: 7.21e+03 Length: 5185  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-628-730-47 (1-5185)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 4544 CACAATGCCACCAC 4558

## RESULT 89

US-09-628-730-59  
; Sequence 59, Application US/09628730  
; Patent No. 6759393

; GENERAL INFORMATION:  
; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE  
; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730  
; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 59  
; LENGTH: 5188

; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pGHRH1-44YTCMV construct  
US-09-628-730-59

Alignment Scores:  
Pred. No.: 7.22e+03 Length: 5188  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-628-730-59 (1-5188)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 4544 CACAATGCCACCAC 4558

## RESULT 90

US-09-173-053-8

; Sequence 8, Application US/09173053  
; Patent No. 6451769

; GENERAL INFORMATION:  
; APPLICANT: HUEBNER, Robert C.

; APPLICANT: NORMAN, Jon A.  
; APPLICANT: LIANG, Xisowu

; APPLICANT: CARNER, Kristin R.  
; APPLICANT: BARBOUR, Alan G.

; APPLICANT: LUKE, Catherine J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING BORRELIA DNA

; FILE REFERENCE: 454312-2440.1  
; CURRENT APPLICATION NUMBER: US/09/173,053  
; CURRENT FILING DATE: 1998-10-15  
; PRIOR APPLICATION NUMBER: 08/663,998  
; PRIOR FILING DATE: 1996-06-14  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8  
; LENGTH: 5215  
; TYPE: DNA

; ORGANISM: Borrelia burgdorferi  
US-09-173-053-8

Alignment Scores:  
Pred. No.: 7.26e+03 Length: 5215  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-173-053-8 (1-5215)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 1500 CACAATGCCACCAC 1514

## RESULT 91

US-09-628-730-60

; Sequence 60, Application US/09628730  
; Patent No. 6759393

; GENERAL INFORMATION:  
; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE  
; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730  
; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 60  
; LENGTH: 5254

; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pGHRH1-44WTGHPep construct  
US-09-628-730-60

Alignment Scores:  
Pred. No.: 7.32e+03 Length: 5254  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-628-730-60 (1-5254)

Qy 1 HisAenAlaHisHis 5  
|||||  
Db 4544 CACAATGCCACCAC 4558

## RESULT 92

US-09-721-480-4

; Sequence 4, Application US/09721480  
; Patent No. 6740323

; GENERAL INFORMATION:  
; APPLICANT: Selby, Mark

; APPLICANT: Glazer, Edward  
; APPLICANT: Houghton, Michael

; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE  
; FILE REFERENCE: PP01635.002

```
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5459
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pCMVII opti
; NAME/KEY: CDS
; LOCATION: (1992)..(3161)
US-09-721-480-4

Alignment Scores:
Pred. No.: 7,64e+03 Length: 5459
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-721-480-4 (1-5459)

Qy 1 HisaenAlaHisHis 5
Db 1662 CACAATGCCACCAC 1676

RESULT 93
US-09-721-480-6
; Sequence 6, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5882
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: CDS
; LOCATION: (1992)..(3584)
US-09-721-480-6

Alignment Scores:
Pred. No.: 8.3e+03 Length: 5882
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-721-480-6 (1-5882)

Qy 1 HisaenAlaHisHis 5
Db 1662 CACAATGCCACCAC 1676

RESULT 94
US-09-770-315-1
; Sequence 1, Application US/09770315
; Patent No. 6429001
; GENERAL INFORMATION:
```

```
; APPLICANT: Chiron Corporation
; TITLE OF INVENTION: Recombinant AAV Packaging Systems
; FILE REFERENCE: 20263-501
; CURRENT APPLICATION NUMBER: US/09/770,315
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,536
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7015
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: recombinant DNA
US-09-770-315-1

Alignment Scores:
Pred. No.: 1.01e+04 Length: 7015
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-770-315-1 (1-7015)

Qy 1 HisaenAlaHisHis 5
Db 2821 CACAATGCCACCAC 2835

RESULT 95
US-08-910-647-1
; Sequence 1, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Polynucleotide Delivery
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/910,647
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-910-647-1

Alignment Scores:
```

Pred. No.: 1.43e+04 Length: 9600  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-910-647-1 (1-9600)

Qy 1 HisAenAlaHis 5

Db 6438 CACAATGCCACCAC 6452

RESULT 96

US-09-620-925-1

; Sequence 1, Application US/09620925

; Patent No. 6468986

; GENERAL INFORMATION:

; APPLICANT: Zuckermann et al.

; TITLE OF INVENTION: Compositions and Methods for

; CORRESPONDENCE ADDRESS: Polynucleotide Delivery

; NUMBER OF SEQUENCES: 4

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94608-2916

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/620,925

; FILING DATE: 21-Jul-2000

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/910,647

; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Fujita, Sharon M.

; REGISTRATION NUMBER: 38,459

; REFERENCE/DOCKET NUMBER: 1218.002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 923-2706

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9600 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-620-925-1

Alignment Scores:  
Pred. No.: 1.43e+04 Length: 9600  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-925-1 (1-9600)

Qy 1 HisAenAlaHis 5

Db 6438 CACAATGCCACCAC 6452

RESULT 97

US-09-554-337-1  
; Sequence 1, Application US/09554337  
; Patent No. 6475780  
; GENERAL INFORMATION:  
; APPLICANT: Parrington, Mark  
; APPLICANT: Li, Xiaomao  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES  
; FILE REFERENCE: 1038-1042 MTS  
; CURRENT APPLICATION NUMBER: US/09/554,337  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/065,791  
; PRIOR FILING DATE: 1997-11-14  
; PRIOR APPLICATION NUMBER: PCT/CA98/01064  
; PRIOR FILING DATE: 1998-11-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 15538  
; TYPE: DNA  
; ORGANISM: respiratory syncytial virus  
US-09-554-337-1

Alignment Scores:  
Pred. No.: 2.43e+04 Length: 15538  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-554-337-1 (1-15538)

Qy 1 HisAenAlaHis 5

Db 1563 CACAATGCCACCAC 1577

RESULT 98

US-09-949-016-16407/C

; Sequence 16407, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 16407

; LENGTH: 21893

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(21893)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16407

Alignment Scores:  
Pred. No.: 3.55e+04 Length: 21893  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0



US-10-029-756-12 (1-5) x US-09-949-016-16407 (1-21893)

Qy 1 HisAsnAlaHisHis 5  
DB 8335 CATAATGCCACCATC 8321

## RESULT 99

US-09-949-016-14958/c  
; Sequence 14958, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14958

; LENGTH: 23406

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14958

## Alignment Scores:

Pred. No.:	3.82e+04	Length:	23406
Score:	34.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-029-756-12 (1-5) x US-09-949-016-14958 (1-23406)

Qy 1 HisAsnAlaHisHis 5

DB 13430 CATAATGCCACCATC 13416

## RESULT 100

US-09-949-016-14320

; Sequence 14320, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14320

; LENGTH: 24056

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14320

## Alignment Scores:

Pred. No.:	3.94e+04	Length:	24056
------------	----------	---------	-------

Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-14320 (1-24056)

Qy 1 HisAsnAlaHisHis 5

DB 19415 CACAATGCCACCATC 19429

Search completed: June 8, 2005, 15:29:24

Job time : 152.316 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 09:39:06 ; Search time 1236.32 Seconds  
(without alignments)  
235.159 Million cell updates/sec

Title: US-10-029-756-20

Perfect score: 36

Sequence: 1 FQIEHH 6

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10029756/runat\_07062005\_122750\_28779/app\_query.fasta.1.597  
-DB=GenEmbl -QFMT=fastcap -SUPFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=1000  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10029756 @CGN 1.1.5965 @runat\_07062005\_122750\_28779 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sv.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	36	100.0	20	6	AX253333 Sequence
2	36	100.0	266	6	AR247897 Sequence
3	36	100.0	291	6	AR246607 Sequence
4	36	100.0	347	6	AR272626 Sequence

C 5	36	100.0	347	6	AR276207 Sequence
C 6	36	100.0	347	6	AR406482 Sequence
C 7	36	100.0	347	6	AR440332 Sequence
C 8	36	100.0	347	6	AR472490 Sequence
C 9	36	100.0	347	6	AR543143 Sequence
C 10	36	100.0	347	6	AX062728 Sequence
C 11	36	100.0	347	6	AX367645 Sequence
C 12	36	100.0	372	6	AR484509 Sequence
C 13	36	100.0	372	6	AX143133 Sequence
C 14	36	100.0	449	6	AR221976 Sequence
15	36	100.0	473	6	AR221975 Sequence
16	36	100.0	480	6	AX840703 Sequence
17	36	100.0	520	6	BD082632 Methods a
18	36	100.0	520	6	BD082647 Methods a
19	36	100.0	520	6	BD092937 Methods a
20	36	100.0	560	6	BD147335 Primer fo
21	36	100.0	560	6	AX867273 Sequence
22	36	100.0	655	6	AR221955 Sequence
23	36	100.0	655	6	BD082635 Methods a
24	36	100.0	655	6	BD082650 Methods a
25	36	100.0	655	6	BD092929 Methods a
26	36	100.0	739	6	BD148047 Primer fo
27	36	100.0	739	6	AX867985 Sequence
28	36	100.0	808	6	CQ780299 Sequence
29	36	100.0	808	6	CQ781966 Sequence
30	36	100.0	808	6	BD125008 Primer fo
31	36	100.0	808	6	BD126675 Primer fo
32	36	100.0	864	6	AR221961 Sequence
33	36	100.0	876	6	AR547128 Sequence
34	36	100.0	1132	1	AF270385 Sequence
35	36	100.0	1132	6	AX486339 Sequence
36	36	100.0	1132	6	AX145703 Sequence
37	36	100.0	1320	6	AR410208 Sequence
38	36	100.0	1320	6	AX467713 Sequence
39	36	100.0	1320	6	AX577003 Sequence
40	36	100.0	1320	6	AX951587 Sequence
41	36	100.0	1320	8	AF489588 Thraustoc
42	36	100.0	1329	6	AX577009 Sequence
43	36	100.0	1335	6	CQ729637 Sequence
44	36	100.0	1335	6	AR221953 Sequence
45	36	100.0	1335	6	AX253297 Sequence
46	36	100.0	1335	6	AX253298 Sequence
47	36	100.0	1335	6	BD091695 Processes f
48	36	100.0	1335	9	AF199596 Homo sapi
49	36	100.0	1335	9	AF226273 Homo sapi
50	36	100.0	1338	6	AX577005 Sequence
51	36	100.0	1341	8	AF536525 Anemone 1
52	36	100.0	1347	8	AY131238 Argania s
53	36	100.0	1347	9	HSA325501
54	36	100.0	1365	5	AF478472 Salmo sal
55	36	100.0	1385	8	AY234126 Primula v
56	36	100.0	1442	10	RNO494720
57	36	100.0	1478	6	BD195601 70 human
58	36	100.0	1478	6	CQ775646 Sequence
59	36	100.0	1478	6	CQ775646 Sequence
60	36	100.0	1498	5	AB074149 Oncorhync
61	36	100.0	1508	10	AF126798 Mus muscu
62	36	100.0	1539	10	BC055950 Mus muscu
63	36	100.0	1546	10	AB021980 Rattus no
64	36	100.0	1576	5	AB069727 Oreochrom
65	36	100.0	1590	5	AF309556 Danio rer
66	36	100.0	1608	10	BC057189 Mus muscu
67	36	100.0	1619	8	AY332747 Pavlova 1
68	36	100.0	1681	8	AY234124 Primula f
69	36	100.0	1684	6	AR076814 Sequence
70	36	100.0	1684	6	AR084177 Sequence
71	36	100.0	1684	6	BD062571 A sunflow
72	36	100.0	1684	6	BD070919 An oleosif
73	36	100.0	1685	6	AR020904 Sequence
74	36	100.0	1685	6	I38430 Sequence 4
75	36	100.0	1685	6	AR200408 Sequence
76	36	100.0	1685	6	AR455421 Sequence
77	36	100.0	1685	8	AF007561 Borago of

78	36	100.0	1686	6	AR221958	Sequence	AR221958	Sequence	151	36	100.0	3131	6	AX416639	Sequence	AX416639	Sequence
79	36	100.0	1686	6	BD082638	Methods a	BD082638	Methods a	152	36	100.0	3149	9	AF084559	Homo sapi	AF084559	Homo sapi
80	36	100.0	1686	6	BD082653	Methods a	BD082653	Methods a	153	36	100.0	3184	6	BD243025	Human oxi	BD243025	Human oxi
81	36	100.0	1686	6	BD092932	Methods a	BD092932	Methods a	154	36	100.0	3334	10	BC063053	Mus muscu	BC063053	Mus muscu
82	36	100.0	1687	8	AX951561	Sequence	AX951561	Sequence	155	36	100.0	3349	10	AB061504	Mus muscu	AB061504	Mus muscu
83	36	100.0	1687	8	BD079010	Sequence	BD079010	Sequence	156	36	100.0	3380	10	AB052085	Rattus no	AB052085	Rattus no
84	36	100.0	1692	5	AB070444	Sequence	AB070444	Sequence	157	36	100.0	3403	5	BC077556	Xenopus l	BC077556	Xenopus l
85	36	100.0	1700	6	BD228694	Delta 6 f	BD228694	Delta 6 f	158	36	100.0	3408	10	AB072976	Mus muscu	AB072976	Mus muscu
86	36	100.0	1705	9	AF134404	Homo sapi	AF134404	Homo sapi	159	36	100.0	3413	10	AF320509	Rattus no	AF320509	Rattus no
87	36	100.0	1706	10	BC081776	Sequence	BC081776	Sequence	160	36	100.0	3415	10	BC022139	Mus muscu	BC022139	Mus muscu
88	36	100.0	1708	5	BC049438	Danio rer	BC049438	Danio rer	161	36	100.0	3416	10	BC026848	Mus muscu	BC026848	Mus muscu
89	36	100.0	1717	5	AR264713	Sequence	AR264713	Sequence	162	36	100.0	3437	10	BC026831	Mus muscu	BC026831	Mus muscu
90	36	100.0	1745	5	AY055749	Sparus au	AY055749	Sparus au	c 163	36	100.0	3765	8	AF481861	Candida a	AF481861	Candida a
91	36	100.0	1757	6	AX035942	Sequence	AX035942	Sequence	c 164	36	100.0	4089	6	AX035941	Sequence	AX035941	Sequence
92	36	100.0	1757	6	AF084560	Homo sapi	AF084560	Homo sapi	165	36	100.0	4103	1	AF270140	Staphyloc	AF270140	Staphyloc
93	36	100.0	1781	5	BC063726	Xenopus l	BC063726	Xenopus l	166	36	100.0	4103	6	AR486094	Sequence	AR486094	Sequence
94	36	100.0	1798	5	AF309557	Cyprinus	AF309557	Cyprinus	167	36	100.0	4205	6	AX145458	Sequence	AX145458	Sequence
95	36	100.0	1798	8	AK058543	Oryza sat	AK058543	Oryza sat	168	36	100.0	4205	6	AX035940	Sequence	AX035940	Sequence
96	36	100.0	1807	9	BC004901	Homo sapi	BC004901	Homo sapi	169	36	100.0	4205	9	AF084558	Homo sapi	AF084558	Homo sapi
97	36	100.0	1816	6	CQ776468	Sequence	CQ776468	Sequence	170	36	100.0	4327	3	ACU13191	Angiostrong	U13191	Angiostrong
98	36	100.0	1818	6	CQ777377	Sequence	CQ777377	Sequence	171	36	100.0	8185	9	BSM807094	Homo sapi	BSM807094	Homo sapi
99	36	100.0	1818	10	AB041560	Mus muscu	AB041560	Mus muscu	c 172	36	100.0	12204	1	AY510074	Listeria	AY510074	Listeria
100	36	100.0	1838	5	AY458652	Salmo sal	AY458652	Salmo sal	c 173	36	100.0	16349	1	AF498420	Pseudomon	AF498420	Pseudomon
101	36	100.0	1843	6	AR221959	Sequence	AR221959	Sequence	c 174	36	100.0	27035	9	AY191837	Homo sapi	AY191837	Homo sapi
102	36	100.0	1843	6	BD082639	Methods a	BD082639	Methods a	175	36	100.0	38060	3	CET13F2	Caenorhabdi	Z81122	Caenorhabdi
103	36	100.0	1843	6	BD082654	Methods a	BD082654	Methods a	c 176	36	100.0	65237	9	AC117450	Homo sapi	AC117450	Homo sapi
104	36	100.0	1843	6	BD092933	Methods a	BD092933	Methods a	c 177	36	100.0	67665	2	AC101324	Mus muscu	AC101324	Mus muscu
105	36	100.0	1856	6	BD157758	Primer fo	BD157758	Primer fo	c 178	36	100.0	79914	9	AC005159	Homo sapi	AC005159	Homo sapi
106	36	100.0	1856	6	AX879291	Sequence	AX879291	Sequence	c 179	36	100.0	89421	9	AP001965	Homo sapi	AP001965	Homo sapi
107	36	100.0	1856	6	AK027427	Homo sapi	AK027427	Homo sapi	c 180	36	100.0	91859	9	AL358133	Human DNA	AL358133	Human DNA
108	36	100.0	1866	5	AF301910	Oncorhinc	AF301910	Oncorhinc	181	36	100.0	95161	8	AP005554	Oryza sat	AP005554	Oryza sat
109	36	100.0	1866	10	BC071266	Mus muscu	BC071266	Mus muscu	c 182	36	100.0	101684	8	AP005847	Oryza sat	AP005847	Oryza sat
110	36	100.0	1887	9	BC007846	Homo sapi	BC007846	Homo sapi	c 183	36	100.0	108205	2	AC102213	Mus muscu	AC102213	Mus muscu
111	36	100.0	1928	6	BD264714	Sequence	BD264714	Sequence	c 184	36	100.0	109041	3	LMFP1408	Leishmani	AL358652	Leishmani
112	36	100.0	1946	6	BD159641	Primer fo	BD159641	Primer fo	185	36	100.0	110000	2	AC129052	Continuation (3 of	AC129052	Continuation (3 of
113	36	100.0	1946	6	AX882292	Sequence	AX882292	Sequence	186	36	100.0	110207	2	AC145157	Medicago	AC145157	Medicago
114	36	100.0	1946	6	AX027522	Homo sapi	AX027522	Homo sapi	187	36	100.0	111911	2	AC145470	Homo sapi	AC145470	Homo sapi
115	36	100.0	1987	5	AY546094	Scophthal	AY546094	Scophthal	188	36	100.0	112485	9	AP001870	Human DNA	AP001870	Human DNA
116	36	100.0	2016	6	BD195657	Sequence	BD195657	Sequence	c 189	36	100.0	119945	8	OSJN00205	Oryza sat	AL662597	Oryza sat
117	36	100.0	2016	6	CQ775702	Sequence	CQ775702	Sequence	c 190	36	100.0	122499	8	OSJN00205	Human DNA	AL109622	Human DNA
118	36	100.0	2016	6	AK352712	Sequence	AK352712	Sequence	c 191	36	100.0	122900	9	BSDJ526F5	Oryza sat	AL034370	Oryza sat
119	36	100.0	2079	9	AK096275	Homo sapi	AK096275	Homo sapi	192	36	100.0	133445	2	AC073440	Homo sapi	AL034370	Oryza sat
120	36	100.0	2146	6	BD157807	Primer fo	BD157807	Primer fo	c 193	36	100.0	140681	8	AC078894	Oryza sat	AC078894	Oryza sat
121	36	100.0	2146	6	AX879386	Sequence	AX879386	Sequence	c 194	36	100.0	143608	9	AC145752	Pan trogl	AC145752	Pan trogl
122	36	100.0	2146	9	AK027459	Homo sapi	AK027459	Homo sapi	c 195	36	100.0	144108	10	BSX936355	Mouse DNA	BSX936355	Mouse DNA
123	36	100.0	2190	6	BD158110	Primer fo	BD158110	Primer fo	196	36	100.0	144201	10	AC087218	Rattus no	AC087218	Rattus no
124	36	100.0	2190	6	AX879945	Sequence	AX879945	Sequence	197	36	100.0	144717	2	AC108901	Felis cat	AC108901	Felis cat
125	36	100.0	2190	9	AK027577	Homo sapi	AK027577	Homo sapi	198	36	100.0	152135	9	AC011199	Homo sapi	AC011199	Homo sapi
126	36	100.0	2236	6	CQ782686	Sequence	CQ782686	Sequence	199	36	100.0	161624	2	AP001493	Homo sapi	AP001493	Homo sapi
127	36	100.0	2236	6	BD127263	Primer fo	BD127263	Primer fo	200	36	100.0	162409	2	AC022184	Homo sapi	AC022184	Homo sapi
128	36	100.0	2236	9	AK074754	Homo sapi	AK074754	Homo sapi	201	36	100.0	162696	2	AC090417	Homo sapi	AC090417	Homo sapi
129	36	100.0	2257	6	AR221960	Sequence	AR221960	Sequence	c 202	36	100.0	163330	10	AL713390	Mouse DNA	AL713390	Mouse DNA
130	36	100.0	2257	6	BD082640	Methods a	BD082640	Methods a	c 203	36	100.0	164229	9	AC092671	Homo sapi	AC092671	Homo sapi
131	36	100.0	2257	6	BD082655	Methods a	BD082655	Methods a	c 204	36	100.0	165201	2	AC149902	Strongylo	AC149902	Strongylo
132	36	100.0	2257	6	BD092934	Methods a	BD092934	Methods a	c 205	36	100.0	166410	8	OSJN00240	Oryza sat	AL713390	Oryza sat
133	36	100.0	2540	6	AK379750	Sequence	AK379750	Sequence	206	36	100.0	167429	9	AC110771	Homo sapi	AC110771	Homo sapi
134	36	100.0	2558	6	CQ783754	Sequence	CQ783754	Sequence	207	36	100.0	168608	2	AC090464	Homo sapi	AC090464	Homo sapi
135	36	100.0	2558	6	BD127815	Primer fo	BD127815	Primer fo	c 208	36	100.0	168608	2	AC092527	Paplo anu	AC092527	Paplo anu
136	36	100.0	2558	9	AK074925	Homo sapi	AK074925	Homo sapi	209	36	100.0	170270	2	AP001548	Homo sapi	AP001548	Homo sapi
137	36	100.0	2621	6	AX770523	Sequence	AX770523	Sequence	c 210	36	100.0	170413	2	AC090405	Homo sapi	AC090405	Homo sapi
138	36	100.0	2621	9	BSM800210	Homo sapi	AL050118	Homo sapi	c 211	36	100.0	170862	9	AC015795	Homo sapi	AC015795	Homo sapi
139	36	100.0	2825	6	CQ782971	Sequence	CQ782971	Sequence	c 212	36	100.0	174645	9	AC091111	Homo sapi	AC091111	Homo sapi
140	36	100.0	2825	6	BD127406	Primer fo	BD127406	Primer fo	c 213	36	100.0	175850	2	AP001399	Homo sapi	AP001399	Homo sapi
141	36	100.0	2825	9	AK074991	Homo sapi	AK074991	Homo sapi	214	36	100.0	177382	2	AC125953	Rattus no	AC125953	Rattus no
142	36	100.0	2872	9	AF486577	Homo sapi	AF486577	Homo sapi	c 215	36	100.0	178148	2	AC149725	Bos tauru	AC149725	Bos tauru
143	36	100.0	2974	9	AF108658	Homo sapi	AF108658	Homo sapi	c 216	36	100.0	179169	2	AC092759	Paplo anu	AC092759	Paplo anu
144	36	100.0	2980	9	AK123240	Homo sapi	AK123240	Homo sapi	c 217	36	100.0	183165	9	AP000802	Homo sapi	AP000802	Homo sapi
145	36	100.0	3007	6	CQ728125	Sequence	CQ728125	Sequence	c 218	36	100.0	184841	9	AC016902	Homo sapi	AC016902	Homo sapi
146	36	100.0	3016	9	AF126799	Homo sapi	AF126799	Homo sapi	c 219	36	100.0	185569	2	AP003099	Homo sapi	AP003099	Homo sapi
147	36	100.0	3075	9	BSM805582	Sequence	AL834479	Homo sapi	c 220	36	100.0	188414	2	CF388091	Danio rer	CF388091	Danio rer
148	36	100.0	3083	6	CQ782909	Sequence	CQ782909	Sequence	c 221	36	100.0	188736	9	CNS0008M	Human chr	AL079305	Human chr
149	36	100.0	3083	6	BD127375	Primer fo	BD127375	Primer fo	c 222	36	100.0	193917	10	AL844153	Mouse DNA	AL844153	Mouse DNA
150	36	100.0	3083	9	AK074939	Homo sapi	AK074939	Homo sapi	223	36	100.0	194487	2	AP002896	Homo sapi	AP002896	Homo sapi

224	36	100.0	196993	9	CNS01DDT	AL132985 Human chr	c 297	35	97.2	80664	2	AC027592	AC027592 Homo sapi
225	36	100.0	198890	10	AC131679	AC131679 Mus muscu	c 298	35	97.2	86820	5	BX890573	BX890573 Zebrafish
c 226	36	100.0	198935	9	AC034268	AC034268 Homo sapi	c 299	35	97.2	88966	2	AP001943	AP001943 Homo sapi
c 227	36	100.0	204340	9	AC091103	AC091103 Homo sapi	c 300	35	97.2	96678	9	HS47710A	AL096755 Human DNA
c 228	36	100.0	206191	10	AC124535	AC124535 Mus muscu	c 301	35	97.2	110000	1	AE017332_4	Continuation (5 of
c 229	36	100.0	206454	9	AC018737	AC018737 Homo sapi	c 302	35	97.2	110000	1	AE017332_5	Continuation (6 of
c 230	36	100.0	208059	2	AC114192	AC114192 Rattus no	c 303	35	97.2	110000	8	CR382125_08	Continuation (9 of
c 231	36	100.0	208492	9	AC062033	AC062033 Homo sapi	c 304	35	97.2	110000	8	CR382126_05	Continuation (6 of
c 232	36	100.0	210474	9	AC148447	AC148447 Pan trogl	c 305	35	97.2	110000	8	CR382126_06	Continuation (7 of
c 233	36	100.0	213989	5	AC145509	AC145509 Gasterost	c 306	35	97.2	110000	8	AE016820_10	Continuation (11 of
c 234	36	100.0	220216	9	AC021019	AC021019 Homo sapi	c 307	35	97.2	119774	10	AL731705	AL731705 Mouse DNA
c 235	36	100.0	222858	2	AC024810	AC024810 Homo sapi	c 308	35	97.2	123236	2	CR384099	CR384099 Danio rer
c 236	36	100.0	224887	2	AC114192	AC114192 Homo sapi	c 309	35	97.2	124895	8	AC135288	AC135288 Solanum d
c 237	36	100.0	227796	2	AC131418	AC131418 Rattus no	c 310	35	97.2	131385	10	AL591417	AL591417 Mouse DNA
c 238	36	100.0	229784	10	AL845171	AL845171 Mouse DNA	c 311	35	97.2	137995	8	AP004688	AP004688 Oryza sat
c 239	36	100.0	230610	5	AC024810	AC024810 Zebrafish	c 312	35	97.2	145293	2	AP003519	AP003519 Oryza sat
c 240	36	100.0	235474	2	AC094786	AC094786 Rattus no	c 313	35	97.2	146227	2	CR628326	CR628326 Danio rer
c 241	36	100.0	238527	10	AC128700	AC128700 Rattus no	c 314	35	97.2	146443	9	AC007488	AC007488 Homo sapi
c 242	36	100.0	240000	2	AC012525	AC012525 Homo sapi	c 315	35	97.2	146671	9	AC093810	AC093810 Homo sapi
c 243	36	100.0	241623	2	AC103008	AC103008 Rattus no	c 316	35	97.2	149319	5	AL929010	AL929010 Zebrafish
c 244	36	100.0	243360	2	AC109684	AC109684 Rattus no	c 317	35	97.2	149741	2	AC148791	AC148791 Otlemur
c 245	36	100.0	250880	10	AC102040	AC102040 Mus muscu	c 318	35	97.2	150331	2	AC145472	AC145472 Rattus no
c 246	36	100.0	256233	2	AC096530	AC096530 Rattus no	c 319	35	97.2	151494	2	AC132989	AC132989 Rattus no
c 247	36	100.0	261824	2	AC128390	AC128390 Rattus no	c 320	35	97.2	157362	2	CR388035	CR388035 Danio rer
c 248	36	100.0	291954	1	AE017328	AE017328 Listeria	c 321	35	97.2	157476	2	CR388035	CR388035 Danio rer
c 249	36	100.0	294415	2	AC121635	AC121635 Rattus no	c 322	35	97.2	158073	9	AC093756	AC093756 Homo sapi
c 250	36	100.0	300029	8	AE017113	AE017113 Oryza sat	c 323	35	97.2	159735	2	AC022627	AC022627 Homo sapi
c 251	36	100.0	300275	1	AE016751	AE016751 Staphyloc	c 324	35	97.2	162077	5	CR294656	CR294656 Zebrafish
c 252	36	100.0	303299	1	CR378676	CR378676 Photobact	c 325	35	97.2	162574	2	CR3800523	CR3800523 Danio rer
c 253	35	97.2	593	11	BV023869	BV023869 S212P6866	c 326	35	97.2	163095	8	AP002523	AP002523 Oryza sat
c 254	35	97.2	638	11	BV016402	BV016402 S212P6380	c 327	35	97.2	164175	5	AC119056	AC119056 Papio anu
c 255	35	97.2	661	11	CNS06409	AL395539 T3 end of	c 328	35	97.2	164857	5	BX248312	BX248312 Zebrafish
c 256	35	97.2	799	11	CNS06409	AL395528 T7 end of	c 329	35	97.2	165969	10	AC122003	AC122003 Mus muscu
c 257	35	97.2	889	11	CNS06409	AL395528 T7 end of	c 330	35	97.2	165969	2	AC120880	AC120880 Mus muscu
c 258	35	97.2	1341	8	AF406816	AF406816 Aquilegia	c 331	35	97.2	166189	2	CR847575	CR847575 Danio rer
c 259	35	97.2	1341	8	AF536526	AF536526 Anemone l	c 332	35	97.2	167208	2	AC034190	AC034190 Homo sapi
c 260	35	97.2	1362	6	AX824969	AX824969 Sequence	c 333	35	97.2	169366	10	AC124467	AC124467 Mus muscu
c 261	35	97.2	1362	6	AX824971	AX824971 Sequence	c 334	35	97.2	170610	2	AC023935	AC023935 Homo sapi
c 262	35	97.2	1410	6	Q0831424	Q0831424 Sequence	c 335	35	97.2	170885	2	AC024378	AC024378 Homo sapi
c 263	35	97.2	1410	6	Q0874858	Q0874858 Sequence	c 336	35	97.2	175337	2	AC022985	AC022985 Homo sapi
c 264	35	97.2	1410	6	AX951581	AX951581 Sequence	c 337	35	97.2	175989	2	CR352248	CR352248 Danio rer
c 265	35	97.2	1410	8	AY234125	AY234125 Primula f	c 338	35	97.2	176032	2	BX510656	BX510656 Danio rer
c 266	35	97.2	1450	8	AY055118	AY055118 Echium pi	c 339	35	97.2	176622	2	AC138566	AC138566 Gallus ga
c 267	35	97.2	1478	8	AY055117	AY055117 Echium ge	c 340	35	97.2	178635	10	AC110257	AC110257 Mus muscu
c 268	35	97.2	1559	8	AY603475	AY603475 Nitzschia	c 341	35	97.2	178738	2	CR847540	CR847540 Danio rer
c 269	35	97.2	1618	8	AY234127	AY234127 Primula v	c 342	35	97.2	180408	2	AC113051	AC113051 Mus muscu
c 270	35	97.2	1652	6	AX481611	AX481611 Sequence	c 343	35	97.2	182902	9	AC092405	AC092405 Papio anu
c 271	35	97.2	1652	6	AX481940	AX481940 Sequence	c 344	35	97.2	183502	2	AC150601	AC150601 Callithri
c 272	35	97.2	1652	8	AY082392	AY082392 Phaeodact	c 345	35	97.2	184704	2	CR385063	CR385063 Danio rer
c 273	35	97.2	1671	10	MCARPEM1	AF189308 Mus carol	c 346	35	97.2	185517	10	AC140231	AC140231 Mus muscu
c 274	35	97.2	1686	10	MSAXPEM1	AF189310 Mus saxic	c 347	35	97.2	186951	9	AC105903	AC105903 Homo sapi
c 275	35	97.2	1788	8	AF031194	AF031194 Tricium	c 348	35	97.2	188189	10	AC137844	AC137844 Mus muscu
c 276	35	97.2	1788	8	BT009556	BT009556 Tricium	c 349	35	97.2	188520	2	AC109298	AC109298 Mus muscu
c 277	35	97.2	3994	10	AL954862	AL954862 Mouse DNA	c 350	35	97.2	188520	2	AC109298	AC109298 Mus muscu
c 278	35	97.2	5593	1	KPCITCDEF	X79817 K.pneumonia	c 351	35	97.2	188520	10	AC134595	AC134595 Mus muscu
c 279	35	97.2	5593	6	AX137631	AX137631 Sequence	c 352	35	97.2	190512	5	BX511303	BX511303 Zebrafish
c 280	35	97.2	5593	6	AX137856	AX137856 Sequence	c 353	35	97.2	191038	10	AC124719	AC124719 Mus muscu
c 281	35	97.2	5593	6	BD014134	BD014134 Process o	c 354	35	97.2	192027	2	AC067715	AC067715 Mus muscu
c 282	35	97.2	6216	6	AR170533	AR170533 Sequence	c 355	35	97.2	192504	5	BX322620	BX322620 Zebrafish
c 283	35	97.2	9437	8	AF195007	AF195007 Brenothec	c 356	35	97.2	192653	9	AC124781	AC124781 Homo sapi
c 284	35	97.2	10961	1	AF001939	AF001939 Deinococc	c 357	35	97.2	192856	10	AC10559	AC10559 Mus muscu
c 285	35	97.2	17752	6	Q0874864	Q0874864 Sequence	c 358	35	97.2	193129	5	AL953908	AL953908 Zebrafish
c 286	35	97.2	17752	6	AX481638	AX481638 Sequence	c 359	35	97.2	195820	2	AC108779	AC108779 Mus muscu
c 287	35	97.2	17752	6	AX481967	AX481967 Sequence	c 360	35	97.2	197853	2	AC132401	AC132401 Mus muscu
c 288	35	97.2	17752	6	AX951606	AX951606 Sequence	c 361	35	97.2	197853	2	AC111423	AC111423 Rattus no
c 289	35	97.2	25002	3	CEC1304	Z92825 Caenorhabdi	c 362	35	97.2	198917	9	AL356157	AL356157 Human DNA
c 290	35	97.2	25002	6	AX481773	AX481773 Sequence	c 363	35	97.2	198973	5	BX247872	BX247872 Zebrafish
c 291	35	97.2	25621	1	PSY548826	AJ548826 Pseudomon	c 364	35	97.2	199918	2	CR751566	CR751566 Danio rer
c 292	35	97.2	38608	3	CEP36H1	Z68760 Caenorhabdi	c 365	35	97.2	204486	2	CR752655	CR752655 Danio rer
c 293	35	97.2	47163	10	AL954297	AL954297 Mouse DNA	c 366	35	97.2	204508	10	AC098711	AC098711 Mus muscu
c 294	35	97.2	56098	5	BX578772	BX578772 Zebrafish	c 367	35	97.2	206131	2	AC101593	AC101593 Mus muscu
c 295	35	97.2	63348	2	AC135176	AC135176 Homo sapi	c 368	35	97.2	208957	10	AC091682	AC091682 Mus muscu
c 296	35	97.2	63750	8	AP004936	AP004936 Lotus cor	c 369	35	97.2	208734	10	AC102675	AC102675 Mus muscu

370	35	97.2	209484	2	AC024116	AC024116 Mus muscu	C 443	34	94.4	1528	6	AX166353	AX166353 Sequence
C 371	35	97.2	209705	10	AC101931	AC101931 Mus muscu	444	34	94.4	1591	8	HACV7BSRN	X87143 Helianthus
C 372	35	97.2	209730	2	AL844860	AL844860 Mus muscu	445	34	94.4	1594	6	AX007239	AX007239 Sequence
C 373	35	97.2	211178	10	AC139209	AC139209 Mus muscu	446	34	94.4	1606	6	AX007273	AX007273 Sequence
C 374	35	97.2	211999	2	AC087039	AC087039 Mus muscu	447	34	94.4	1610	8	ENAJ4160	AD224160 Brassica
C 375	35	97.2	212101	2	AC148782	AC148782 Otlemur	448	34	94.4	1633	8	AF001394	AF001394 Arabidops
C 376	35	97.2	213050	1	AL646079	AL646079 Ralstonia	449	34	94.4	1652	8	AY087345	AY087345 Arabidops
C 377	35	97.2	213438	2	AC125903	AC125903 Rattus no	450	34	94.4	1678	6	AX007241	AX007241 Sequence
C 378	35	97.2	213524	2	AL390792	AL390792 Homo sapi	451	34	94.4	1702	6	AR200409	AR200409 Sequence
C 379	35	97.2	216410	2	AC140457	AC140457 Mus muscu	452	34	94.4	1702	6	AR455422	AR455422 Sequence
C 380	35	97.2	216609	2	AC142133	AC142133 Rattus no	453	34	94.4	1704	8	AF428420	AF428420 Arabidops
C 381	35	97.2	220823	10	AC108827	AC108827 Mus muscu	454	34	94.4	1705	8	ATAJ4161	AJ224161 Arabidops
C 382	35	97.2	223392	10	AL670238	AL670238 Mouse DNA	455	34	94.4	1743	8	BT000442	BT000442 Arabidops
C 383	35	97.2	224402	2	AC096500	AC096500 Rattus no	C 456	34	94.4	1840	6	AX166371	AX166371 Sequence
C 384	35	97.2	224607	2	AC107176	AC107176 Mus muscu	457	34	94.4	1857	5	AY398379	AY398379 Danio rer
C 385	35	97.2	224740	2	AC018986	AC018986 Mus muscu	458	34	94.4	1869	8	AF133728	AF133728 Borago of
C 386	35	97.2	225065	2	AC127370	AC127370 Mus muscu	459	34	94.4	1924	6	AX166373	AX166373 Sequence
C 387	35	97.2	225654	5	AL953842	AL953842 Zebrafish	C 460	34	94.4	1924	6	AX166385	AX166385 Sequence
C 388	35	97.2	227922	10	AC120547	AC120547 Mus muscu	C 461	34	94.4	1980	6	AR564554	AR564554 Sequence
C 389	35	97.2	229678	2	AC103232	AC103232 Rattus no	C 462	34	94.4	2034	8	AB080193	AB080193 Pisum sat
C 390	35	97.2	231755	2	AC109091	AC109091 Rattus no	C 463	34	94.4	2688	6	AR388599	AR388599 Sequence
C 391	35	97.2	232552	2	AC103111	AC103111 Rattus no	C 464	34	94.4	2762	9	AF222985	AF222985 Homo sapi
C 392	35	97.2	233168	2	AC099164	AC099164 Rattus no	C 465	34	94.4	6876	6	AR354068	AR354068 Sequence
C 393	35	97.2	234724	10	AL683854	AL683854 Mouse DNA	C 466	34	94.4	6876	6	AR535624	AR535624 Sequence
C 394	35	97.2	235133	2	AC115375	AC115375 Rattus no	C 467	34	94.4	7291	9	AF222983	AF222983 Homo sapi
C 395	35	97.2	235198	10	AL645571	AL645571 Mouse DNA	C 468	34	94.4	9466	6	CQ574109	CQ574109 Sequence
C 396	35	97.2	235915	2	AC134944	AC134944 Rattus no	C 469	34	94.4	10029	1	AE009551	AE009551 Brucella
C 397	35	97.2	241385	2	AC128785	AC128785 Rattus no	C 470	34	94.4	12145	1	AE014388	AE014388 Brucella
C 398	35	97.2	243282	2	AC096473	AC096473 Rattus no	C 471	34	94.4	15002	9	AF222981	AF222981 Homo sapi
C 399	35	97.2	244677	2	AC129545	AC129545 Mus muscu	C 472	34	94.4	31048	3	U80447	U80447 Caenorhabdi
C 400	35	97.2	246322	2	AC133966	AC133966 Homo sapi	C 473	34	94.4	33376	9	AF222987	AF222987 Homo sapi
C 401	35	97.2	247984	2	AC130984	AC130984 Rattus no	C 474	34	94.4	33780	6	AX151213	AX151213 Sequence
C 402	35	97.2	248864	2	AC129403	AC129403 Rattus no	C 475	34	94.4	35660	8	SPBC16H5	AL022104 S-Pombe c
C 403	35	97.2	249942	2	AC111088	AC111088 Mus muscu	C 476	34	94.4	39964	2	AC145671	AC145671 Homo sapi
C 404	35	97.2	250510	2	AC110837	AC110837 Rattus no	C 477	34	94.4	40400	3	CEF26584	Z81070 Caenorhabdi
C 405	35	97.2	251228	2	AC097036	AC097036 Rattus no	C 478	34	94.4	41564	3	AF067937	AF067937 Caenorhab
C 406	35	97.2	253701	2	AC106658	AC106658 Rattus no	C 479	34	94.4	41564	3	AF067937	AF067937 Caenorhab
C 407	35	97.2	254057	2	AC094747	AC094747 Rattus no	C 480	34	94.4	57250	2	AC083997	AC083997 Homo sapi
C 408	35	97.2	254581	2	AC130626	AC130626 Rattus no	C 481	34	94.4	59777	3	AC084454	AC084454 Caenorhab
C 409	35	97.2	260967	2	AC091771	AC091771 Mus muscu	C 482	34	94.4	61246	2	AL359032_4	Continuation (5 of
C 410	35	97.2	262895	2	CR387980	CR387980 Danio rer	C 483	34	94.4	65283	2	AC101475	AC101475 Mus muscu
C 411	35	97.2	272577	2	AC097684	AC097684 Rattus no	C 484	34	94.4	71302	2	AC087760	AC087760 Homo sapi
C 412	35	97.2	301042	1	AE016967	AE016967 Mycoplasma	C 485	34	94.4	72281	2	HSF20148	AL109765 Homo sapi
C 413	35	97.2	308147	1	AE016915	AE016915 Chromobac	C 486	34	94.4	73078	9	AC122132	AC122132 Homo sapi
C 414	35	97.2	349980	6	CQ870463	CQ870463 Sequence	C 487	34	94.4	77728	9	AP000146	AP000146 Homo sapi
C 415	34	94.4	33	6	AR080602	AR080602 Sequence	C 488	34	94.4	77728	9	AP000231	AP000231 Homo sapi
C 416	34	94.4	33	6	AR098445	AR098445 Sequence	C 489	34	94.4	79442	9	AL139037	AL139037 Human DNA
C 417	34	94.4	33	6	AR136022	AR136022 Sequence	C 490	34	94.4	86516	9	AC009493	AC009493 Homo sapi
C 418	34	94.4	33	6	AR215240	AR215240 Sequence	C 491	34	94.4	86894	2	AL390319	AL390319 Homo sapi
C 419	34	94.4	33	6	BD082625	BD082625 Methods a	C 492	34	94.4	87577	2	BX640459	BX640459 Danio rer
C 420	34	94.4	33	6	BD092921	BD092921 Methods a	C 493	34	94.4	87960	2	AC017906	AC017906 Drosophila
C 421	34	94.4	315	6	BR388367	BR388367 Sequence	C 494	34	94.4	90019	8	TM021B04	AF007271 Arabidops
C 422	34	94.4	317	11	BX640487	BX640487 Arabidops	C 495	34	94.4	95993	8	ATF2A19	AL132962 Arabidops
C 423	34	94.4	447	6	AS0348	AS0348 Sequence 3	C 496	34	94.4	97375	9	AL353898	AL353898 Human DNA
C 424	34	94.4	447	6	AS0352	AS0352 Sequence 7	C 497	34	94.4	98476	8	AP003706	AP003706 Oryza sat
C 425	34	94.4	447	6	AR127512	AR127512 Sequence	C 498	34	94.4	101033	9	AC104090	AC104090 Homo sapi
C 426	34	94.4	447	6	AR127514	AR127514 Sequence	C 499	34	94.4	109321	9	AC021079	AC021079 Homo sapi
C 427	34	94.4	447	14	HPCCOREE1T	L39299 Hepatitis C	C 500	34	94.4	109864	9	AF096876	AF096876 Homo sapi
C 428	34	94.4	447	14	HPCCOREE1W	L39302 Hepatitis C	C 501	34	94.4	110000	1	BX571856_05	Continuation (6 of
C 429	34	94.4	488	9	BC062656	BC062656 Homo sapi	C 502	34	94.4	110000	1	BX571857_05	Continuation (6 of
C 430	34	94.4	609	6	AX620466	AX620466 Sequence	C 503	34	94.4	110000	2	AC150872_2	Continuation (3 of
C 431	34	94.4	634	11	G40519	G40519 Z7223 Zebra	C 504	34	94.4	110000	2	AP006497_4	Continuation (5 of
C 432	34	94.4	662	6	AX166383	AX166383 Sequence	C 505	34	94.4	110000	2	AP006497_5	Continuation (6 of
C 433	34	94.4	702	7	AF536823	AF536823 Bacterioph	C 506	34	94.4	110000	8	CR382124_10	Continuation (11 of
C 434	34	94.4	1051	3	AY057996	AY057996 Entamoeba	C 507	34	94.4	110149	8	CR382134_01	Continuation (12 of
C 435	34	94.4	1238	6	AX166375	AX166375 Sequence	C 508	34	94.4	111255	8	AC005397	AC005397 Arabidops
C 436	34	94.4	1350	6	AX505863	AX505863 Sequence	C 509	34	94.4	112582	9	AC125478	AC125478 Medicago
C 437	34	94.4	1365	6	AR564555	AR564555 Sequence	C 510	34	94.4	113345	8	AC120778	AC120778 Homo sapi
C 438	34	94.4	1428	6	AX166358	AX166358 Sequence	C 511	34	94.4	114078	2	AX640498	AX640498 Danio rer
C 439	34	94.4	1428	6	AX166359	AX166359 Sequence	C 512	34	94.4	114804	9	AC094080	AC094080 Homo sapi
C 440	34	94.4	1464	6	AX166350	AX166350 Sequence	C 513	34	94.4	118504	5	BX649415	BX649415 Zebrafish
C 441	34	94.4	1491	8	BT003379	BT003379 Arabidops	C 514	34	94.4	119427	5	BX890584	BX890584 Mouse DNA
C 442	34	94.4	1524	9	AF465766	AF465766 Homo sapi	C 515	34	94.4	120359	10	BX890584	BX890584 Mouse DNA

516	34	94.4	122223	9	AC007880	AC007880 Homo sapi	589	34	94.4	182146	10	AC137128	Mus muscu
517	34	94.4	124531	9	AL049710	Human DNA	590	34	94.4	182360	9	AC137128	Mus muscu
518	34	94.4	126087	8	AF147264	Arabidops	591	34	94.4	182577	5	EX640466	Zebrafish
519	34	94.4	129271	8	AC005687	Arabidops	592	34	94.4	182591	10	AC127272	Mus muscu
520	34	94.4	129921	8	AC146568	Medicago	593	34	94.4	182838	2	AC115855	Mus muscu
521	34	94.4	131414	9	AL109763	Homo sapi	594	34	94.4	183604	9	AC022022	Homo sapi
522	34	94.4	132072	9	AC004841	Homo sapi	595	34	94.4	183779	9	AC123023	Homo sapi
523	34	94.4	133968	9	AL136171	Human DNA	596	34	94.4	184362	2	AL450268	Homo sapi
524	34	94.4	134804	8	AP004888	Oryza sat	597	34	94.4	184362	2	AL450268	Homo sapi
525	34	94.4	137408	2	AC151098	Homo sapi	598	34	94.4	185132	9	CNS01DUB	Human chr
526	34	94.4	139292	2	AC149664	Homo sapi	599	34	94.4	185324	9	AC087828	Homo sapi
527	34	94.4	139966	9	AC004820	Homo sapi	600	34	94.4	185947	9	AC092630	Homo sapi
528	34	94.4	141944	9	AC122108	Homo sapi	601	34	94.4	186084	9	AP002768	Homo sapi
529	34	94.4	142436	2	AC140695	Rattus no	602	34	94.4	186834	5	EX004687	Zebrafish
530	34	94.4	143220	9	AL1389887	Human DNA	603	34	94.4	187752	10	AC124689	Mus muscu
531	34	94.4	143708	2	AC141659	Apis mell	604	34	94.4	187931	8	AP005319	Oryza sat
532	34	94.4	144075	2	AC013763	Homo sapi	605	34	94.4	188037	2	AC147929	Ovis arie
533	34	94.4	144590	8	AP006452	Oryza sat	606	34	94.4	188320	2	AC092085	Homo sapi
534	34	94.4	144610	2	CR387981	Danio rer	607	34	94.4	188907	2	AC150945	Bos tauru
535	34	94.4	148123	2	AC151083	Bos tauru	608	34	94.4	189421	9	BS000043	Pan trogl
536	34	94.4	148344	10	AC090432	Mus muscu	609	34	94.4	189502	2	AC119087	Rattus no
537	34	94.4	148555	2	AC126921	Bos tauru	610	34	94.4	191923	2	AP001846	Homo sapi
538	34	94.4	150052	9	AC006481	Homo sapi	611	34	94.4	193554	2	AC151137	Bos tauru
539	34	94.4	150325	2	AC018535	Homo sapi	612	34	94.4	193593	10	AC111008	Mus muscu
540	34	94.4	150817	8	AP003323	Oryza sat	613	34	94.4	194068	2	AC115327	Rattus no
541	34	94.4	151959	2	AC036192	Homo sapi	614	34	94.4	194311	9	AC091245	Homo sapi
542	34	94.4	152838	2	AC011589	Homo sapi	615	34	94.4	194546	9	AC142286	Pan trogl
543	34	94.4	154862	9	AC139310	Bos tauru	616	34	94.4	194641	4	AC150690	Bos tauru
544	34	94.4	156195	9	AC093799	Homo sapi	617	34	94.4	194721	5	EX470232	Zebrafish
545	34	94.4	156337	2	AC009938	Homo sapi	618	34	94.4	196301	10	AC109217	Mus muscu
546	34	94.4	156813	9	HSJ6731M13	Human DNA	619	34	94.4	196455	2	AC151138	Bos tauru
547	34	94.4	156870	2	AC149695	Bos tauru	620	34	94.4	197064	8	ATCHRIV18	Arabidops
548	34	94.4	157174	2	AC151222	Bos tauru	621	34	94.4	197646	2	AC011041	Homo sapi
549	34	94.4	157371	2	AC147844	Ovis arie	622	34	94.4	198160	2	AC013569	Homo sapi
550	34	94.4	157801	2	AC058814	Homo sapi	623	34	94.4	198503	2	AC107734	Mus muscu
551	34	94.4	157857	2	AC072032	Homo sapi	624	34	94.4	199503	9	AC018901	Homo sapi
552	34	94.4	159922	2	AC072032	Homo sapi	625	34	94.4	201673	2	AC099747	Bos tauru
553	34	94.4	161346	5	EX511013	Zebrafish	626	34	94.4	201673	2	AC099747	Bos tauru
554	34	94.4	162591	2	AC151214	Bos tauru	627	34	94.4	204617	3	AC006074	Drosophila
555	34	94.4	162739	9	AL353788	Human DNA	628	34	94.4	205011	5	AL954168	Zebrafish
556	34	94.4	163056	2	AL359968	Homo sapi	629	34	94.4	206352	2	AL392238	Mus muscu
557	34	94.4	163461	2	AC150853	Bos tauru	630	34	94.4	206383	10	AC008160	Mus muscu
558	34	94.4	164686	4	AC098686	Bos tauru	631	34	94.4	206569	10	AC133968	Mus muscu
559	34	94.4	164792	2	AC119551	Rattus no	632	34	94.4	207555	2	AC104557	Mus muscu
560	34	94.4	164950	2	EX088696	Danio rer	633	34	94.4	210675	2	AC036272	Homo sapi
561	34	94.4	165067	9	AL138927	Human DNA	634	34	94.4	211084	2	AC092804	Bos tauru
562	34	94.4	165095	2	AC138665	Mus muscu	635	34	94.4	211542	2	AC073206	Homo sapi
563	34	94.4	165363	9	HS45914	Human DNA	636	34	94.4	212974	2	AC121452	Rattus no
564	34	94.4	165765	2	AC117979	Rattus no	637	34	94.4	213599	2	AC140764	Rattus no
565	34	94.4	165807	2	AL391810	Homo sapi	638	34	94.4	215399	2	AC116268	Rattus no
566	34	94.4	166655	5	EX537129	Zebrafish	639	34	94.4	216877	9	AC106791	Homo sapi
567	34	94.4	169947	2	AC130631	Rattus no	640	34	94.4	216887	2	AC113676	Rattus no
568	34	94.4	169968	2	AC099745	Bos tauru	641	34	94.4	216958	2	AC115959	Mus muscu
569	34	94.4	170156	2	AP002412	Homo sapi	642	34	94.4	217844	2	EX927392	Danio rer
570	34	94.4	170365	9	AL390920	Human DNA	643	34	94.4	218080	10	AC125208	Mus muscu
571	34	94.4	170770	9	AP240627	Homo sapi	644	34	94.4	218739	2	AC111863	Rattus no
572	34	94.4	172456	2	AC151080	Homo sapi	645	34	94.4	222632	2	AC106115	Rattus no
573	34	94.4	172579	9	AC008064	Homo sapi	646	34	94.4	223526	2	AC150549	Bos tauru
574	34	94.4	172641	2	AC150489	Bos tauru	647	34	94.4	225165	2	AC149666	Bos tauru
575	34	94.4	172641	2	AC150489	Bos tauru	648	34	94.4	225658	10	AC127353	Mus muscu
576	34	94.4	172680	9	AL512641	Human DNA	649	34	94.4	226674	2	AC131171	Rattus no
577	34	94.4	173660	2	AC151128	Homo sapi	650	34	94.4	226924	10	AC13490	Mus muscu
578	34	94.4	175092	2	AC150576	Bos tauru	651	34	94.4	227340	2	AC095000	Rattus no
579	34	94.4	175177	10	AC124383	Mus muscu	652	34	94.4	228826	2	AC135589	Rattus no
580	34	94.4	175590	9	AC027119	Homo sapi	653	34	94.4	228950	2	AC111512	Rattus no
581	34	94.4	176245	2	AC016197	Homo sapi	654	34	94.4	229231	4	AC096139	Rattus no
582	34	94.4	176551	2	EX537283	Danio rer	655	34	94.4	233345	4	AJ421481	Bos tauru
583	34	94.4	178095	2	CR753874	Danio rer	656	34	94.4	233345	4	AJ421481	Bos tauru
584	34	94.4	178262	3	AC093049	Drosophila	657	34	94.4	234844	2	AC111734	Rattus no
585	34	94.4	179779	2	AP005315	Oryza sat	658	34	94.4	236612	2	AC109678	Rattus no
586	34	94.4	180574	9	AC092807	Homo sapi	659	34	94.4	240664	2	AC094875	Rattus no
587	34	94.4	181817	2	AC141133	Rattus no	660	34	94.4	240741	2	AC126133	Rattus no
588	34	94.4	181842	2	AL391823	Homo sapi	661	34	94.4	243313	3	AE003834	Drosophila

662	34	94.4	243510	5	BX005415	Zebraphish	735	33	91.7	1374	8	AF465282	Mortierel
663	34	94.4	244170	2	AC130152	Rattus no	736	33	91.7	1404	6	BD178222	Fatty aci
C 664	34	94.4	244595	2	AC098435	Rattus no	737	33	91.7	1434	3	AY493438	Thalassio
665	34	94.4	247239	2	AC091376	Rattus no	738	33	91.7	1461	3	AF114440	Caenorhab
666	34	94.4	250064	2	AC103494	Rattus no	739	33	91.7	1461	6	BD242778	Desaturas
667	34	94.4	250629	2	AC114044	Rattus no	740	33	91.7	1463	3	AF031477	Caenorhab
C 668	34	94.4	258819	2	AC118292	Rattus no	741	33	91.7	1463	6	BD138943	Desaturas
669	34	94.4	259210	2	AC073368	Homo sapi	742	33	91.7	1463	6	AX003603	Sequence
670	34	94.4	259553	2	AC135140	Rattus no	743	33	91.7	1482	8	AY320288	Rhizopus
C 671	34	94.4	261024	1	AE017256	Wolbachia	744	33	91.7	1521	8	AB070555	Mortierel
C 672	34	94.4	262101	2	AC113760	Rattus no	745	33	91.7	1537	8	AY583316	Rhizopus
C 673	34	94.4	266631	2	AC130916	Rattus no	746	33	91.7	1546	8	AB052086	Muor c1r
C 674	34	94.4	267172	9	BS000177	Pan trogl	C 747	33	91.7	1581	5	XL428P50	Z19545 X.laevis mR
675	34	94.4	272952	2	AC109685	Rattus no	748	33	91.7	1590	8	AB020032	Mortierel
C 676	34	94.4	296821	2	AC127127	Rattus no	749	33	91.7	1617	6	AR080598	Sequence
C 677	34	94.4	300821	1	AE017250	Treponema	750	33	91.7	1617	6	AR098439	Sequence
C 678	34	94.4	301050	1	AP003130	Staphyloc	751	33	91.7	1617	6	ARI36018	Sequence
C 679	34	94.4	302881	2	BX323850	Danio rer	752	33	91.7	1617	6	AR215236	Sequence
C 680	34	94.4	309473	2	AC098042	Rattus no	753	33	91.7	1617	6	AR235375	Sequence
C 681	34	94.4	325350	1	AP004823	Staphyloc	754	33	91.7	1617	6	BD082621	Methods a
C 682	34	94.4	325643	2	AL512381	Homo sapi	755	33	91.7	1617	6	BD092914	Methods a
C 683	34	94.4	329709	1	AP002997	Mesorhizo	756	33	91.7	1617	6	AF110510	Mortierel
C 684	34	94.4	334963	2	AC114019	Rattus no	757	33	91.7	1644	8	AF307942	Mortierel
685	34	94.4	340000	9	AP001692	Homo sapi	C 758	33	91.7	1650	8	AY035052	Arabidops
686	34	94.4	340000	9	AP001707	Homo sapi	759	33	91.7	1667	8	SCMET8	X17271 Saccharomyc
C 687	34	94.4	340000	9	HS21C018	Homo sapi	760	33	91.7	1743	8	AB070556	Mortierel
C 688	34	94.4	343590	1	AP003359	Staphyloc	761	33	91.7	1831	8	AY392409	Amylomyce
C 689	34	94.4	347356	1	BX640437	Bordetell	762	33	91.7	1856	8	AF005096	Ricinusc c
C 690	34	94.4	348093	2	AC128471	Rattus no	C 763	33	91.7	1900	1	AXACEA	X93149 A.xylinum a
C 691	34	94.4	348251	1	BX640423	Bordetell	764	33	91.7	1947	8	AF465283	Mortierel
692	34	94.4	348517	1	BX248354	Corynebac	C 765	33	91.7	1980	6	AR484379	Sequence
C 693	34	94.4	349726	1	BX640421	Bordetell	C 766	33	91.7	1980	6	AX142873	Sequence
C 694	33	91.7	36	6	AX577011	Sequence	C 767	33	91.7	2000	6	AX656198	Sequence
C 695	33	91.7	260	11	AU025619	Rattus no	768	33	91.7	2004	6	AX813737	Sequence
C 696	33	91.7	306	6	AR554370	Sequence	C 769	33	91.7	2014	14	TRA272198	Tobacco r
C 697	33	91.7	336	6	AX072791	Sequence	770	33	91.7	2175	8	AJ601391	Mortierel
C 698	33	91.7	386	6	AX315800	Sequence	C 771	33	91.7	2200	5	XLEFLAA	X52975 X.laevis mR
C 699	33	91.7	480	6	CQ049477	Sequence	772	33	91.7	2207	8	AB070557	Mortierel
C 700	33	91.7	480	6	CQ064504	Sequence	C 773	33	91.7	2279	9	AB025159	Homo sapi
C 701	33	91.7	480	6	CQ091451	Sequence	774	33	91.7	3004	1	AF270259	Staphyloc
C 702	33	91.7	480	6	CQ130277	Sequence	775	33	91.7	3004	6	AR486213	Sequence
C 703	33	91.7	480	6	CQ168902	Sequence	776	33	91.7	3004	6	AX145577	Sequence
C 704	33	91.7	480	6	CQ198020	Sequence	C 777	33	91.7	3177	1	AF269675	Staphyloc
C 705	33	91.7	480	6	CQ213480	Sequence	C 778	33	91.7	3177	6	AR485631	Sequence
C 706	33	91.7	480	6	CQ252060	Sequence	C 779	33	91.7	3177	6	AX144995	Sequence
C 707	33	91.7	480	6	CQ289208	Sequence	C 780	33	91.7	3216	14	TRV9833	Tobacco r
C 708	33	91.7	480	6	CQ326198	Sequence	781	33	91.7	3227	8	SCNGR1	Z14097 S.cerevisia
C 709	33	91.7	657	3	AY142706	Onchocerc	782	33	91.7	3235	8	SCYBR212W	S.cerevisia
C 710	33	91.7	682	6	AX840707	Sequence	783	33	91.7	3248	8	AK106248	Oryza sat
C 711	33	91.7	684	4	BOSZEV2	Bos tauru	C 784	33	91.7	3320	1	AF269607	Staphyloc
C 712	33	91.7	709	6	BD146231	Primer fo	C 785	33	91.7	3320	6	AR485563	Sequence
C 713	33	91.7	709	6	AX866169	Sequence	C 786	33	91.7	3320	6	AX144927	Sequence
C 714	33	91.7	862	8	PSP16751	Y16751 Piromyces s	C 787	33	91.7	3414	6	BD159244	Primer fo
C 715	33	91.7	943	11	G39469	G39469 222313 Zebr	C 788	33	91.7	3414	6	AX881738	Sequence
C 716	33	91.7	1044	6	AX617312	Sequence	C 789	33	91.7	3414	9	BD012417	A novel g
C 717	33	91.7	1071	8	AX621305	Mortierel	C 790	33	91.7	3414	9	AK027344	Homo sapi
C 718	33	91.7	1071	8	AF307941	Mortierel	C 791	33	91.7	3459	6	AR270800	Sequence
C 719	33	91.7	1207	8	AF244921	Spinacia	792	33	91.7	3459	6	HSNGM07EG	Sequence
C 720	33	91.7	1266	6	CQ831420	Sequence	C 793	33	91.7	3643	1	AF269971	Staphyloc
C 721	33	91.7	1275	6	BD242779	Desaturas	C 794	33	91.7	3643	6	AR485925	Sequence
C 722	33	91.7	1275	8	AF139720	Euglena g	C 795	33	91.7	3643	6	AX145289	Sequence
C 723	33	91.7	1344	3	AF078796	Caenorhab	C 796	33	91.7	3751	6	AX704751	Sequence
C 724	33	91.7	1344	6	BD140482	Desaturas	C 797	33	91.7	3780	3	AF388524	Dictyoste
C 725	33	91.7	1344	6	CQ831426	Sequence	798	33	91.7	3854	14	AF368033	Ndelle vi
C 726	33	91.7	1344	6	AX020906	Sequence	C 799	33	91.7	3947	3	AY280695	Platypalp
C 727	33	91.7	1344	6	AX951583	Sequence	C 800	33	91.7	4048	1	AF444794	Vibrio ch
C 728	33	91.7	1374	6	BD232180	Compositi	C 801	33	91.7	4073	6	AX269342	Sequence
C 729	33	91.7	1374	6	AX413720	Sequence	C 802	33	91.7	4473	8	AF030976	Ascobolus
C 730	33	91.7	1374	6	AX415732	Sequence	803	33	91.7	4828	3	AK103435	Oryza sat
C 731	33	91.7	1374	6	AX951591	Sequence	804	33	91.7	5000	3	AF482397	Dictyoste
C 732	33	91.7	1374	8	AF306634	Mortierel	805	33	91.7	5227	14	AY008144	Spodopter
C 733	33	91.7	1374	8	AF307940	Mortierel	806	33	91.7	5325	8	AY583466	Marchanti
C 734	33	91.7	1374	8	AF465281	Mortierel	C 807	33	91.7	5941	8	AIMASC2	Ascobolus i



C 808	33	91.7	7047	1	LSEXOGC	X98238	L.sake gene	C 881	33	91.7	83881	8	AP004917	AP004917	Lotus cor
C 809	33	91.7	7099	3	HROAMD1	D13507	Holocynthia	882	33	91.7	84554	8	AC123571	AC123571	Medicago
C 810	33	91.7	7673	14	HPV12	X74466	Human papill	883	33	91.7	84554	8	AC123571	AC123571	Medicago
C 811	33	91.7	7722	14	HPU31785	U31785	Human papill	C 884	33	91.7	87428	3	CEY64G10A	CEY64G10A	Caenorhab
C 812	33	91.7	7726	14	PH477CG	M32305	Human papill	885	33	91.7	89703	8	AC005223	AC005223	Arabidops
C 813	33	91.7	7731	14	HPU85660	U85660	Human papill	C 886	33	91.7	89703	8	AL356134	AL356134	Human DNA
C 814	33	91.7	7746	14	PHH5CG	M17466	Human papill	C 887	33	91.7	90291	9	AP000173	AP000173	Homo sapi
C 815	33	91.7	7746	14	PHHDELGC	M22961	Human papill	C 888	33	91.7	91186	2	AC118415_3	AC118415_3	Continuation (4 of
C 816	33	91.7	8133	1	AF060119	AF060119	Pasteurel	C 889	33	91.7	91186	2	AC118415_3	AC118415_3	Continuation (4 of
C 817	33	91.7	8546	6	AX828406	AX828406	Sequence	890	33	91.7	92728	8	CNS08C9D	CNS08C9D	Oriza sat
C 818	33	91.7	8546	9	HS306906	HS306906	Homo sapi	891	33	91.7	93196	2	AC022085	AC022085	Homo sapi
C 819	33	91.7	10066	1	U67598	U67598	Methanocald	892	33	91.7	93268	3	AC024204	AC024204	Caenorhab
C 820	33	91.7	10383	1	AE006705	AE006705	Sulfolobu	C 893	33	91.7	93268	3	AC024862	AC024862	Caenorhab
C 821	33	91.7	11367	1	AE006168	AE006168	Pasteurel	C 894	33	91.7	96337	9	AC087349	AC087349	Homo sapi
C 822	33	91.7	11831	1	AE006172	AE006172	Pasteurel	C 895	33	91.7	96597	6	AX695914	AX695914	Sequence
C 823	33	91.7	13680	3	AC024820	AC024820	Caenorhab	C 896	33	91.7	97862	2	AC120823_4	AC120823_4	Continuation (5 of
C 824	33	91.7	13935	3	PP156DSA	X96616	P. primaurel	C 897	33	91.7	97862	2	AC120823_4	AC120823_4	Continuation (5 of
C 825	33	91.7	15249	6	AR353984	AR353984	Sequence	C 898	33	91.7	99848	9	HS34417	HS34417	Human DNA
C 826	33	91.7	15249	6	AR353540	AR353540	Sequence	C 899	33	91.7	100400	9	AC119744	AC119744	Homo sapi
C 827	33	91.7	15453	6	BD093329	BD093329	Atopy gen	C 900	33	91.7	101333	8	AP004030	AP004030	Oriza sat
C 828	33	91.7	17986	3	U23451	U23451	Caenorhabdi	C 901	33	91.7	101365	2	AP004748	AP004748	Oriza sat
C 829	33	91.7	17986	3	U23451	U23451	Caenorhabdi	C 902	33	91.7	101589	5	AL113963	AL113963	Zebratfish
C 830	33	91.7	18207	6	AX828384	AX828384	Sequence	903	33	91.7	101589	9	HSJ717M23	HSJ717M23	Human DNA
C 831	33	91.7	18207	9	AF156100	AF156100	Homo sapi	C 904	33	91.7	103550	2	AP004003	AP004003	Oriza sat
C 832	33	91.7	19230	3	AC024821	AC024821	Caenorhab	C 905	33	91.7	105741	2	AC140160	AC140160	Rattus no
C 833	33	91.7	22348	9	AP000332	AP000332	Homo sapi	C 906	33	91.7	105741	2	AC140160	AC140160	Rattus no
C 834	33	91.7	22683	3	AC006656	AC006656	Caenorhab	C 907	33	91.7	106562	2	AP004055	AP004055	Rattus no
C 835	33	91.7	22683	3	AC006656	AC006656	Caenorhab	C 908	33	91.7	108036	9	AC084352	AC084352	Homo sapi
C 836	33	91.7	24171	3	CEC31A11	Z83218	Caenorhabdi	C 909	33	91.7	109501	10	AC084213	AC084213	Mus muscu
C 837	33	91.7	26076	3	CEP14D7	Z77658	Caenorhabdi	910	33	91.7	109964	2	AP005677	AP005677	Oriza sat
C 838	33	91.7	26258	3	U41018	Z77658	Caenorhabdi	911	33	91.7	110964	2	AP005677	AP005677	Oriza sat
C 839	33	91.7	27884	8	AP006537	AP006537	Lotus cor	C 910	33	91.7	110000	1	AS017308_5	AS017308_5	Continuation (6 of
C 840	33	91.7	29324	1	BS16829KB	UJ22587	Bacillus	912	33	91.7	110000	1	AS017332_1	AS017332_1	Continuation (2 of
C 841	33	91.7	29727	2	CEH32E01	UJ22587	Bacillus	913	33	91.7	110000	1	AP006618_47	AP006618_47	Continuation (48 o
C 842	33	91.7	31361	3	AF016437	AF016437	Caenorhab	C 914	33	91.7	110000	1	AP006840_13	AP006840_13	Continuation (14 o
C 843	33	91.7	31361	3	AF016437	AF016437	Caenorhab	915	33	91.7	110000	1	BX571856_21	BX571856_21	Continuation (22 o
C 844	33	91.7	32723	3	CEM88	Z34802	Caenorhabdi	C 916	33	91.7	110000	1	BX571856_22	BX571856_22	Continuation (22 o
C 845	33	91.7	32856	9	AC139700	AC139700	Homo sapi	C 917	33	91.7	110000	1	CF000001_18	CF000001_18	Continuation (19 o
C 846	33	91.7	33539	3	U00067	U00067	Caenorhabdi	C 918	33	91.7	110000	2	AC095237_1	AC095237_1	Continuation (4 of
C 847	33	91.7	35257	2	AC149339	AC149339	Phakopsor	919	33	91.7	110000	2	AC095424_0	AC095424_0	Rattus no
C 848	33	91.7	35257	2	CEZK1320	Z46934	Caenorhabdi	C 920	33	91.7	110000	2	AC095424_0	AC095424_0	Rattus no
C 849	33	91.7	35989	3	CEZK1320	Z46934	Caenorhabdi	C 921	33	91.7	110000	2	AC096204_2	AC096204_2	Continuation (3 of
C 850	33	91.7	36116	2	AC149332	AC149332	Phakopsor	C 922	33	91.7	110000	2	AC105872_0	AC105872_0	Rattus no
C 851	33	91.7	37176	3	CEP44G3	Z83109	Caenorhabdi	923	33	91.7	110000	2	AC109746_3	AC109746_3	Continuation (4 of
C 852	33	91.7	37717	3	U53150	Z83109	Caenorhabdi	C 924	33	91.7	110000	2	AC109746_3	AC109746_3	Continuation (4 of
C 853	33	91.7	38094	3	AF040647	AF040647	Caenorhab	C 925	33	91.7	110000	2	AC112426_2	AC112426_2	Continuation (3 of
C 854	33	91.7	38383	3	CEP35H8	Z36752	Caenorhabdi	C 926	33	91.7	110000	2	AC115558_1	AC115558_1	Continuation (2 of
C 855	33	91.7	39266	3	CEP20E11	Z81508	Caenorhabdi	C 927	33	91.7	110000	2	AC117408_2	AC117408_2	Continuation (3 of
C 856	33	91.7	40647	9	HSU53583	U53583	Human chrom	928	33	91.7	110000	2	AC118415_2	AC118415_2	Continuation (3 of
C 857	33	91.7	41151	3	CEC48B4	Z29117	Caenorhabdi	929	33	91.7	110000	2	AC129442_4	AC129442_4	Continuation (5 of
C 858	33	91.7	41258	3	AF025453	AF025453	Caenorhab	C 930	33	91.7	110000	2	AC130739_2	AC130739_2	Continuation (3 of
C 859	33	91.7	42300	3	U80452	U80452	Caenorhabdi	C 931	33	91.7	110000	2	AP006502_09	AP006502_09	Continuation (10 o
C 860	33	91.7	46022	5	GGA289777	AJ289777	Gallus ga	C 932	33	91.7	110000	6	AR271569_15	AR271569_15	Continuation (16 o
C 861	33	91.7	46022	5	GGA289778	AJ289778	Gallus ga	933	33	91.7	110000	8	AR406002_6	AR406002_6	Continuation (7 of
C 862	33	91.7	46022	5	GGA289779	AJ289779	Gallus ga	C 934	33	91.7	110000	8	CR380953_05	CR380953_05	Continuation (6 of
C 863	33	91.7	46148	3	AC006624	AC006624	Caenorhab	C 935	33	91.7	110000	8	CR382124_11	CR382124_11	Continuation (12 o
C 864	33	91.7	48084	9	HSBA259P1	AL080273	Human DNA	936	33	91.7	110000	8	CR382127_12	CR382127_12	Continuation (13 o
C 865	33	91.7	48874	6	AR161611	AR161611	Sequence	C 937	33	91.7	110098	8	AP004144	AP004144	Oriza sat
C 866	33	91.7	48974	6	BD080745	BD080745	Preseilli	C 938	33	91.7	110494	8	AP004139	AP004139	Oriza sat
C 867	33	91.7	49974	10	AF007560	AF007560	Mus muscu	C 939	33	91.7	111128	9	AC125421	AC125421	Homo sapi
C 868	33	91.7	56675	2	AC101826	AC101826	Mus muscu	C 940	33	91.7	111183	9	AC008950	AC008950	Homo sapi
C 869	33	91.7	57499	2	AC123371_4	Continuation (5 of	941	33	91.7	112241	8	AP003857	AP003857	Oriza sat	
C 870	33	91.7	58464	2	AC110049	AC110049	Homo sapi	C 942	33	91.7	112404	8	OSJN00288	OSJN00288	Oriza sat
C 871	33	91.7	61635	9	AC110812	AC110812	Homo sapi	C 943	33	91.7	112518	2	AC151142	AC151142	Bos tauru
C 872	33	91.7	65000	8	AP006752	AP006752	Oriza sat	C 944	33	91.7	112928	9	AC105242	AC105242	Homo sapi
C 873	33	91.7	68254	2	AC117408_3	Continuation (4 of	C 945	33	91.7	113326	8	AP003999	AP003999	Oriza sat	
C 874	33	91.7	74049	2	AC135331	AC135331	Homo sapi	946	33	91.7	113415	2	AP004860	AP004860	Oriza sat
C 875	33	91.7	74166	2	AC151820	AC151820	Xenopus t	C 947	33	91.7	114032	9	AC104395	AC104395	Homo sapi
C 876	33	91.7	74319	5	AL139162	AL139162	Human DNA	C 948	33	91.7	114493	2	AC142483	AC142483	Rattus no
C 877	33	91.7	74910	9	AL606722	AL606722	Zebratfish	C 949	33	91.7	114493	2	AC142483	AC142483	Rattus no
C 878	33	91.7	75556	2	AC025993	AC025993	Homo sapi								

954	33	91.7	119535	8	OSJN00016	AL606446	Oryza sat
955	33	91.7	119691	8	AP003743	AP003743	Oryza sat
956	33	91.7	120228	9	AC112514	AC112514	Oryza sat
957	33	91.7	120492	9	AC092580	AC092580	Homo sapi
958	33	91.7	121470	8	AC133608	AC133608	Oryza sat
959	33	91.7	121755	9	AP001181	AP001181	Homo sapi
960	33	91.7	123897	2	AC144684	AC144684	Rattus no
961	33	91.7	124026	8	AP004086	AP004086	Oryza sat
962	33	91.7	124028	8	AP005567	AP005567	Oryza sat
963	33	91.7	124166	8	AC137074	AC137074	Genomic s
964	33	91.7	124489	9	HSDJ760C5	AL078587	Human DNA
965	33	91.7	124920	9	BS000193	BS000193	Pan trogl
966	33	91.7	125380	8	AC145388	AC145388	Oryza sat
967	33	91.7	125829	9	AC127002	AC127002	Homo sapi
968	33	91.7	128229	9	AC087547	AC087547	Oryza sat
969	33	91.7	129539	2	CNS095BM	BS569687	Oryza sat
970	33	91.7	129540	8	CNS08CAW	AL844499	Oryza sat
971	33	91.7	129641	9	AC008560	AC008560	Homo sapi
972	33	91.7	129656	2	AC141351	AC141351	Rattus no
973	33	91.7	129856	9	AC016620	AC016620	Homo sapi
974	33	91.7	130130	2	AC117804	AC117804	Mus muscu
975	33	91.7	130805	2	AC116524	AC116524	Mus muscu
976	33	91.7	130907	8	AP003848	AP003848	Oryza sat
977	33	91.7	130954	8	CNS08CCJ	AL935067	Oryza sat
978	33	91.7	130954	8	CNS08CCJ	AL935067	Oryza sat
979	33	91.7	131689	8	AC010588	AC010588	Homo sapi
980	33	91.7	133085	8	AC137668	AC137668	Medicago
981	33	91.7	133106	8	AP004759	AP004759	Oryza sat
982	33	91.7	133741	10	AL606930	AL606930	Mouse DNA
983	33	91.7	133896	8	AC125496	AC125496	Oryza sat
984	33	91.7	134246	9	AC125617	AC125617	Homo sapi
985	33	91.7	135934	10	AL929095	AL929095	Mouse DNA
986	33	91.7	135940	8	AC137699	AC137699	Genomic s
987	33	91.7	136073	2	AP004773	AP004773	Oryza sat
988	33	91.7	137073	8	AP005843	AP005843	Oryza sat
989	33	91.7	137779	8	AC138111	AC138111	Mus muscu
990	33	91.7	138646	5	BX088562	BX088562	Zebrafish
991	33	91.7	138668	8	AC092749	AC092749	Genomic s
992	33	91.7	138249	8	AC148658	AC148658	Oryza sat
993	33	91.7	139342	14	AF325155	AF325155	Spodopter
994	33	91.7	139953	9	HGBA504H3	AL121585	Human DNA
995	33	91.7	140055	2	AC023003	AC023003	Homo sapi
996	33	91.7	140063	8	AP005314	AP005314	Oryza sat
997	33	91.7	140142	2	AC143959	AC143959	Macaca mu
998	33	91.7	140261	8	AP005490	AP005490	Oryza sat
999	33	91.7	140720	8	AC135792	AC135792	Oryza sat
1000	33	91.7	141041	8	AC087550	AC087550	Oryza sat

  

RESULT 1	AX253333/c	20 bp	DNA	linear	PAT 10-OCT-2001
LOCUS	AX253333	Sequence 39 from Patent WO0170993.			
DEFINITION	AX253333				
ACCESSION	AX253333.1	GI:16073873			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					

  

ORIGIN					
Alignment Scores:	2.81	Length:	20		
Pred. No.:	36.00	Matches:	6		
Score:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-10-029-756-20 (1-6) x AX253333 (1-20)					
Qy	1 PheGlnIleGluHisHis 6				
Db	20 TTCCAGATTCGAGCACCAC 3				
RESULT 2					
AR247897	AR247897	266 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	Sequence 3256 from patent US 6476212.				
DEFINITION	AR247897				
ACCESSION	AR247897				
VERSION	AR247897.1	GI:27295771			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					

  

ORIGIN					
Alignment Scores:	52	Length:	266		
Pred. No.:	36.00	Matches:	6		
Score:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-10-029-756-20 (1-6) x AR247897 (1-266)					
Qy	1 PheGlnIleGluHisHis 6				
Db	78 TTCCAGATTCGAGCACCAC 95				
RESULT 3					
AR246607	AR246607	291 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	Sequence 1966 from patent US 6476212.				
DEFINITION	AR246607				
ACCESSION	AR246607.1	GI:27294481			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					

  

ORIGIN					
Alignment Scores:	57.6	Length:	291		
Pred. No.:	36.00	Matches:	6		
Score:					

Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 100.00%    Indels: 0  
DB: 6    Gaps: 0

US-10-029-756-20 (1-6) x AR246607 (1-291)

QY 1 PheGlnIleGluHisHis 6  
DB 228 TTCCAGATTCGACCCAT 245

RESULT 4  
AR272626/c    AR272626    347 bp    DNA    linear    PAT 10-APR-2003  
LOCUS    Sequence 355 from patent US 6504010.  
DEFINITION    AR272626  
ACCESSION    AR272626  
VERSION    AR272626.1    GI:29704511  
KEYWORDS  
SOURCE    Unknown.  
ORGANISM    Unknown.

REFERENCE    1 (bases 1 to 347)  
AUTHORS    Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,  
Carter, D., Retter, M.W., Mannion, J. and Fan, L.  
TITLE    Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL    Patent: US 6504010-A 355 07-JAN-2003;  
FEATURES    Location/Qualifiers  
source    1..347  
         /organism="unknown"  
         /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 70.2    Length: 347  
Score: 36.00    Matches: 6  
Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 100.00%    Indels: 0  
DB: 6    Gaps: 0

US-10-029-756-20 (1-6) x AR272626 (1-347)

QY 1 PheGlnIleGluHisHis 6  
DB 284 TTCCAGATTCGACCCAT 267

RESULT 5  
AR276207/c    AR276207    347 bp    DNA    linear    PAT 10-APR-2003  
LOCUS    Sequence 355 from patent US 6509448.  
DEFINITION    AR276207  
ACCESSION    AR276207  
VERSION    AR276207.1    GI:29709852  
KEYWORDS  
SOURCE    Unknown.  
ORGANISM    Unknown.

REFERENCE    1 (bases 1 to 347)  
AUTHORS    Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,  
Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.  
TITLE    Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL    Patent: US 6509448-A 355 21-JAN-2003;  
FEATURES    Location/Qualifiers  
source    1..347  
         /organism="unknown"  
         /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 70.2    Length: 347  
Score: 36.00    Matches: 6  
Percent Similarity: 100.00%    Conservative: 0

Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 100.00%    Indels: 0  
DB: 6    Gaps: 0

US-10-029-756-20 (1-6) x AR276207 (1-347)

QY 1 PheGlnIleGluHisHis 6  
DB 284 TTCCAGATTCGACCCAC 267

RESULT 6  
AR406482/c    AR406482    347 bp    DNA    linear    PAT 18-DEC-2003  
LOCUS    Sequence 355 from patent US 6630574.  
DEFINITION    AR406482  
ACCESSION    AR406482  
VERSION    AR406482.1    GI:40156293  
KEYWORDS  
SOURCE    Unknown.  
ORGANISM    Unknown.

REFERENCE    1 (bases 1 to 347)  
AUTHORS    Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,  
Carter, D., Retter, M.W., Mannion, J. and Fan, L.  
TITLE    Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL    Patent: US 6630574-A 355 07-OCT-2003;  
FEATURES    Location/Qualifiers  
source    1..347  
         /organism="unknown"  
         /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 70.2    Length: 347  
Score: 36.00    Matches: 6  
Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 100.00%    Indels: 0  
DB: 6    Gaps: 0

US-10-029-756-20 (1-6) x AR406482 (1-347)

QY 1 PheGlnIleGluHisHis 6  
DB 284 TTCCAGATTCGACCCAC 267

RESULT 7  
AR440332/c    AR440332    347 bp    DNA    linear    PAT 20-FEB-2004  
LOCUS    Sequence 355 from patent US 6667154.  
DEFINITION    AR440332  
ACCESSION    AR440332  
VERSION    AR440332.1    GI:42666492  
KEYWORDS  
SOURCE    Unknown.  
ORGANISM    Unknown.

REFERENCE    1 (bases 1 to 347)  
AUTHORS    Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,  
Carter, D., Retter, M.W., Mannion, J. and Fan, L.  
TITLE    Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL    Patent: US 6667154-A 355 23-DEC-2003;  
FEATURES    Location/Qualifiers  
source    1..347  
         /organism="unknown"  
         /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 70.2    Length: 347  
Score: 36.00    Matches: 6  
Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0

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Query Match:      100.00%      Indels:      0
DB:               6              Gaps:      0

US-10-029-756-20 (1-6) x AR440332 (1-347)

Qy      1 PheGlnIleGluHis 6
Db      284 TTCCAGATCGAGCACCAC 267

RESULT 8
AR472490/c
LOCUS   AR472490          347 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 355 from patent US 6686447.
ACCESSION AR472490
VERSION   AR472490.1 GI:42707819
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 347)
AUTHORS  Wang, T., and Fan, L.
TITLE     Compositions and methods for the therapy and diagnosis of lung
          cancer
JOURNAL   Patent: US 6686447-A 355 03-FEB-2004;
FEATURES  Location/Qualifiers
          source
            1..347
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:      70.2      Length:      347
Score:          36.00     Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:      0

US-10-029-756-20 (1-6) x AR472490 (1-347)

Qy      1 PheGlnIleGluHis 6
Db      284 TTCCAGATCGAGCACCAC 267

RESULT 9
AR543143/c
LOCUS   AR543143          347 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 355 from patent US 6746846.
ACCESSION AR543143
VERSION   AR543143.1 GI:53935819
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 347)
AUTHORS  Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
          Carter, D., Retter, M.W., Mannion, J., and Fan, L.
TITLE     Methods for diagnosing lung cancer
JOURNAL   Patent: US 6746846-A 355 08-JUN-2004;
FEATURES  Location/Qualifiers
          source
            1..347
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:      70.2      Length:      347
Score:          36.00     Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:      0

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US-10-029-756-20 (1-6) x AR543143 (1-347)

Qy      1 PheGlnIleGluHis 6
Db      284 TTCCAGATCGAGCACCAC 267

RESULT 10
AX062728/c
LOCUS   AX062728          347 bp      DNA      linear      PAT 24-JAN-2001
DEFINITION Sequence 355 from Patent WO0100828.
ACCESSION AX062728
VERSION   AX062728.1 GI:12540586
KEYWORDS  .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
          Carter, D., Retter, M.W., and Mannion, J.
TITLE     Compositions and methods for the therapy and diagnosis of lung
          cancer
JOURNAL   Patent: WO 0100828-A 355 04-JAN-2001;
FEATURES  Location/Qualifiers
          source
            1..347
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.:      70.2      Length:      347
Score:          36.00     Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:      0

US-10-029-756-20 (1-6) x AX062728 (1-347)

Qy      1 PheGlnIleGluHis 6
Db      284 TTCCAGATCGAGCACCAC 267

RESULT 11
AX367645/c
LOCUS   AX367645          347 bp      DNA      linear      PAT 16-FEB-2002
DEFINITION Sequence 355 from Patent WO0204514.
ACCESSION AX367645
VERSION   AX367645.1 GI:18855732
KEYWORDS  .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,
          Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S.,
          McNabb, A., Fanger, N., Switzer, A., McNeill, P.D., and Clapper, J.D.
TITLE     Compositions and methods for the therapy and diagnosis of lung
          cancer
JOURNAL   Patent: WO 0204514-A 355 17-JAN-2002;
FEATURES  Location/Qualifiers
          source
            1..347
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.:      70.2      Length:      347

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Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX367645 (1-347)

QY 1 PheGlnIleGluHis 6  
|||||  
Db 284 TTCCAGATCGAGCACCAT 267

RESULT 12  
LOCUS AR484509/c 372 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 1855 from patent US 6703492.  
ACCESSION AR484509  
VERSION AR484509.1 GI:47247612  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 372)  
AUTHORS Kimmerly, W.J.  
TITLE Staphylococcus epidermidis nucleic acids and proteins  
JOURNAL Patent: US 6703492-A 1855 09-MAR-2004;  
FEATURES Location/Qualifiers  
source  
1..372  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 75.9 Length: 372  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR484509 (1-372)

QY 1 PheGlnIleGluHis 6  
|||||  
Db 154 TTCCAAATCGAGCACCAT 137

RESULT 13  
LOCUS AX143133/c 372 bp DNA linear PAT 31-MAY-2001  
DEFINITION Sequence 1855 from Patent WO0134809.  
ACCESSION AX143133  
VERSION AX143133.1 GI:14282438  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Kimmerly, W.J.  
TITLE Staphylococcus epidermidis nucleic acids and proteins  
JOURNAL Patent: WO 0134809-A 1855 17-MAY-2001;  
FEATURES Location/Qualifiers  
source  
1..372  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic nucleic acid sequence"

ORIGIN  
Alignment Scores:  
Pred. No.: 75.9 Length: 372  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX143133 (1-372)

QY 1 PheGlnIleGluHis 6  
|||||  
Db 154 TTCCAAATCGAGCACCAT 137

RESULT 14  
LOCUS AR221976 449 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 38 from patent US 6428990.  
ACCESSION AR221976  
VERSION AR221976.1 GI:23329279  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 449)  
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.  
TITLE Human desaturase gene and uses thereof  
JOURNAL Patent: US 6428990-A 38 06-AUG-2002;  
FEATURES Location/Qualifiers  
source  
1..449  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 93.9 Length: 449  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR221976 (1-449)

QY 1 PheGlnIleGluHis 6  
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Db 248 TTCCAGATTGAGCACCAT 265

RESULT 15  
LOCUS AR221975 473 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 37 from patent US 6428990.  
ACCESSION AR221975  
VERSION AR221975.1 GI:23329278  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 473)  
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.  
TITLE Human desaturase gene and uses thereof  
JOURNAL Patent: US 6428990-A 37 06-AUG-2002;  
FEATURES Location/Qualifiers  
source  
1..473  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 99.6 Length: 473  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR221975 (1-473)

Qy 1 PheGlnIleGluHisHis 6  
 Db 279 TTCAGATTCGAGCACCAT 296

RESULT 16  
 AX840703  
 LOCUS AX840703 480 bp DNA linear PAT 17-DEC-2003  
 DEFINITION Sequence 5 from Patent WO03078639.  
 ACCESSION AX840703  
 VERSION AX840703.1 GI:39978890  
 KEYWORDS Pavlova lutheri  
 SOURCE Pavlova lutheri  
 ORGANISM Pavlova lutheri  
 Eukaryota; Haptophyceae; Pavlovaales; Pavlova.

REFERENCE 1  
 AUTHORS Graham, I.A. and Tonon, T.D.  
 TITLE Transgenic plants expressing enzymes involved in fatty acid biosynthesis  
 JOURNAL Patent: WO 03078639-A 5 25-SEP-2003;  
 THE UNIVERSITY OF YORK (GB)

FEATURES  
 source location/Qualifiers  
 1..480  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:2832"

ORIGIN  
 Alignment Scores: 101 Length: 480  
 Pred. No.: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX840703 (1-480)

Qy 1 PheGlnIleGluHisHis 6  
 Db 55 TTCAGATTCGAGCACCAT 72

RESULT 17  
 BD082632  
 LOCUS BD082632 520 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Methods and compositions for synthesis of long chain poly-unsaturated fatty acids.  
 ACCESSION BD082632  
 VERSION BD082632.1 GI:22628242  
 KEYWORDS JP 2001523091-A/12.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 520)  
 AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Loenard, A.E.Y.  
 TITLE Methods and compositions for synthesis of long chain poly-unsaturated fatty acids  
 JOURNAL Patent: JP 2001523091-A 12 20-NOV-2001;  
 CALGENE LLC, ABBOTT LABORATORIES

COMMENT PN JP 2001523091-A/12  
 PD 20-NOV-2001  
 PF 10-APR-1998 JP 1998544053  
 PR 11-APR-1997 US 08/834655  
 PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,  
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD  
 PC C12N15/53, C12N15/81, C12N5/02, C12N5/10, C12N1/19, C12P7/64 PC  
 C11B1/00, A61K31/20,  
 PC A23L1/30  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
 source location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

source 1..520  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

ORIGIN  
 Alignment Scores: 111 Length: 520  
 Pred. No.: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD082632 (1-520)

Qy 1 PheGlnIleGluHisHis 6  
 Db 273 TTCAGATTCGAGCACCAC 290

RESULT 18  
 BD082647  
 LOCUS BD082647 520 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids.  
 ACCESSION BD082647  
 VERSION BD082647.1 GI:22628257  
 KEYWORDS JP 2001523092-A/7.  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 520)  
 AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Loenard, A.E.Y.  
 TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids  
 JOURNAL Patent: JP 2001523092-A 7 20-NOV-2001;  
 CALGENE LLC, ABBOTT LABORATORIES

COMMENT PN JP 2001523092-A/7  
 PD 20-NOV-2001  
 PF 10-APR-1998 JP 1998544176  
 PR 11-APR-1997 US 08/833610  
 PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,  
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD  
 PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC  
 C30, A23K1/00  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
 source location/Qualifiers  
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 /organism="unidentified"  
 /mol\_type="genomic DNA"  
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ORIGIN  
 Alignment Scores: 111 Length: 520  
 Pred. No.: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD082647 (1-520)

Qy 1 PheGlnIleGluHisHis 6  
 Db 273 TTCAGATTCGAGCACCAC 290

RESULT 19  
 BD092937

LOCUS BD092937 520 bp DNA linear PAT 27-AUG-2002  
DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants.  
ACCESSION BD092937  
VERSION BD092937.1 GI:22638548  
KEYWORDS JP 2001527395-A/24.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 520)  
AUTHORS Knutzen,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.  
TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants  
JOURNAL Patient: JP 2001527395-A 24 25-DEC-2001;  
COMMENT CALGENE LLC,ABBOTT LABORATORIES  
PN JP 2001527395-A/24  
PD 25-DEC-2001  
PR 10-APR-1998 JP 1998544175  
PF 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR  
11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI  
DEBORAH KNUTZEN, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,  
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD  
PC  
C12N15/53,C12N15/82,C12N5/10,C12P7/64,C11B1/00,A61K31/20,A23L1/ PC  
30,A23K1/00  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source  
1..520  
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/db\_xref="taxon:32630"  
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Alignment Scores: 111 Length: 520  
Pred. No.: 36.00 Matches: 6  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 6 Gaps: 0  
DB:  
US-10-029-756-20 (1-6) x BD092937 (1-520)  
Qy 1 PheGlnIleGluHis 6  
Db 273 TTTCAGATCGAGCACCAC 290  
RESULT 20  
BD147335 560 bp DNA linear PAT 17-JAN-2003  
LOCUS BD147335  
DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
ACCESSION BD147335  
VERSION BD147335.1 GI:27853093  
KEYWORDS JP 2002191363-A/2178.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 560)  
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.  
TITLE Primer for synthesizing full-length cDNA and use thereof  
JOURNAL Patient: JP 2002191363-A 2178 09-JUL-2002;  
COMMENT HELIX RESEARCH INSTITUTE  
PN JP 2002191363-A/2178  
PD 09-JUL-2002  
PF 28-JUL-2000 JP 2000280990  
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,  
PI KEIICHI NAGAI,TETSUJI OTSUKI  
PC  
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
10,C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC  
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC  
Primer for synthesizing full-length cDNA and use thereof FH Key  
FT source 1..560  
FT Location/Qualifiers  
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FEATURES  
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1..560  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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Alignment Scores: 120 Length: 560  
Pred. No.: 36.00 Matches: 6  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 6 Gaps: 0  
DB:  
US-10-029-756-20 (1-6) x BD147335 (1-560)  
Qy 1 PheGlnIleGluHis 6  
Db 294 TTCCAGATTGAGCACCAC 311  
RESULT 21  
AX867273 560 bp DNA linear PAT 17-DEC-2003  
LOCUS AX867273  
DEFINITION Sequence 2178 from Patent EP1074617.  
ACCESSION AX867273  
VERSION AX867273.1 GI:40021651  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 560)  
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.  
TITLE Primers for synthesizing full-length cDNA and their use  
JOURNAL Patent: EP 1074617-A 2178 07-FEB-2001;  
COMMENT Research Association for Biotechnology (JP)  
FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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Alignment Scores: 120 Length: 560  
Pred. No.: 36.00 Matches: 6  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 6 Gaps: 0  
DB:  
US-10-029-756-20 (1-6) x AX867273 (1-560)  
Qy 1 PheGlnIleGluHis 6  
Db 294 TTCCAGATTGAGCACCAC 311  
RESULT 22  
AR221955 655 bp DNA linear PAT 26-SEP-2002  
LOCUS AR221955  
DEFINITION Sequence 3 from patent US 6428990.

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ACCESSION AR221955
VERSION AR221955.1 GI:23329258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 655)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 642890-A 3 06-AUG-2002;
FEATURES
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            /mol_type="genomic DNA"
ORIGIN
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Pred. No.: 144 Length: 655
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x AR221955 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 23
BD082635
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082635
VERSION BD082635.1 GI:22628245
KEYWORDS JP 2001523091-A/15.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 655)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
JOURNAL CALGENE LLC ABBOTT LABORATORIES
COMMENT PN JP 2001523091-A/15
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544053
PR 11-APR-1997 US 08/834655
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C11B1/00, A61K31/20,
C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC
CC A23L1/30
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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            /db_xref="taxon:32644"
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Pred. No.: 144 Length: 655
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082635 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 24
BD082650
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082650
VERSION BD082650.1 GI:22628260
KEYWORDS JP 2001523092-A/10.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 655)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
JOURNAL CALGENE LLC ABBOTT LABORATORIES
COMMENT PN JP 2001523092-A/10
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/
C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 144 Length: 655
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082650 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 25
BD092929
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION BD092929
VERSION BD092929.1 GI:22638540
KEYWORDS JP 2001527395-A/16.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 655)

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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082635 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 24
BD082650
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082650
VERSION BD082650.1 GI:22628260
KEYWORDS JP 2001523092-A/10.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 655)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
JOURNAL CALGENE LLC ABBOTT LABORATORIES
COMMENT PN JP 2001523092-A/10
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
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        location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 144 Length: 655
Score: 36.00 Matches: 6
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082650 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 25
BD092929
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION BD092929
VERSION BD092929.1 GI:22638540
KEYWORDS JP 2001527395-A/16.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 655)

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AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.  
 TITLE Methods and compositions for synthesis of long chain  
 JOURNAL polyunsaturated fatty acids in plants  
 COMMENT Patent: JP 2001527395-A 16 25-DEC-2001;  
 CALGENE LLC, ABBOTT LABORATORIES  
 PN JP 2001527395-A/16  
 PD 25-DEC-2001  
 PF 10-APR-1998 JP 1998544175  
 PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR  
 11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI  
 DEBORAH KUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI  
 THURMOND,  
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD  
 PC C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC  
 30, A23K1/00  
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 CC topology: Linear;  
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 /db\_xref="taxon:32630"

ORIGIN  
 Alignment Scores:  
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 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD092929 (1-655)

Qy 1 PheGlnIleGluHis 6  
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 Db 242 TTCCAGATTGACACCAT 259

RESULT 26  
 BD148047  
 LOCUS 739 bp DNA linear PAT 17-JAN-2003  
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD148047  
 VERSION BD148047.1 GI:27853805  
 KEYWORDS JP 2002191363-A/2890.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 739)  
 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,  
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.  
 Primer for synthesizing full-length cDNA and use thereof  
 Patent: JP 2002191363-A 2890 09-JUL-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002191363-A/2890  
 PD 09-JUL-2002  
 PF 28-JUL-2000 JP 2000280990  
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU  
 PI SAITO,  
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
 PI KEIICHI NAGAI, TETSUJI OTSUKI  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
 10, C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
 Primer for synthesizing full-length cDNA and use thereof FH Key  
 Location/Qualifiers  
 1. 739  
 FT source

AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.  
 TITLE Methods and compositions for synthesis of long chain  
 JOURNAL polyunsaturated fatty acids in plants  
 COMMENT Patent: JP 2001527395-A 16 25-DEC-2001;  
 CALGENE LLC, ABBOTT LABORATORIES  
 PN JP 2001527395-A/16  
 PD 25-DEC-2001  
 PF 10-APR-1998 JP 1998544175  
 PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR  
 11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI  
 DEBORAH KUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI  
 THURMOND,  
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD  
 PC C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC  
 30, A23K1/00  
 CC Strandedness: Single;  
 CC topology: Linear;  
 FH Key Location/Qualifiers.  
 FE Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Alignment Scores:  
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 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD148047 (1-739)

Qy 1 PheGlnIleGluHis 6  
 |||||  
 Db 339 TTCCAGATTGACACCCAC 356

RESULT 27  
 AX867985  
 LOCUS 739 bp DNA linear PAT 17-DEC-2003  
 DEFINITION Sequence 2890 from Patent EP1074617.  
 ACCESSION AX867985  
 VERSION AX867985.1 GI:40022848  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,  
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.  
 Primers for synthesizing full-length cDNA and their use  
 Patent: EP 1074617-A 2890 07-FEB-2001;  
 Research Association for Biotechnology (JP)  
 Location/Qualifiers  
 1. 739  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 165 Length: 739  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX867985 (1-739)

Qy 1 PheGlnIleGluHis 6  
 |||||  
 Db 339 TTCCAGATTGACACCCAC 356

RESULT 28  
 CQ780299  
 LOCUS 808 bp DNA linear PAT 17-MAR-2004  
 DEFINITION Sequence 439 from Patent EP1396543.  
 ACCESSION CQ780299  
 VERSION CQ780299.1 GI:45536371  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,

Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H. for synthesizing full length cDNA clones and their use  
Patent: EP 1396543-A 439 10-MAR-2004;  
Research Association for Biotechnology (JP)

FEATURES  
source  
1. .808  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 182 Length: 808  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CQ780299 (1-808)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 706 TTTCAGATTGAGCACCAC 723

RESULT 29  
CQ781966  
LOCUS CQ781966 808 bp DNA linear PAT 17-MAR-2004  
DEFINITION Sequence 2106 from Patent EP1396543.  
ACCESSION CQ781966  
VERSION CQ781966.1 GI:45538022  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
Koga,H.  
TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Patent: EP 1396543-A 2106 10-MAR-2004;  
Research Association for Biotechnology (JP)

FEATURES  
source  
1. .808  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 182 Length: 808  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CQ781966 (1-808)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 706 TTTCAGATTGAGCACCAC 723

RESULT 30  
BD125008  
LOCUS BD125008 808 bp DNA linear PAT 18-SEP-2002  
DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
ACCESSION BD125008  
VERSION BD125008.1 GI:23219953  
KEYWORDS JP 2002017375-A/439.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
Koga,H.  
TITLE Primer for synthesizing full-length cDNA and use thereof  
JOURNAL Patent: JP 2002017375-A 439 22-JAN-2002;  
HELEX RESEARCH INSTITUTE

COMMENT  
OS Homo sapiens (human)  
PN JP 2002017375-A/439  
PD 22-JAN-2002  
PF 07-JUL-2000 JP 2000253172  
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO  
PI ISHII,  
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI  
SHINICHI KOJIMA,  
PI TETSUJI OTSUKI,HISASHI KOGA  
PC  
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
10,  
C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC  
Primer for synthesizing full-length cDNA and use thereof FH Key

FT source 1. .808  
/organism="Homo sapiens (human)".  
FT Location/Qualifiers  
1. .808  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 182 Length: 808  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD125008 (1-808)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 706 TTTCAGATTGAGCACCAC 723

RESULT 31  
BD126675  
LOCUS BD126675 808 bp DNA linear PAT 18-SEP-2002  
DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
ACCESSION BD126675  
VERSION BD126675.1 GI:23221620  
KEYWORDS JP 2002017375-A/2106.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
Koga,H.  
TITLE Primer for synthesizing full-length cDNA and use thereof  
JOURNAL Patent: JP 2002017375-A 2106 22-JAN-2002;  
HELEX RESEARCH INSTITUTE

COMMENT  
OS Homo sapiens (human)  
PN JP 2002017375-A/2106  
PD 22-JAN-2002  
PF 07-JUL-2000 JP 2000253172  
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO  
PI ISHII,  
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI

SHINICHI KOJIMA,  
PI TETSUJI OTSUKI, HISASHI KOGA  
PC  
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
PC, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
Primer for synthesizing full-length cDNA and use thereof FH Key  
Location/Qualifiers  
FT source 1..808  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source  
1..808  
Location/Qualifiers  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN  
Alignment Scores:  
Pred. No.: 182 Length: 808  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-029-756-20 (1-6) x BD126675 (1-808)  
Qy 1 PheGlnIleGluHisHis 6  
Db 706 TTTCAGATTGACACCAT 723  
RESULT 32  
LOCUS AR221961 864 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 12 from patent US 6428990.  
ACCESSION AR221961  
VERSION AR221961.1 GI:23329264  
KEYWORDS  
SOURCE  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 864)  
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.  
TITLE Human desaturase gene and uses thereof  
JOURNAL Patent: US 6428990-A 12 06-AUG-2002;  
FEATURES  
source  
1..864  
Location/Qualifiers  
/organism='unknown'  
/mol\_type='genomic DNA'  
ORIGIN  
Alignment Scores:  
Pred. No.: 196 Length: 864  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-029-756-20 (1-6) x AR221961 (1-864)  
Qy 1 PheGlnIleGluHisHis 6  
Db 670 TTTCAGATTGACACCAT 687  
RESULT 33  
LOCUS AR547128/c 876 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 2259 from patent US 6747137.  
ACCESSION AR547128  
VERSION AR547128.1 GI:53940303  
KEYWORDS  
SOURCE  
Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 876)  
AUTHORS Weinstein, K.G. and Bush, D.  
TITLE Nucleic acid sequences relating to *Candida albicans* for diagnostics and therapeutics  
JOURNAL Patent: US 6747137-A 2259 08-JUN-2004;  
FEATURES  
source  
1..876  
Location/Qualifiers  
/organism='unknown'  
/mol\_type='genomic DNA'  
ORIGIN  
Alignment Scores:  
Pred. No.: 200 Length: 876  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-029-756-20 (1-6) x AR547128 (1-876)  
Qy 1 PheGlnIleGluHisHis 6  
Db 478 TTCCAAATTGAACACCAT 461  
RESULT 34  
LOCUS AF270385 1132 bp DNA linear BCT 01-AUG-2000  
DEFINITION *Staphylococcus epidermidis* strain SRI clone step.4043f09a genomic sequence.  
ACCESSION AF270385  
VERSION AF270385.1 GI:9624299  
KEYWORDS  
SOURCE  
ORGANISM  
*Staphylococcus epidermidis*  
*Staphylococcus epidermidis*  
Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
REFERENCE 1 (bases 1 to 1132)  
AUTHORS Kimmerly, W.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenebee, S., Ashanti, C., Althuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and Furdon, P.J.  
TITLE Transposon-mediated sequencing of the *Staphylococcus epidermidis* genome  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1132)  
AUTHORS Taylor, J. David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenebee, S., Ashanti, C., Althuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and Furdon, P.J.  
TITLE Direct Submission  
JOURNAL Submitted (22-MAY-2000) Departments of Genomic Sciences and Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore Drive, Research Triangle Park, North Carolina 27709-3398, USA  
FEATURES  
source  
1..1132  
Location/Qualifiers  
/organism='Staphylococcus epidermidis'  
/mol\_type='genomic DNA'  
/strain='SRI'  
/db\_xref='taxon:1282'  
/clone='step.4043f09a'  
ORIGIN  
Alignment Scores:  
Pred. No.: 266 Length: 1132  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AF270385 (1-1132)

Qy 1 PheGlnIleGluHisHis 6  
 Db 359 TTTCAATCGAGCACCAC 376

## RESULT 35

AR486339 AR486339 1132 bp DNA linear PAT 14-MAY-2004  
 LOCUS  
 DEFINITION Sequence 4425 from patent US 6703492.  
 ACCESSION AR486339  
 VERSION AR486339.1 GI:47249442  
 KEYWORDS  
 SOURCE Unknown.

## ORGANISM

REFERENCE 1 (bases 1 to 1132)

AUTHORS Kimmerly,W.J.

TITLE Staphylococcus epidermidis nucleic acids and proteins

JOURNAL Patent: US 6703492-A 4425 09-MAY-2004;

## FEATURES

source

1. .1132

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 266 Length: 1132  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR486339 (1-1132)

Qy 1 PheGlnIleGluHisHis 6  
 Db 359 TTTCAATCGAGCACCAC 376

## RESULT 36

AX145703 AX145703 1132 bp DNA linear PAT 31-MAY-2001  
 LOCUS  
 DEFINITION Sequence 4425 from Patent WO0134809.  
 ACCESSION AX145703  
 VERSION AX145703.1 GI:14284268  
 KEYWORDS  
 SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

## REFERENCE

1 Kimmerly,W.J.

AUTHORS Staphylococcus epidermidis nucleic acids and proteins

TITLE Patent: WO 0134809-A 4425 17-MAY-2001;

## JOURNAL

GLAXO GROUP LIMITED (GB)

## FEATURES

source

1. .1132

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="synthetic nucleic acid sequence"

## ORIGIN

## Alignment Scores:

Pred. No.: 266 Length: 1132  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX145703 (1-1132)

Qy 1 PheGlnIleGluHisHis 6  
 Db 359 TTTCAATCGAGCACCAC 376

## RESULT 37

AR410208 AR410208 1320 bp DNA linear PAT 18-DEC-2003  
 LOCUS  
 DEFINITION Sequence 28 from patent US 6635451.  
 ACCESSION AR410208  
 VERSION AR410208.1 GI:40161449  
 KEYWORDS  
 SOURCE Unknown.

## ORGANISM

REFERENCE 1 (bases 1 to 1320)

AUTHORS Mukerji,P., Huang,Y.-S., Das,T., Thurmond,J. and Pereira,S.L.

TITLE Desaturase genes and uses thereof

JOURNAL Patent: US 6635451-A 28 21-OCT-2003;

## FEATURES

source

1. .1320

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 317 Length: 1320  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR410208 (1-1320)

Qy 1 PheGlnIleGluHisHis 6  
 Db 1123 TTTCAATCGAGCACCAC 1140

## RESULT 38

AX467713 AX467713 1320 bp DNA linear PAT 16-JUL-2002  
 LOCUS  
 DEFINITION Sequence 3 from Patent WO0226946.  
 ACCESSION AX467713  
 VERSION AX467713.1 GI:21900886  
 KEYWORDS  
 SOURCE Thraustochytrium sp.

ORGANISM Thraustochytrium sp.

REFERENCE 1

AUTHORS Qiu,X. and Hong,H.

TITLE Fad4, fad5, fad6, and fad6, novel fatty acid desaturase family

JOURNAL Patent: WO 0226946-A 3 04-APR-2002;

Biological Food & Science Corp. (CA)

## FEATURES

source

1. .1320

/organism="Thraustochytrium sp."

/mol\_type="unassigned DNA"

/db\_xref="taxon:145168"

/note="unnamed protein product"

## CDS

1. .1320

/codon\_start=1

/protein\_id="CAD42497.1"

/db\_xref="GI:21900887"

/translation="MGKSGRGAAREMTAEANGDKRKTILIEGLYDATNFKHPGGS

IINPLTRGEAGVDATQAYREFHQRSGKADYKLSPLKLDASKVSRSFSAKEQARRDAM

TRDYAAPREELVAEGYFDPSPHMIYRVVVEIVAFSLFSLMSKASPTSLVLGVVMNG

IAQRCGGMVMEHMGHSFTGVILDDRMCEFFYGVGCGMSGHYKWNKSHKHAAPNRL

EHDVDLNTLFLVAFNERVVRKVPKPSLLALNLRVQAYLFAPVSCLLGLGTLVLRP

YMLTRKHEMFVWIFPIYIGVIFSLMGALGYSFGTSVGMVLCSPGIGCIYIFLPFAVSH

THLFTVNTNPDLHLWLEYAADHTVNISTKSWLVTWMSNLNFQIEHHILFPTAPQRFKE

ISPRVEALFKRHNLPYYDLPTYSVSTTFANLYSVGHSVGADTKKQD"

```
ORIGIN
Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX467713 (1-1320)

Qy 1 PheGlnIleGluHisHis 6
Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 39
AX577003 AX577003 1320 bp DNA linear PAT 08-JAN-2003
LOCUS Sequence 28 from Patent WO02081668.
DEFINITION AX577003
ACCESSION AX577003
VERSION AX577003.1 GI:27646347
KEYWORDS
SOURCE
ORGANISM
Thraustochytrium aureum
Thraustochytrium aureum
Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae;
Thraustochytrium.
REFERENCE
1 Mukerji, P., Huang, Y.S., Das, T., Thurmond, J. and Pereira, S.L.
AUTHORS Desaturase genes and uses thereof
TITLE Patent: WO 02081668-A 28 17-OCT-2002;
JOURNAL Abbott Laboratories (US)
FEATURES
Location/Qualifiers
source
1. 1320
/organism="Thraustochytrium aureum"
/mol_type="unassigned DNA"
/db_xref="taxon:42467"

ORIGIN
Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX577003 (1-1320)

Qy 1 PheGlnIleGluHisHis 6
Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 40
AX951587 AX951587 1320 bp DNA linear PAT 08-JAN-2004
LOCUS Sequence 27 from Patent WO03093482.
DEFINITION AX951587
ACCESSION AX951587
VERSION AX951587.1 GI:40781945
KEYWORDS
SOURCE
ORGANISM
Thraustochytrium
Thraustochytrium
Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae.
REFERENCE
1 Cirpus, P., Renz, A., Lerchl, J. and Kuijpers, A.M.
AUTHORS Method for producing multiple unsaturated fatty acids in plants
TITLE Patent: WO 03093482-A 27 13-NOV-2003;
JOURNAL BASF Plant Science GmbH (DE)
FEATURES
Location/Qualifiers
source
1. 1320
/organism="Thraustochytrium"
/mol_type="unassigned DNA"
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CDS

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/db_xref="taxon:4774"
1. 1320
/note="unnamed protein product; Delta-5-Desaturase"
/codon_start=1
/protein_id="CAF05420.1"
/db_xref="GI:40781946"
/translation="MGKSGRSRARENTAEANGDKRKTILIEGVLYDATNFKHPGGS
IINFLTEGEAGVDATQAYREFHQSGKADKYLSPLKLDASKVSRFSAKQQRDAM
TRDYAAPREELVAEGYFDPISPHMIYRVEIVAFALFALMSKASPTSLVGVVMMG
IAQRCGVVHEMGHSGFTGVIWLDRCCEFFYVGCGMSGHYWKNQSHKHAAPNRL
EHDVDLNTPLVAENRVRKVPKGSLLALWLQVAYLFAVPSCLLIGLWTLVLPFR
YMLTKRHRMEFVWIFARYIGWFSLMGALGYSPGTSVGMVLCFGLGCIYIFLQPAVSH
THLPVTNPEDQLHWLEYAADHTVNISTKSHLVTWMSNLNFQIEHFLPPTAPQRFKE
ISPRVEALFKRHNLPYYDLPTYSVSTTFANLYSVGHSVGADTKKQD"

ORIGIN
Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX951587 (1-1320)

Qy 1 PheGlnIleGluHisHis 6
Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 41
AF489588 AF489588 1320 bp mRNA linear PLN 09-APR-2002
LOCUS Thraustochytrium sp. ATCC21685 delta-5 fatty acid desaturase mRNA,
DEFINITION complete cds.
ACCESSION AF489588
VERSION AF489588.1 GI:20069122
KEYWORDS
SOURCE
ORGANISM
Thraustochytrium sp. ATCC21685
Thraustochytrium sp. ATCC21685
Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae;
Thraustochytrium.
REFERENCE
1 (bases 1 to 1320)
AUTHORS Qiu, X., Hong, H. and MacKenzie, S.L.
TITLE Identification of a Delta 4 fatty acid desaturase from
Thraustochytrium sp. involved in the biosynthesis of docosaenoic
acid by heterologous expression in Saccharomyces cerevisiae and
Brassica juncea
JOURNAL J. Biol. Chem. 276 (34), 31561-31566 (2001)
MEDLINE 21402888
PUBMED 11397798
REFERENCE
2 (bases 1 to 1320)
AUTHORS Qiu, X., Hong, H. and MacKenzie, S.L.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2002) Research & Development, Bioriginal Food &
Science Corporation, 102 Melville Street, Saskatoon, SK S7J 0R1,
Canada
FEATURES
Location/Qualifiers
source
1. 1320
/organism="Thraustochytrium sp. ATCC21685"
/mol_type="mRNA"
/strain="ATCC 21685"
/db_xref="ATCC:21685"
/db_xref="taxon:191040"
1. 1320
/note="FAD5"
/codon_start=1
/product="delta-5 fatty acid desaturase"
/protein_id="AA009687.1"
/db_xref="GI:20069123"
/translation="MGKSGRSRARENTAEANGDKRKTILIEGVLYDATNFKHPGGS
IINFLTEGEAGVDATQAYREFHQSGKADKYLSPLKLDASKVSRFSAKQQRDAM
TRDYAAPREELVAEGYFDPISPHMIYRVEIVAFALFALMSKASPTSLVGVVMMG
IAQRCGVVHEMGHSGFTGVIWLDRCCEFFYVGCGMSGHYWKNQSHKHAAPNRL
EHDVDLNTPLVAENRVRKVPKGSLLALWLQVAYLFAVPSCLLIGLWTLVLPFR
YMLTKRHRMEFVWIFARYIGWFSLMGALGYSPGTSVGMVLCFGLGCIYIFLQPAVSH
THLPVTNPEDQLHWLEYAADHTVNISTKSHLVTWMSNLNFQIEHFLPPTAPQRFKE
ISPRVEALFKRHNLPYYDLPTYSVSTTFANLYSVGHSVGADTKKQD"

CDS
```

IAQRCGWMHEMGHSFTGVIWLDRCMCEFFYGVGCMGSHYWNQKSHKHAAPNRL  
EHDVLDNTPLVAVNERVRKVPQSLALWLRVOAYLPAVPSCLLGLGWTLVLRH  
YMLRTKRMEDFWIIPAXYIGWFSLMGALGYSFGTSGMYLCSFGLGCIYIFLOPAVSH  
THLPVTNPEDQLHLEAYADHTVNISTKSMLVTTWNSNLNFQIEHHLLFFTAPQPRFKE  
ISPRVEALFKRHNLFPYDLPYTSVSTTFANLYSVGHSVGADTKQD"

ORIGIN

Alignment Scores:  
Pred. No.: 317 Length: 1320  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8 Indels: 0  
DB: Gaps: 0

US-10-029-756-20 (1-6) x AF489588 (1-1320)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1123 TTTCAGATCGAGACCAC 1140

RESULT 42  
AX577009  
LOCUS AX577009 1329 bp DNA linear PAT 08-JAN-2003  
DEFINITION Sequence 34 from Patent WO02081668.  
ACCESSION AX577009  
VERSION AX577009.1 GI:27646350  
KEYWORDS Isochrysis galbana  
SOURCE Isochrysis galbana  
ORGANISM Isochrysis galbana  
Eukaryota; Haptophyceae; Isochrysidales; Isochrysis.

REFERENCE 1  
AUTHORS Mukerji, P., Huang, Y.S., Dae, T., Thurmond, J. and Pereira, S.L.  
TITLE Desaturase genes and uses thereof  
JOURNAL Patent: WO 02081668-A 34 17-OCT-2002;  
Abbott Laboratories (US)

FEATURES  
source  
1..1329  
/organism="Isochrysis galbana"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:37099"

ORIGIN

Alignment Scores:  
Pred. No.: 319 Length: 1329  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6 Indels: 0  
DB: Gaps: 0

US-10-029-756-20 (1-6) x AX577009 (1-1329)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1132 TTTCAGATCGAGACCAC 1149

RESULT 43  
CQ729637  
LOCUS CQ729637 1335 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 15571 from Patent WO02068579.  
ACCESSION CQ729637  
VERSION CQ729637.1 GI:42301265  
KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
human exons or transcripts, for detecting expression and other uses  
thereof

JOURNAL Patent: WO 02068579-A 15571 06-SEP-2002;

PE Corporation (NY) (US)  
FEATURES  
source  
1..1335  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 321 Length: 1335  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6 Indels: 0  
DB: Gaps: 0

US-10-029-756-20 (1-6) x CQ729637 (1-1335)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1141 TTCCAGATTGAGCACCAT 1158

RESULT 44  
AR221953  
LOCUS AR221953 1335 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 1 from patent US 6428990.  
ACCESSION AR221953  
VERSION AR221953.1 GI:23329256  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1335)  
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.  
TITLE Human desaturase gene and uses thereof  
JOURNAL Patent: US 6428990-A 1 06-AUG-2002;  
FEATURES  
source  
1..1335  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 321 Length: 1335  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6 Indels: 0  
DB: Gaps: 0

US-10-029-756-20 (1-6) x AR221953 (1-1335)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1141 TTCCAGATTGAGCACCAT 1158

RESULT 45  
AX253297  
LOCUS AX253297 1335 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 3 from Patent WO0170993.  
ACCESSION AX253297  
VERSION AX253297.1 GI:16073841  
KEYWORDS Rattus sp.

SOURCE Rattus sp.  
ORGANISM Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1  
AUTHORS Winther, M.D., Smith, H.L., Allen, S.J., Ponton, A. and de Antueno, R.J.  
TITLE Polynucleotides that control delta-6-desaturase genes and methods  
for identifying compounds for modulating delta-6-desaturase

```

JOURNAL Patent: WO 0170993-A 3 27-SEP-2001;
AUTHORS Scotia Holdings plc (GB)
FEATURES Location/Qualifiers
source 1..1335
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"

ORIGIN
Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX253297 (1-1335)

Qy 1 PheGlnIleGluHis 6
Db 1141 TTCAGATTGAGCACCAC 1158

RESULT 46
AX253298 AX253298 1335 bp DNA linear PAT 10-OCT-2001
LOCUS Sequence 4 from Patent WO0170993.
DEFINITION AX253298
ACCESSION AX253298
VERSION AX253298.1 GI:16073842
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Winther,M.D., Smith,H.L., Allen,S.J., Ponton,A. and de Antueno,R.J.
TITLE Polynucleotides that control delta-6-desaturase genes and methods
for identifying compounds for modulating delta-6-desaturase
JOURNAL Patent: WO 0170993-A 4 27-SEP-2001;
AUTHORS Scotia Holdings plc (GB)
FEATURES Location/Qualifiers
source 1..1335
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX253298 (1-1335)

Qy 1 PheGlnIleGluHis 6
Db 1141 TTCAGATTGAGCACCAC 1158

RESULT 47
BD091695 BD091695 1335 bp DNA linear PAT 27-AUG-2002
LOCUS Process for producing lipid and microorganism secreting lipid.
DEFINITION BD091695
ACCESSION BD091695
VERSION BD091695.1 GI:22637306
KEYWORDS WO 0175069-A/1.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

```

REFERENCE 1 (bases 1 to 1335)
AUTHORS Suzuki,O., Ono,K., Aki,T., Shimauchi,T., Nakajima,T. and Kondo,A.
TITLE Process for producing lipid and microorganism secreting lipid
JOURNAL Patent: WO 0175069-A 1 11-OCT-2001;
IDEMITSU PETROCHEMICAL CO LTD.OSAMU SUZUKI,KAZUHIISA ONO, TSUNEHIRO
AKI, TOSHITSUGU SHIMAUCHI,TOSHIAKI NAKAJIMA,AKIHIRO KONDO
COMMENT AKI, Rattus norvegicus (rat)
PN WO 0175069-A/1
PD 11-OCT-2001
PF 31-MAR-2000 WO 2000JP002129
PI OSAMU SUZUKI,KAZUHIISA ONO, TSUNEHIRO AKI,TOSHITSUGU SHIMAUCHI,
PI TOSHIAKI NAKAJIMA,AKIHIRO KONDO
PC C12N1/19,C12N15/53,C12P7/64//C12N1/19,C12R1.865), (C12P7/64,
PC C12R1.865)
CC
FH Key Location/Qualifiers
FT CDS (1)..(1332).
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"

ORIGIN
Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD091695 (1-1335)

Qy 1 PheGlnIleGluHis 6
Db 1141 TTCAGATTGAGCACCAC 1158

RESULT 48
AF199596 AF199596 1335 bp mRNA linear PRI 21-JUN-2000
LOCUS Homo sapiens delta-5 desaturase mRNA, complete cds.
DEFINITION Homo sapiens delta-5 desaturase mRNA, complete cds.
ACCESSION AF199596
VERSION AF199596.1 GI:6842049
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Cho,H.P., Nakamura,M. and Clarke,S.D.
TITLE Cloning, expression, and fatty acid regulation of the human delta-5
desaturase
JOURNAL J. Biol. Chem. 274 (52), 37335-37339 (1999)
MEDLINE 20069725
PUBMED 10601301
REFERENCE 2 (bases 1 to 1335)
AUTHORS Cho,H.P. and Clarke,S.D.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Nutritional Sciences, University of Texas
at Austin, PAI 5.30, Austin, TX 78751, USA
FEATURES Location/Qualifiers
source 1..1335
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q12.2-q13"
1..1335
/codon_start=1
/product="delta-5 desaturase"
/protein_id="AAF29378.1"
/db_xref="GI:6842050"

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/translation="MADPVAETAAGQTPRYFTWDEVAQRSCCEERWLVIDRKVN  
ISETRRHGGSRVISHVAGQATDPFVAHINKGLVKYKNSLLIGELSPQSPFP  
TKNKLTDFPRELRATVERGMKANHVFLLYLHLLDGAALWLTWVGTSFLPF  
LLCAVLASVAQAQAGLQHDGCHLSVFSTSKWHLHHFVIGHLKGAPASWNNHMFQ  
LHAKPNCFRKDPDINMHPFFPALGKILSVELGCKKKNYPYNHOKKYPFLIGPPALLP  
LYFQWYIFYFYVQIRKKWVDLAWMITFYVRFLLTVPLGLKAFGLGFLFVRFLESNMF  
VWVQNMHHPMHIHIDHRMDWVSTQLATCNVHKSAPFNDWFSGLHNFQIBHLPPTMP  
RHNHYKVAPLVQSLCAKHGIEYQSKPLLSAFADIHLSKESGQLWLDAYLHQ"

## ORIGIN

Alignment Scores:  
Pred. No.: 321 Length: 1335  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x AF199596 (1-1335)

Qy 1 PheGlnIleGluHisHis 6

Db 1141 TTCAGATTGACCAT 1158

## RESULT 49

AF226273 1335 bp mRNA linear PRI 17-MAY-2000  
LOCUS Homo sapiens delta-5 fatty acid desaturase (FADS5) mRNA, complete cds.

ACCESSION AF226273

VERSION AF226273.1 GI:7861969

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 1335)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Leonard, A.E., Kelder, B., Bobik, E.G., Chuang, L.T.,  
Parker-Barnes, J.M., Thurmond, J.M., Kroeger, P.E., Kopchick, J.J.,  
Huang, Y.-S. and Mukerji, P.  
cDNA cloning and characterization of human Delta5-desaturase  
involved in the biosynthesis of arachidonic acid  
Biochem. J. 347 Pt 3, 719-724 (2000)

## JOURNAL

20233676

10769175

## REFERENCE

2 (bases 1 to 1335)  
Leonard, A.E., Kelder, B., Bobik, E.G., Chuang, L.-T.,  
Parker-Barnes, J.M., Thurmond, J.M., Kroeger, P.E., Kopchick, J.J.,  
Huang, Y.-S. and Mukerji, P.  
Direct Submission

Submitted (18-JAN-2000) Strategic Discovery Research, RPD of Abbott  
Laboratories, 3300 Steiner Rd., Columbus, OH 43219, USA

## FEATURES

source

1. .1335

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/map="between FEN1 and FTH1"

1. .1335

/gene="FADS5"

1. .1335

/gene="FADS5"

/note="involved in arachidonic acid biosynthesis"

/codon\_start=1

/product="delta-5 fatty acid desaturase"

/protein\_id="AAF70457.1"

/db\_xref="GI:7861970"

/translation="MADPVAETAAGQTPRYFTWDEVAQRSCCEERWLVIDRKVN  
ISETRRHGGSRVISHVAGQATDPFVAHINKGLVKYKNSLLIGELSPQSPFP  
TKNKLTDFPRELRATVERGMKANHVFLLYLHLLDGAALWLTWVGTSFLPF  
LLCAVLASVAQAQAGLQHDGCHLSVFSTSKWHLHHFVIGHLKGAPASWNNHMFQ  
LHAKPNCFRKDPDINMHPFFPALGKILSVELGCKKKNYPYNHOKKYPFLIGPPALLP

LYFQWYIFYFYVQIRKKWVDLAWMITFYVRFLLTVPLGLKAFGLGFLFVRFLESNMF  
VWVQNMHHPMHIHIDHRMDWVSTQLATCNVHKSAPFNDWFSGLHNFQIBHLPPTMP  
RHNHYKVAPLVQSLCAKHGIEYQSKPLLSAFADIHLSKESGQLWLDAYLHQ"

## ORIGIN

Alignment Scores:  
Pred. No.: 321 Length: 1335  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x AF226273 (1-1335)

Qy 1 PheGlnIleGluHisHis 6

Db 1141 TTCAGATTGACCAT 1158

## RESULT 50

AX577005 1338 bp DNA linear PAT 08-JAN-2003  
LOCUS AX577005  
DEFINITION Sequence 30 from Patent WO02081668.  
ACCESSION AX577005

VERSION AX577005.1 GI:27646348

KEYWORDS

SOURCE

ORGANISM

Thraustochytrium aureum

Thraustochytrium aureum

Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae;

Thraustochytrium.

## REFERENCE

1

AUTHORS

TITLE

JOURNAL

Desaturase genes and uses thereof

Patent: WO 02081668-A 30 17-OCT-2002;

Abbott Laboratories (US)

FEATURES

source

1. .1338

/organism="Thraustochytrium aureum"

/mol\_type="unassigned DNA"

/db\_xref="taxon:42467"

## ORIGIN

Alignment Scores:  
Pred. No.: 322 Length: 1338  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX577005 (1-1338)

Qy 1 PheGlnIleGluHisHis 6

Db 1135 TTCAGATCGACCAT 1152

## RESULT 51

AF536525 1341 bp mRNA linear PLN 18-NOV-2003  
LOCUS AF536525  
DEFINITION Anemone leveillei delta-6-fatty acid desaturase mRNA, complete cds.  
ACCESSION AF536525

VERSION AF536525.1 GI:33330960

KEYWORDS

SOURCE

ORGANISM

Anemone leveillei

Anemone leveillei

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;

Ranunculaceae; Anemone.

1 (bases 1 to 1341)

Whitney, H.M., Michaelson, L.V., Sayanova, O., Pickett, J.A. and

Napier, J.A.

TITLE

Functional characterisation of two cytochrome b5-fusion desaturases

from Anemone leveillei: the unexpected identification of a fatty



```

JOURNAL      acid delta6-desaturase
MEDLINE      Planta 217 (6), 983-992 (2003)
PUBMED       22882798
REFERENCE    2 (bases 1 to 1341)
AUTHORS      Whitney, H.M., Pickett, J.A., Sayanova, O. and Napier, J.A.
TITLE        Direct Submission
JOURNAL      Submitted (08-AUG-2002) Crop Performance & Improvement, Long Ashton
              Research Station, Long Ashton, Bristol BS41 9AP, UK
              Location/Qualifiers
FEATURES     source
              1..1341
              /organism="Anemone leveillei"
              /mol_type="mRNA"
              /db_xref="taxon:212809"
              1..1341
              /note="All; cytochrome b5 fusion desaturase"
              /codon_start=1
              /product="delta-6-fatty acid desaturase"
              /protein_id="AAQ10731.1"
              /db_xref="GI:33330961"
              /translation="MAEKRRISDDLSRHNKPGDWISIQKIYDVTEWGHKHPGGE
              GPLNLAQDVTDAFVAHPGSAWKNLDFHIGLYQDVSDVSKDYKLVSEFSKAG
              LVEKKGHGLRLVMSLVFTASVGVLSKTSVHVGSAVLAVIWMQFGFIGHDSG
              HYNIMTSELNMQIFSNVYVSGVSCWKKRYNAHIAVNSLEYDPLQVYPLVY
              STALPDSLTSFYRKMTFDVARFLVSFQHWTFYPLMAIGKVSFLAQSILVLSKPP
              LPDRHLEFGLVFWAMVYSLTISCLPNWVERVIFIANVAVTGHQVFCILNHSYQV
              YIGAPCANDWEKOTKGISDISCPWDFHGLQFQIEHHLFPMRPRCNLKISPFV
              KELCKRNLVTVTSVFFEGNRRLTLAKNALKARDLTSPIPKNLVMEAVHTG"

ORIGIN
Alignment Scores:
Pred. No.:      323      Length:      1341
Score:          36.00    Matches:      6
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match:    100.00%    Indels:      0
DB:             8        Gaps:        0

US-10-029-756-20 (1-6) x AFS36525 (1-1341)

Qy      1 PheGlnIleGluHis 6
      |||||
Db      1108 TTTCAGATTGAGCATCAT 1125

RESULT 52
LOCUS     AY131238      1347 bp      mRNA      linear      PLN 17-AUG-2002
DEFINITION Argania spinosa delta-6-desaturase mRNA, complete cds.
ACCESSION AY131238
VERSION   AY131238.1  GI:22296825
KEYWORDS  Argania spinosa
SOURCE    Argania spinosa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Sapotaceae; Argania.
REFERENCE 1 (bases 1 to 1347)
AUTHORS   El Filali, A., Anderson, M. and Abbas, K.
TITLE     Characterization and cloning of delta-6-desaturase in Argania
              spinosa fruit
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1347)
AUTHORS   El Filali, A., Anderson, M. and Abbas, K.
TITLE     Direct Submission
JOURNAL   Submitted (12-JUN-2002) Biologie Moleculaire, Faculte des Sciences,
              Ibn Batouta, Rabat, Rabat 1014, Morocco
              Location/Qualifiers
FEATURES     source
              1..1347
              /organism="Argania spinosa"
              /mol_type="mRNA"
              /db_xref="taxon:85884"
              1..1347
              /codon_start=1

CDS

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/product="delta-6-desaturase"
/protein_id="AAM94345.1"
/db_xref="GI:22296826"
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SPPLKSLAGQVTDADFVAFHPTASTWKNLDFKFTGYLKYDYSVSESKYSLVPEFSK
MGLYDKAGHIMFATLCFTAMLFAMSVGVLCRCEGLVHLFSGCLMGFLWIOSGMWIGH
PGHYVVSDELNLKPMGIFPANCLSGISIGSKWNAHIAHIAVNSLEYDPLQVYPLFL
VVSXKFGSLTSHFYERKLTIDSLSRFPVSKQHWTFYTIMCAARLNMYVQSILMLTK
RNVSYRAHELGLCLVFSIWIYPLVSLPNWGERIMFVIAISVGTGMQVQFSLNHFSS
SVYVKGPNGNWTFETDGTLDISCPPMMDWFHGLQFQIEHHLFPMRPRCNLRTISP
YVIELCKKHNLPLYNVASFSKANEMTLRLNTALQARDITKPLPKNLVMEALHTHG"

ORIGIN
Alignment Scores:
Pred. No.:      324      Length:      1347
Score:          36.00    Matches:      6
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match:    100.00%    Indels:      0
DB:             8        Gaps:        0

US-10-029-756-20 (1-6) x AY131238 (1-1347)

Qy      1 PheGlnIleGluHis 6
      |||||
Db      1114 TTCCAAATTGAGCATCAT 1131

RESULT 53
LOCUS     HSA325501/c  1347 bp      DNA      linear      PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding Not1 site, clone
              NB6-702R.
ACCESSION AJ325501
VERSION   AJ325501.1  GI:15869895
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1347)
AUTHORS   Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
              Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
              Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
              Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
              Not1 flanking sequences: a tool for gene discovery and verification
              of the human genome
TITLE     Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL   Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE   22131767
PUBMED    12136098
REFERENCE 2 (bases 1 to 1347)
AUTHORS   Zabarovsky, E.R.
TITLE     Direct Submission
JOURNAL   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
              Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
              Sweden
              Location/Qualifiers
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Best Local Similarity: 100.00%    Mismatches: 0
Query Match:    100.00%    Indels:      0
DB:             9        Gaps:        0

US-10-029-756-20 (1-6) x HSA325501 (1-1347)

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AUTHORS Legrand,P.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JUL-2002) Legrand P., Sciences Animales, Laboratoire  
 de Biochimie ENSAR-INRA, 65, Rue de Saint-Brieuc, 35000 Rennes,  
 France

FEATURES  
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 /db\_xref="taxon:10116"  
 /tissue\_type="liver"  
 /clone\_lib="marathon-ready cdna"  
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 /db\_xref="GI:21742819"  
 /db\_xref="GOA:Q8K1P9"  
 /db\_xref="UniProt/TREMBL:Q8K1P9"  
 /translation="MGVGEGGGPGPGPGAPLPIFRWQIRQHDLPQDKWL  
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 GPGWSSVLAALILAIISOACWCICLQHDIGHASIPKSRWNHVAQFVNGQLKFSAHW  
 WNFRRHQHAKPNIFHKDPDVTVPVLLGSSVEYKCKERYLPYNHQLXFLYLG  
 PLLTLVFEVENLAYMLVCMQWTLDLAAASFYSFFLSPYFGATGTLFLFVAVRL  
 ESHFWVTQNNHPIKPIGHEKRDWASSQAATCNVPSLFDIMFSGHLNFQIEHHL  
 PPTMPRHRYRVAFLVKAFCARHGLHYEVKPLTALVDIIGSLKKSGDIWLDAIYHQ"

ORIGIN  
 Alignment Scores: 350 Length: 1442  
 Pred. No.: 36.00 Matches: 6  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 10

US-10-029-756-20 (1-6) x RN0494720 (1-1442)

Oy 1 PheGlnIleGluHisHis 6  
 Db 1244 TTCAGATTGACACCAC 1261

RESULT 57  
 BD195601 1478 bp DNA linear PAT 17-JUL-2003  
 LOCUS 70 human secreted proteins.  
 DEFINITION  
 ACCESSION BD195601  
 VERSION BD195601.1 GI:33005371  
 KEYWORDS JP 2002519990-A/62.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 REFERENCE 1 (bases 1 to 1478)  
 AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,  
 Bednarek,D.P., Endress,G.A., Yu,G.L., N.J., Feng,P., Young,P.E.,  
 Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A.,  
 Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,  
 Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.  
 70 human secreted proteins  
 Patent: JP 2002519990-A 62 02-JUL-2002;  
 HUMAN GENOME SCIENCES INC  
 COMMENT OS Unidentified  
 PN JP 2002519990-A/62  
 PD 02-JUL-2002  
 PF 06-MAR-1998 JP 1998538875  
 PR 07-MAR-1997 US 60/040162,07-MAR-1997 US 60/040333 PR  
 07-MAR-1997 US 60/038621,07-MAR-1997 US 60/040161 PR

07-MAR-1997 US 60/040626,07-MAR-1997 US 60/040334 PR  
 07-MAR-1997 US 60/040336,07-MAR-1997 US 60/040163 PR  
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 23-MAY-1997 US 60/047587,23-MAY-1997 US 60/047492 PR  
 23-MAY-1997 US 60/047598,23-MAY-1997 US 60/047613 PR  
 23-MAY-1997 US 60/047582,23-MAY-1997 US 60/047596 PR  
 23-MAY-1997 US 60/047612,23-MAY-1997 US 60/047632 PR  
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 22-AUG-1997 US 60/056662,22-AUG-1997 US 60/056872 PR  
 22-AUG-1997 US 60/056882,22-AUG-1997 US 60/056637 PR  
 22-AUG-1997 US 60/056903,22-AUG-1997 US 60/056880 PR  
 22-AUG-1997 US 60/056879,22-AUG-1997 US 60/056911 PR  
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 22-AUG-1997 US 60/056892,22-AUG-1997 US 60/056632 PR  
 22-AUG-1997 US 60/056664,22-AUG-1997 US 60/056876 PR  
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 22-AUG-1997 US 60/056875,22-AUG-1997 US 60/056862 PR  
 22-AUG-1997 US 60/056887,22-AUG-1997 US 60/056908 PR  
 22-AUG-1997 US 60/056884,05-SEP-1997 US 60/057761 PR  
 05-SEP-1997 US 60/057650  
 PI STEVEN M RUBEN,CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET,  
 PI KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY  
 A ENDRESS,GUO LIANG  
 PI YU,JIAN NI,  
 PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN  
 M FERRIE,ROXANNE DUAN,  
 PI JING SHAN HU,KIMBERLY A FLORENCE,HENRIK  
 S OLSEN,REINHARDT EBNER,  
 PI LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR PI  
 ,YI LI,ZHIZHEN ZENG,  
 PI HLA KYAW  
 PC C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/69, PC  
 GO1N33/50,  
 PC GO1N33/53,GO1N33/68,A61K38/17  
 CC Strandedness: Double;  
 CC Topology: Linear;  
 CC 70 human secreted proteins  
 FH Key Location/Qualifiers  
 FT source 1..1478  
 FT /organism='Unidentified'.  
 FEATURES  
 source Location/Qualifiers  
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-029-756-20 (1-6) x BD195601 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCCAGATCGAGCACCAC 964

RESULT 58
LOCUS CQ775646 1478 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 63 from Patent EP1394252.
ACCESSION CQ775646
VERSION CQ775646.1 GI:45379034
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Olsen,H.S., Yu,G.L., Endress,G.A., Bednarik,D.P., Carter,K.C.,
Feng,P., Soppet,D.R., Young,P.E., Duan,D.R., Florence,K.A.,
Greene,J.M., Fischer,C.L., Hu,J.S., Ruben,S.M., Ebner,R.,
Brewer,L.A., Ferrie,A.M., Moore,P.A., Ni,J., Shi,Y., Lafleur,D.W.,
Li,Y., Zeng,Z., Kyaw,H. and Rosen,C.A.
70 human secreted proteins
TITLE Patent: EP 1394252-A 63 03-MAR-2004;
JOURNAL HUMAN GENOME SCIENCES, INC. (US)
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x CQ775646 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCCAGATCGAGCACCAC 964

RESULT 59
LOCUS AR352656 1478 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6590075.
ACCESSION AR352656
VERSION AR352656.1 GI:33757914
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1478)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
Olsen,H.S., Ebner,R., Brewer,L.A. and Shi,Y.
Secreted protein H0A250
TITLE Patent: US 6590075-A 63 08-JUL-2003;
JOURNAL Location/Qualifiers
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source
1. .1478
/organism="unknown"

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ORIGIN
/mol_type="genomic DNA"

Alignment Scores: 360 Length: 1478
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x AR352656 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCCAGATCGAGCACCAC 964

RESULT 60
LOCUS AB074149 1498 bp mRNA linear VRT 13-NOV-2001
DEFINITION Oncorhynchus masou mRNA for putative delata 6-desaturase, complete
cde.
ACCESSION AB074149
VERSION AB074149.1 GI:16904664
KEYWORDS
SOURCE Oncorhynchus masou (cherry salmon)
ORGANISM Oncorhynchus masou
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1
AUTHORS Sirisunay,S., Yoshizaki,G., Kiron,V., Takeuchi,T. and Gen,K.
TITLE delta6-desaturase-like cDNA in masou salmon form2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1498)
AUTHORS Sirisunay,S., Yoshizaki,G., Kiron,V., Takeuchi,T. and Gen,K.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2001) Soranuth Sirisunay, Tokyo University of
Fisheries, Aquatic Bioscience; 4-5-7 Konan, Minato-ku, Tokyo
108-8477, Japan (E-mail:soranuth@yahoo.com, Tel:81-3-5463-0555,
Fax:81-3-5463-0553)
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IGPLLIVFENIQLFETMFSQRDWDLAWMTFLRFCCYYPFGFGFSGVALISFV
RFLSHWFVVTQMSHLPMDMHERHQDWLTQMLSATCNIEQSTFNDFWFSGLHNFQIE
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HK"

ORIGIN
Alignment Scores: 365 Length: 1498
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 5

US-10-029-756-20 (1-6) x AB074149 (1-1498)

Qy 1 PheGlnIleGluHisHis 6

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Db 1243 TTTCCAGATTGACACCAT 1260
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RESULT 61
AF126798 1508 bp mRNA linear ROD 21-JUN-2000
LOCUS Mus musculus delta-6 fatty acid desaturase mRNA, complete cds.
DEFINITION AF126798
ACCESSION AF126798
VERSION AF126798.1 GI:4406525
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1508)
AUTHORS Cho, H.P., Nakamura, M.T. and Clarke, S.D.
TITLE Delta-6 desaturase
JOURNAL J. Biol. Chem. 274 (1), 471-477 (1999)
MEDLINE 99085046
PUBMED 9867867
REFERENCE 2 (bases 1 to 1508)
AUTHORS Cho, H.P., Nakamura, M.T. and Clarke, S.D.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-1999) Nutritional Sciences, University of Texas
at Austin, Painter 5.30 (A2700), Austin, TX 78712, USA
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/note="D6D"
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/db_xref="GI:4406526"
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TLTAVFLATSOAQGMWLQHDYCHLSYVYKYSIWNHVKFVYGHKLGASANWNRHHP
QHAKPNIIFHKDPPDKLSLVFVLGWEQPLRYKKKLYLPYLNHQHVEFPLIGPPLIP
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VWVTQMHLVMEIDLDHYDRDWFSSQLAATCNVEQSFNDWFSGHLNFOIEHHLFPPTMP
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Pred. No.: 368 Length: 1508
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-029-756-20 (1-6) x AF126798 (1-1508)
Qy 1 PheGlnIleGluHis 6
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Db 1215 TTCCAGATTGACACCAT 1232
|||||
RESULT 62
BC055950 1539 bp mRNA linear ROD 04-NOV-2003
LOCUS Mus musculus fatty acid desaturase 3, mRNA (cdna clone
DEFINITION IMAGE:4208582), partial cds.
ACCESSION BC055950
VERSION BC055950.1 GI:33585850
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1539)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Sheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huly, S.M.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smallos, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1539)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.sbgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 120 Row: k Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208582"
/tissue_type="Colon, normal. 5 month old male mouse."
/clone_lib="NCI CGAP_C024"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/protein_id="AAH5950.1"
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/db_xref="LocusID:60527"
/db_xref="MGI:1928740"
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CDS
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FVMQQLGFSAGWFRFHQHHKPNIFHKDPDVTVPVLLGESSVEYGGKKRRYLP
YNHQHLFFLIGPPLLTLVNFEVENLAYMLVCMQWTDLLWAASFYRFFLSYSPFYGA
TGTLFVAVRVLESHWFVMTQNMHFKETGHEKRDWASSQLAATCNVPSLFDWM
PSGHLNFQIEHHLFPTPRHNRVAVPLVAKFCAKHGLHYEVKPFALTVDIIIGSLKK
SGDIWLDAYLHQ"
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misc\_feature

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/gene="Fads3"
/note="Heme 1; Region: Heme/Steroid binding domain. This
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of proteins. This family also includes proteins that bind
to steroids. The family includes progesterone receptors.
Many members of this subfamily are membrane anchored by an
N-terminal transmembrane alpha helix. This family also
includes a domain in some chitin synthases. There is no
known ligand for this domain in the chitin synthases"
/db_xref="CDD:pfam00173"
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misc\_feature

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/db_xref="CDD:pfam00487"
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## ORIGIN

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Pred. No.: 377 Length: 1539
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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US-10-029-756-20 (1-6) x BC055950 (1-1539)

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Qy 1 PheGlnIleGluHis 6
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Db 1021 TTCAGATTGACACCAC 1038
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## RESULT 63

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AB021980
LOCUS AB021980.1 1546 bp mRNA linear ROD 09-APR-1999
DEFINITION Rattus norvegicus mRNA for delta-6 fatty acid desaturase, complete
cDS.
ACCESSION AB021980
VERSION AB021980.1 GI:4514721
KEYWORDS delta-6 fatty acid desaturase.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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## REFERENCE

```
1 (sites)
Aki,T., Shimada,Y., Inagaki,K., Higashimoto,H., Kawamoto,S.,
Shigeta,S., Ono,K. and Suzuki,O.
```

## AUTHORS

```
Molecular cloning and functional characterization of rat delta-6
fatty acid desaturase
```

## JOURNAL

```
Biochem. Biophys. Res. Commun. 255 (3), 575-579 (1999)
```

## MEDLINE

```
99160394
```

## PUBMED

```
10049752
```

## REFERENCE

```
2 (bases 1 to 1546)
```

## AUTHORS

```
Aki,T.
```

## TITLE

```
Direct Submission
```

## JOURNAL

```
Submitted (31-DEC-1998) Tsunehiro Aki, Hiroshima University,
```

```
Department of Molecular Biotechnology; 1-4-1 Kagamiyama,
```

```
Higashi-Hiroshima, Hiroshima 739-8527, Japan
```

```
(E-mail: aki@ipc.hiroshima-u.ac.jp, Tel:81-824-24-7755,
```

```
Fax:81-824-22-7191)
```

```
Sequence updated (25-Feb-1999).
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US-10-029-756-20 (1-6) x AB021980 (1-1546)

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Db 1237 TTCAGATTGACACCAC 1254
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## RESULT 64

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LOCUS AB069727.1 1576 bp mRNA linear VRT 11-AUG-2001
DEFINITION Oreochromis niloticus Fads6 mRNA for putative delta-6 fatty acyl
desaturase, complete cds.
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## ACCESSION

```
AB069727
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## VERSION

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AB069727.1 GI:15147882
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## KEYWORDS

## SOURCE

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Oreochromis niloticus (Nile tilapia)
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## ORGANISM

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Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidae; Cichlidae; Oreochromis.
```

## REFERENCE

```
1 Sirisua,S., Yoshizaki,G., Kiron,V., Takeuchi,T., Satoh,S. and
Watanabe,T.
```

## AUTHORS

```
Molecular cloning, Expression, and Activity of the Nile Tilapia
(Oreochromis niloticus) Delta-6 Fatty Acyl Desaturase
```

## JOURNAL

```
Unpublished
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## REFERENCE

```
2 (bases 1 to 1576)
```

## AUTHORS

```
Sirisua,S., Yoshizaki,G., Kiron,V., Takeuchi,T., Satoh,S. and
Watanabe,T.
```

## TITLE

```
Direct Submission
```

## JOURNAL

```
Submitted (09-AUG-2001) Soranuth Sirisua, Tokyo University of
Fisheries, Aquatic Biosciences, Konan 4-5-7, Minato, Tokyo
```

```
108-8477, Japan (E-mail:soranuth@yahoo.com, Tel:81-3-5463-0555,
```

```
Fax:81-3-5463-0553)
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## FEATURES

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Location/Qualifiers
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1..1576
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110..1447
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AF309556 1590 bp mRNA linear VRT 05-DEC-2001
LOCUS
DEFINITION
Danio rerio putative delta-6 fatty acyl desaturase (Fadad6) mRNA,
complete cds.
ACCESSION
AF309556
VERSION
AF309556.1 GI:10954034
KEYWORDS
Danio rerio (zebrafish)
SOURCE
Danio rerio
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 1590)
Hastings,N., Agaba,M., Tocher,D.R., Leaver,M.J., Dick,J.R.,
Sargent,J.R. and Teale,A.J.
A vertebrate fatty acid desaturase with Delta 5 and Delta 6
activities
Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)
11724940
JOURNAL
PUBMED
2 (bases 1 to 1590)
Hastings,N., Agaba,M.K., Tocher,D.R., Teale,A.J. and Sargent,J.R.
Direct Submission
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Stirling PK9 4LA, Scotland
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QHAKPNIFKKQDPQNMNLNAGVQVPEYGVKIKHLPYNOHHQKFFFGPPLIIP
VYFQFQPHNMISGHWVDLLWCISYYVRYFLCYTFQYGFVFWAILFNVFNESHPF
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Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
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Qy 1 PheGlnlleGluHis 6
Db 1141 TTTCAGATCGAGCATCAT 1158
RESULT 66
BC057189 1608 bp mRNA linear ROD 30-JUN-2004
LOCUS
DEFINITION
Mus musculus fatty acid desaturase 2, mRNA (cDNA clone MGC:68002
IMAGE:5137343), complete cds.
ACCESSION
BC057189
VERSION
BC057189.1 GI:34785343
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1608)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.B., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL
PUBMED
2 (bases 1 to 1608)
Strausberg,R.
Direct Submission
TITLE
Submitted (29-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Ahter,N., Ayel,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
```

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,  
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,  
Tsurgou,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IPAK Plate: 123 Row: i Column: 2  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 9790070.

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/tissue\_type="Liver, normal. 5 month old male mouse."  
/clone\_lib="NCI CGAP\_Li9"  
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note="Vector: PCMV-SPORT6"  
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63. .1397  
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TLTAVFLATSOAQAOLHVDYHLSVYKSIWNHVKFVIGHLKASANWNNRHF  
OHAAPNIHKDPDIKSLHVLGEMQPLEYKKKLXVLPYNHCHYEFLIGPPLLIP  
MYFQQLIMTISRDRVDLAWAISYMRFFTYIPFYGILGALVFLNFRFLSHWF  
RVVTOMHLVNEIDLHDYRWFSSQLAATCNVEQSFNDWFSGLNFQIEHHLFFPTMP  
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Db 1203 TTCCAGATTGACACCAC 1220  
RESULT 67  
AY332747  
LOCUS  
DEFINITION  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Pavlova lutheri  
Eukaryota; Haptophyceae; Pavlova; Pavlova.  
REFERENCE  
1 (bases 1 to 1619)  
Tonon,T., Harvey,D., Larson,T.R. and Graham,I.A.  
Identification of a very long chain polyunsaturated fatty acid  
delta4-desaturase from the microalga Pavlova lutheri

ORIGIN  
Alignment Scores:  
Pred. No.: 396 Length: 1608  
Score: 36.00 Matches: 6  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Db 1194 TTCCAGATCGACCAT 1211  
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AY234124  
LOCUS  
DEFINITION  
AY234124  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Primula farinosa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; Ericales; Primulaceae; Primula.  
REFERENCE  
1 (bases 1 to 1681)  
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and  
Napier,J.A.  
Identification of Primula fatty acid Delta(6)-desaturases with n-3  
substrate preferences(1)  
FBBS Lett. 542 (1-3), 100-104 (2003)  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 1681)  
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and  
Napier,J.A.  
Direct Submission  
TITLE

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 1619)  
Tonon,T., Harvey,D., Larson,T.R. and Graham,I.A.  
Direct Submission  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 1619)  
Tonon,T., Harvey,D., Larson,T.R. and Graham,I.A.  
Submitted (30-JUN-2003) Biology (Area 7), University of York, CNAP,  
Heslington, York YO10 5YW, UK  
FEATURES  
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Location/Qualifiers  
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Alignment Scores:  
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Query Match: 100.00% Indels: 0  
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US-10-029-756-20 (1-6) x AY332747 (1-1619)  
Qy 1 PheGlnIleGluHisHis 6  
Db 1194 TTCCAGATCGACCAT 1211  
RESULT 68  
AY234124  
LOCUS  
DEFINITION  
AY234124  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Primula farinosa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; Ericales; Primulaceae; Primula.  
REFERENCE  
1 (bases 1 to 1681)  
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and  
Napier,J.A.  
Identification of Primula fatty acid Delta(6)-desaturases with n-3  
substrate preferences(1)  
FBBS Lett. 542 (1-3), 100-104 (2003)  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 1681)  
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and  
Napier,J.A.  
Direct Submission  
TITLE



JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton  
 Research Station, Long Ashton, Bristol BS41 9AP, UK  
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 LFSSKVPDRVQEIFGIGVFWWYPLLVSLCPNMGEMFVVASFSVTGIQHVQCLN  
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## ORIGIN

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US-10-029-756-20 (1-6) x AY234124 (1-1681)

Qy 1 PheGlnlleGluHis 6  
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 Db 1178 TTTCAGATCGAGCACCAT 1195

RESULT 69  
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 DEFINITION Sequence 1 from patent US 5959175.  
 ACCESSION AR076814  
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 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 1684)  
 Thomas, T.L., Nunberg, A.N. and Beremand, P.D.  
 Sunflower albumin 5', regulatory region for the modification of  
 plant seed lipid composition  
 Patent: US 5959175-A 1 28-SEP-1999;  
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## ORIGIN

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US-10-029-756-20 (1-6) x AR076814 (1-1684)

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RESULT 70  
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 DEFINITION Sequence 1 from patent US 5977436.  
 ACCESSION AR084177  
 VERSION AR084177.1 GI:10010948  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 1684)  
 Thomas, T.L. and Li, Z.  
 Olesin 5' regulatory region for the modification of plant seed  
 lipid composition  
 Patent: US 5977436-A 1 02-NOV-1999;  
 JOURNAL Location/Qualifiers  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 417 Length: 1684  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR084177 (1-1684)

Qy 1 PheGlnlleGluHis 6  
 |||||  
 Db 1156 TTCCAAATTGAGCATCAT 1173

RESULT 71  
 LOCUS BD062571 1684 bp DNA linear PAT 27-AUG-2002  
 DEFINITION A sunflower albumin 5' regulatory region for the modification of  
 plant seed lipid composition.  
 ACCESSION BD062571  
 VERSION BD062571.1 GI:22608174  
 KEYWORDS JP 2001518795-A/1.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 1684)  
 Thomas, T.L., Beremand, P.D. and Nunberg, A.N.  
 A sunflower albumin 5' regulatory region for the modification of  
 plant seed lipid composition  
 Patent: JP 2001518795-A 1 16-OCT-2001;  
 JOURNAL RHONE POULENC AGRO  
 COMMENT PN JP 2001518795-A/1  
 PD 16-OCT-2001  
 PF 09-APR-1998 JP 1998543140  
 PR 09-APR-1997 US 08/831570  
 PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC  
 C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC Strandedness:  
 Double;  
 CC Topology: Linear;  
 FH Key 43..1387.  
 FT CDS Location/Qualifiers  
 source 1..1684  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 417 Length: 1684  
 Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD062571 (1-1684)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1156 TTCCAATTGAGCATCAT 1173

RESULT 72  
BD070919 1684 bp DNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION An oleosin 5'regulatory region for the modification of plant seed  
lipid composition.  
ACCESSION BD070919  
VERSION BD070919.1 GI:22616522  
KEYWORDS JP 2001519668-A/1.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 1684)  
AUTHORS Thomas,T.L. and Li,Z.  
TITLE An oleosin 5'regulatory region for the modification of plant seed  
lipid composition  
JOURNAL Patent: JP 2001519668-A 1 23-OCT-2001;  
COMMENT RHONE POULENC AGRO  
OS Unidentified  
PN JP 2001519668-A/1  
PD 23-OCT-2001  
PF 09-APR-1998 JP 1998543141  
PR 09-APR-1997 US 08/831575  
PI TERRY L THOMAS, ZHONGSEN LI  
PC C12N15/82,C12N15/29,C12N15/53,A01H5/00,A01H5/10 CC  
Strandedness: Double;  
CC Topology: linear;  
CC An oleosin 5'regulatory region for the modification of plant  
seed lipid  
CC composition  
FH Key 43..1387.  
FT CDS Location/Qualifiers  
source 1..1684  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN  
Alignment Scores:  
Pred. No.: 417 Length: 1684  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD070919 (1-1684)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1156 TTCCAATTGAGCATCAT 1173

RESULT 73  
AR020904 1685 bp DNA linear PAT 05-DEC-1998  
LOCUS  
DEFINITION Sequence 4 from patent US 5789220.  
ACCESSION AR020904  
VERSION AR020904.1 GI:3975519  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 1685)  
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freyasiniet,G.L.  
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase  
JOURNAL Patent: US 5789220-A 4 04-AUG-1998;  
FEATURES Location/Qualifiers  
source 1..1685  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 417 Length: 1685  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR020904 (1-1685)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1157 TTCCAATTGAGCATCAT 1174

RESULT 74  
I38430 1685 bp DNA linear PAT 13-MAY-1997  
LOCUS  
DEFINITION Sequence 4 from patent US 5614393.  
ACCESSION I38430  
VERSION I38430.1 GI:2084484  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 1685)  
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freyasiniet,G.L.  
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase  
JOURNAL Patent: US 5614393-A 4 25-MAR-1997;  
FEATURES Location/Qualifiers  
source 1..1685  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 417 Length: 1685  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x I38430 (1-1685)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 1157 TTCCAATTGAGCATCAT 1174

RESULT 75  
AR200408 1685 bp DNA linear PAT 20-APR-2002  
LOCUS  
DEFINITION Sequence 4 from patent US 6355861.  
ACCESSION AR200408  
VERSION AR200408.1 GI:20250482  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 1685)  
AUTHORS Thomas,T.L.  
TITLE Production of gamma linolenic acid by a .DELTA.6-desaturase

JOURNAL Patent: US 6355861-A 4 12-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..1685  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 417 Length: 1685  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR200408 (1-1685)

Oy 1 PheGlnIleGluHis 6  
 Db 1157 TTCCAAATTGAGCATCAT 1174

## RESULT 76

LOCUS AR455421 1685 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 4 from patent US 6683232.

ACCESSION AR455421

VERSION AR455421.1 GI:42689973

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1685)

AUTHORS Thomas,T.L.

TITLE Production of gamma. linolenic acid by a DELTA.6-desaturase

JOURNAL Patent: US 6683232-A 4 27-JAN-2004;

FEATURES Location/Qualifiers

source 1..1685  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 417 Length: 1685  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR455421 (1-1685)

Oy 1 PheGlnIleGluHis 6  
 Db 1157 TTCCAAATTGAGCATCAT 1174

## RESULT 77

LOCUS AF007561 1685 bp mRNA linear PLN 05-JAN-1999

DEFINITION Borago officinalis delta 6-desaturase mRNA, complete cds.

ACCESSION AF007561

VERSION AF007561.1 GI:4102020

KEYWORDS

SOURCE

ORGANISM

Borago officinalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Boraginaceae; Borago.

REFERENCE 1 (bases 1 to 1685)

AUTHORS Nunberg,A.N., Beremand,P.D. and Thomas,T.L.

TITLE Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid

JOURNAL (GLA)

REFERENCE 2 (bases 1 to 1685)

AUTHORS Nunberg,A.N., Beremand,P.D. and Thomas,T.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JUN-1997) Biology, Texas A&M University, College Station, TX 77843, USA

## FEATURES

source

Location/Qualifiers

1..1685  
 /organism="Borago officinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:13363"  
 /tissue\_type="seed"  
 /dev\_stage="12 day post pollination"  
 /note="membrane bound polysomal RNA"  
 44..1390  
 /function="fatty acid desaturase"  
 /function="produces gamma. linolenic acid from linoleic acid"  
 /functions="produces octadecatetraenoic acid from alpha linolenic acid"  
 /codon\_start=1  
 /product="delta 6-desaturase"  
 /protein\_id="AAD01410.1"  
 /db\_xref="GI:4102021"  
 /translation="MAAQIKKITSDELKNHDKPDLWISIQGKAYDVSDVVKDHPGG  
 SPFLKSLAGDEVTDFAVAFHPASTWKNLDFEFTGYLKDYSVSVSKDYRKLVEFSK  
 MGLYDKKHIMFATLCFIAMLFAMSVYGVLFCEGLVHLFSGCLMGFLMIQSGIHGD  
 AGHYMVVSDSLNKFMGIFAANCLSGISIGWKNHNAHIACTNSLEYDPLQIIPFL  
 VVSKKFGSLTSHFYEKRLTFDSLRFVSYQHWTFYIMCAARLNMYVQSLMLLT  
 RNYVQRAQLGCLVFIWYPLLVSLCPNMGERIMFVIAISLVTCMQVQPSLNHFSS  
 SVYVGKPGNNWFEKQTDGLDISCPNMDWFGHGLQFQIEHLFPKMPRCNLAKISP  
 YVIELCKHNLPYNYASFKNENMTLTLRLTALQARDITKPLPKNLWEALHTHG"

## ORIGIN

Alignment Scores:  
 Pred. No.: 417 Length: 1685  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AF007561 (1-1685)

Oy 1 PheGlnIleGluHis 6  
 Db 1157 TTCCAAATTGAGCATCAT 1174

## RESULT 78

LOCUS AR221958 1686 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 6 from patent US 6428990.

ACCESSION AR221958

VERSION AR221958.1 GI:23329261

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1686)

AUTHORS Mukerji,P., Leonard,A.E.Y., Huang,Y.-S. and Parker-Barnes,J.M.

TITLE Human desaturase gene and uses thereof

JOURNAL Patent: US 6428990-A 6 06-AUG-2002;

FEATURES Location/Qualifiers

source 1..1686  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 418 Length: 1686  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

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US-10-029-756-20 (1-6) x AR221958 (1-1686)

Qy 1 PheGlnIleGluHisHis 6
Db 534 TTCAGATTGAGCACCAC 551

RESULT 79
BD082638 1686 bp DNA linear PAT 27-AUG-2002
LOCUS Methods and compositions for synthesis of long chain
DEFINITION poly-unsaturated fatty acids.
ACCESSION BD082638
VERSION BD082638.1 GI:22628248
KEYWORDS JP 2001523091-A/18.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1686)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
JOURNAL poly-unsaturated fatty acids
COMMENT Patent: JP 2001523091-A 18 20-NOV-2001; CALGENE LLC,ABBOTT LABORATORIES
PN JP 2001523091-A/18
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544053
PR 11-APR-1997 US 08/834655
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND.
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC
,C11B1/00, A61K31/20,
PC A23K1/30
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source 1..1686
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores: 418 Length: 1686
Pred. No.: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082653 (1-1686)
Qy 1 PheGlnIleGluHisHis 6
Db 534 TTCAGATTGAGCACCAC 551

RESULT 81
BD092932 1686 bp DNA linear PAT 27-AUG-2002
LOCUS Methods and compositions for synthesis of long chain
DEFINITION polyunsaturated fatty acids in plants.
ACCESSION BD092932
VERSION BD092932.1 GI:22638543
KEYWORDS JP 2001527395-A/19.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1686)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
JOURNAL polyunsaturated fatty acids in plants
COMMENT Patent: JP 2001527395-A 19 25-DEC-2001; CALGENE LLC,ABBOTT LABORATORIES
PN JP 2001527395-A/19
PD 25-DEC-2001
PF 10-APR-1998 JP 1998544175
PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR 11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI
DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND.
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
30, A23K1/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source 1..1686
/organism="synthetic construct"

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 418 Length: 1686
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD092932 (1-1686)

Qy 1 PheGlnIleGluHis 6
|||||
Db 534 TTCCAGATTGACACCAC 551

RESULT 82
AX951561
LOCUS AX951561 1687 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 1 from Patent WO03093482.
ACCESSION AX951561
VERSION AX951561.1 GI:40781919
KEYWORDS
SOURCE
ORGANISM Borago officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Boraginaceae; Borago.

REFERENCE
1 Cirpus, P., Renz, A., Lerchl, J. and Kuijpers, A.M.
METHOD for producing multiple unsaturated fatty acids in plants
PATENT: WO 03093482-A 1 13-NOV-2003;
BASF Plant Science GmbH (DE)
LOCATION/Qualifiers
source 1..1687
/organism="Borago officinalis"
/mol_type="unassigned DNA"
/db_xref="taxon:13363"
42..1388
/feature="unnamed protein product; Delta-6-Desaturase"
/codon_start=1
/protein_id="CAF05407.1"
/db_xref="GI:40781920"
/translation="MAAQIKKVIITSDLNKDKPGDLWISIQKAYDVSDWKDHPGG
SPPLKSLAGQVTDFAVAFHDPASTWKNLDFEFTGYLYKDYSEVSKDYKLVFEFSK
MGLYDKKHIMPATLCFTAMLPAMSVYGVLPCEGVVHLFGCLMGFLMIOSGWIHGD
AGHYNVVSDSLNKPFGIPFAANCLSGISIGWKNHNAHIAACNSLEYDPLQYIPFL
VSSKFFGSLTSHFYKRLTDFSLRSFVSYOHWTFFYIMCAARLNMYVQSLIMLLTK
RNVSYRAHELGLCVFSIWYPLLVSLCPNMGIRIMFVIAISLVTCMQQVQFSLNHFSS
SVYVCKPKNWFEKQTDGTLDISCPNMDWPHGGLQFQIEHLPKPRCNLRKISP
YVIELCKKHNLPYNYASFSKANEMTLRLTALQARDITKPLPKNLWEALHTHG"

CDS
ORIGIN
Alignment Scores:
Pred. No.: 418 Length: 1687
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX951561 (1-1687)

Qy 1 PheGlnIleGluHis 6
|||||
Db 1155 TTCCAAATTGACATCAT 1172

RESULT 83
BOU79010
LOCUS BOU79010 1687 bp mRNA linear PLN 02-MAY-1997
DEFINITION Borago officinalis delta 6 desaturase mRNA, complete cds.

ORIGIN
Alignment Scores:
Pred. No.: 418 Length: 1687
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BOU79010 (1-1687)

Qy 1 PheGlnIleGluHis 6
|||||
Db 1155 TTCCAAATTGACATCAT 1172

RESULT 84
AB070444
LOCUS AB070444 1692 bp mRNA linear VRT 23-AUG-2001
DEFINITION Oncorhynchus masou FD6D mRNA for putative delata 6-desaturase,
complete cds.
ACCESSION AB070444
VERSION AB070444.1 GI:15281353
KEYWORDS
SOURCE
ORGANISM Oncorhynchus masou (cherry salmon)
Oncorhynchus masou
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE
1 Yoshizaki, G., Ishikawa, A., Takeuchi, T. and Gen, K.
delta6-desaturase-like cDNA in masou salmon
```

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U79010
U79010.1 GI:2062402
KEYWORDS
SOURCE
ORGANISM Borago officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Boraginaceae; Borago.

REFERENCE
1 (bases 1 to 1687)
AUTHORS Sayanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G.,
Christie, W.W., Shewry, P.R. and Napier, J.A.
TITLE Expression of a borago desaturase cDNA containing an N-terminal
cytochrome b5 domain results in the accumulation of high levels of
delta6-desaturated fatty acids in transgenic tobacco
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
MEDLINE 97268723
PUBMED 9108131
REFERENCE 2 (bases 1 to 1687)
AUTHORS Sayanova, O., Smith, M.A., Shewry, P.R. and Napier, J.A.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1996) Cell Biology, IACR-Long Ashton Research
Station, Long Ashton, Bristol BS18 9AF, UK
FEATURES
source 1..1687
/organism="Borago officinalis"
/mol_type="mRNA"
/db_xref="taxon:13363"
42..1388
/function="haem-binding protein"
/codon_start=1
/product="delta 6 desaturase"
/protein_id="AAC49700.1"
/db_xref="GI:2062403"
/translation="MAAQIKKVIITSDLNKDKPGDLWISIQKAYDVSDWKDHPGG
SPPLKSLAGQVTDFAVAFHDPASTWKNLDFEFTGYLYKDYSEVSKDYKLVFEFSK
MGLYDKKHIMPATLCFTAMLPAMSVYGVLPCEGVVHLFGCLMGFLMIOSGWIHGD
AGHYNVVSDSLNKPFGIPFAANCLSGISIGWKNHNAHIAACNSLEYDPLQYIPFL
VSSKFFGSLTSHFYKRLTDFSLRSFVSYOHWTFFYIMCAARLNMYVQSLIMLLTK
RNVSYRAHELGLCVFSIWYPLLVSLCPNMGIRIMFVIAISLVTCMQQVQFSLNHFSS
SVYVCKPKNWFEKQTDGTLDISCPNMDWPHGGLQFQIEHLPKPRCNLRKISP
YVIELCKKHNLPYNYASFSKANEMTLRLTALQARDITKPLPKNLWEALHTHG"

ORIGIN
Alignment Scores:
Pred. No.: 418 Length: 1687
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x BOU79010 (1-1687)

Qy 1 PheGlnIleGluHis 6
|||||
Db 1155 TTCCAAATTGACATCAT 1172

RESULT 84
AB070444
LOCUS AB070444 1692 bp mRNA linear VRT 23-AUG-2001
DEFINITION Oncorhynchus masou FD6D mRNA for putative delata 6-desaturase,
complete cds.
ACCESSION AB070444
VERSION AB070444.1 GI:15281353
KEYWORDS
SOURCE
ORGANISM Oncorhynchus masou (cherry salmon)
Oncorhynchus masou
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE
1 Yoshizaki, G., Ishikawa, A., Takeuchi, T. and Gen, K.
delta6-desaturase-like cDNA in masou salmon
```

```
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1692)
AUTHORS Yoshizaki,G., Ishikawa,A., Takeuchi,T. and Gen,K.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-2001) Goro Yoshizaki, Tokyo University of
Fisheries; 4-5-7 Kounan, Minato-ku 108-8477, Japan
(E-mail:goro@o Tokyo-u-fish.ac.jp, Tel:81-3-5463-0558,
Fax:81-3-5463-0558)
FEATURES
source Location/Qualifiers
1..1692
/organism="Oncorhynchus masou"
/mol_type="mRNA"
/db_xref="taxon:8020"
1..1692
/gene="FD6D"
174..1538
/gene="PD6D"
/codon_start=1
/product="putative delata 6-desaturase"
/protein_id="BAB63440.1"
/db_xref="GI:15281354"
/translation="MGGGQQTSESEPAKGVGVPDGGRGSSAVTWEVQKHCHRS
QMLVIDRWYNIITWAKHGGPGIRVISHFAGEDATEAFVAFHLEPNFVRKPLKLLIG
ELATPEQDQKNAVLQVDFQALRDVSEGLLRARPLFSLYLGHLLLEALALGL
LWVGTSMSTLLCSLMLATSOAAGLQHDYGLSVCKKSGWNHKLKHPVYHGHQYE
SANWNRHFOHAKPNVSKDPDINSIHVFLGDKQPVVEGIIKKLYMPVYHGHQYE
FLVGGPLIVPFFNIQIPRIFMSORDWDVLAWMTFYLRPFCCYPPFFGFGSVALLS
FVRLESHFWFVVTOMSHLPMEMDHERHQDLWTWOLSATNCIEOSTDNWFSGLHNFQ
IEHLFTPMRHHYHLVAPLVRALCEKHGVPYQVKTQLQGMTDVVRSLKSGDMLDA
YLHK"
ORIGIN
Alignment Scores:
Pred. No.: 419 Length: 1692
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-029-756-20 (1-6) x AB070444 (1-1692)
Qy 1 PheGlnIleGluHis 6
|||||
Db 1344 TTTCAGATTGAACCAT 1361
RESULT 85
BD228694 1700 bp DNA linear PAT 17-JUL-2003
LOCUS Delta 6 fatty acid desaturase.
DEFINITION BD228694
ACCESSION BD228694.1 GI:33038464
VERSION BD228694.1
KEYWORDS JP 2002527051-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1700)
AUTHORS Petrukhin,K. and Caskey,T.C.
TITLE Delta 6 fatty acid desaturase
JOURNAL Patent: JP 2002527051-A 2 27-AUG-2002;
MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002527051-A/2
PD 27-AUG-2002
PF 05-OCT-1999 JP 2000575530
PR 09-OCT-1998 US 60/103760
PI KONSTANTIN PETRUKHIN,THOMAS C CASKEY
PC C12N15/09,A61P3/10,A61P17/00,A61P27/02,A61P29/00, PC
A61P31/12,
PC C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/88,C12Q1/
PC 02,C12Q1/68,
PC G01N33/15,G01N33/50//A61K38/55,A61K39/395,A61K39/395,A61K39/
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PC 395,A61K45/00,
PC A61K48/00 G01N33/68,C12N15/00,C12N5/00,A61K37/64 CC Delta 6
fatty acid desaturase
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 422 Length: 1700
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD228694 (1-1700)
Qy 1 PheGlnIleGluHis 6
|||||
Db 1214 TTCCAGATCGAGCACCAC 1231
RESULT 86
AF134404 1705 bp mRNA linear PRI 19-MAY-1999
LOCUS Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA, complete
cde.
DEFINITION AF134404
ACCESSION AF134404.1 GI:4868365
VERSION AF134404.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1705)
AUTHORS Li,W., Metzker,M.L., Caskey,C.T. and Petrukhin,K.
TITLE Human retina-specific delta 6 fatty acid desaturase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1705)
AUTHORS Li,W., Metzker,M.L., Caskey,C.T. and Petrukhin,K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-1999) Human Genetics, Merck Research
Laboratories, P.O. Box 4, West Point, PA 19486, USA
FEATURES
source Location/Qualifiers
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71..1408
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VPSALAFILAIQAQSCWCLQHDIGHASIFKKSWMNHVAOKFVMQGLKGFSAHWNFR
HFQHAKPNIFHKDPDVTVAFLGSSVEYKKERYLPYNOOHLYFFLIGPPLLT
LVNFEVNLHMLVCMOWADLLWAASFYAFFFLFYGVGVLFFVAVRYVLESHW
FVMTQNNHLPKEIGEKHRDWSSQAAATCNVEPSLFTNWFSGHLNFIQIEHLLFFRM
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## Alignment Scores:

Pred. No.: 423 Length: 1705  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x AF134404 (1-1705)

Qy 1 PheGlnIleGluHis 6

Db 1214 TTCAGATCGAGCACCAC 1231

## RESULT 87

BC081776 1706 bp mRNA linear ROD 15-SEP-2004  
 LOCUS BC081776  
 DEFINITION Rattus norvegicus fatty acid desaturase 2, mRNA (CDNA clone  
 MGC:93365 IMAGE:7128630), complete cds.

## ACCESSION

BC081776.1 GI:51858587

## KEYWORDS

MGC.

## SOURCE

Rattus norvegicus (Norway rat)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

## REFERENCE

1 (bases 1 to 1706)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Viala, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Green, E.D.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Shevchenko, Y.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

## TITLE

12477932

## JOURNAL

PUBMED

## REFERENCE

2 (bases 1 to 1706)  
 Director MGC Project.  
 Direct Submission  
 Submitted (01-SEP-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

## REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-sngc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

## FEATURES

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 /lab\_host="DH10B"  
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 /db\_xref="RGD:68339"  
 167..1501  
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 /db\_xref="RGD:68339"

## gene

## CDS

Alignment Scores:  
 Pred. No.: 423 Length: 1706  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

## ORIGIN

US-10-029-756-20 (1-6) x BC081776 (1-1706)  
 Qy 1 PheGlnIleGluHis 6  
 Db 1307 TTCAGATCGAGCACCAC 1324

## RESULT 88

## LOCUS

BC049438 1708 bp mRNA linear VRT 30-JUN-2004  
 DEFINITION Danio rerio fatty acid desaturase 2, mRNA (CDNA clone MGC:56438  
 IMAGE:5612204), complete cds.

## ACCESSION

BC049438

## VERSION

BC049438.1 GI:29436932

## KEYWORDS

MGC.

## SOURCE

Danio rerio (zebrafish)

## ORGANISM

Danio rerio

## REFERENCE

## AUTHORS

1 (bases 1 to 1708)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)  
12477932  
2 (bases 1 to 1708)  
Strausberg, R.  
Direct Submission  
Submitted (31-MAR-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
Tissue Procurement: Dr. Sumio Sugano  
cDNA Library Preparation: Dr. Sumio Sugano  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth  
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,  
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,  
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,  
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,  
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie  
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 104 Row: e Column: 4  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis, similarity but not identity to protein.

FEATURES  
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/clone\_lib="Sugano SUD adult male"  
/lab\_host="DH10B"  
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/note="synonyms: DRD5/D6, fb64c04, wu:fb64c04, Fadsd6,  
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## gene

## CDS

ORIGIN  
RHHYWRAPRVRSLCEKYGKYGKQKTYGAPADIIIRSLSEKSGELMWLDAYLNK"  
Alignment Scores:  
Pred. No.: 424 Length: 1708  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0  
US-10-029-756-20 (1-6) x BC049438 (1-1708)  
Qy 1 PheGlnIleGluHisHis 6  
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Db 1235 TTCCAGATCGAGCATCAT 1252  
RESULT 89  
LOCUS AR264713 1717 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 2 from patent US 6492108.  
ACCESSION AR264713  
VERSION AR264713.1 GI:29693075  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1717)  
AUTHORS Hallman, J.L., Guegler, K.J., Corley, N.C. and Shah, P.  
TITLE Delta-6 desaturase homologs  
JOURNAL Patent: US 6492108-A 2 10-DEC-2002;  
FEATURES Location/Qualifiers  
source 1..1717  
/organism="unknown"  
/mol\_type="genomic DNA"  
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Pred. No.: 426 Length: 1717  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-029-756-20 (1-6) x AR264713 (1-1717)  
Qy 1 PheGlnIleGluHisHis 6  
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Db 1218 TTCCAGATCGAGCACCAC 1235  
RESULT 90  
LOCUS AY055749 1745 bp mRNA linear VRT 31-JUL-2003  
DEFINITION Sparus aurata putative delta 6-desaturase (FD6D) mRNA, complete  
cds.  
ACCESSION AY055749  
VERSION AY055749.1 GI:23428437  
KEYWORDS  
SOURCE Sparus aurata (gilthead seabream)  
ORGANISM Sparus aurata  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
Percoidae; Sparidae; Sparus.  
REFERENCE 1 (bases 1 to 1745)  
AUTHORS Seilliez, I., Panserat, S., Corraze, G., Kaushik, S. and Bergot, P.  
TITLE Cloning and nutritional regulation of a Delta6-desaturase-like  
enzyme in the marine teleost gilthead seabream (Sparus aurata)  
JOURNAL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 135 (3), 449-460  
(2003)  
MEDLINE 22715572  
PUBMED 12831765



```
REFERENCE 2 (bases 1 to 1745)
AUTHORS Sellies,I., Panserat,S., Kaushik,S. and Bergot,P.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2001) Fish Nutrition Laboratory, INRA,
St-Pee-sur-Nivelle 64310, France
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Pred. No.: 434 Length: 1745
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x AY055749 (1-1745)
Qy 1 PheGlnIleGluHisHis 6
Db 1299 TTTCAGATCGAGCACCAC 1316

RESULT 91
AX035942
LOCUS AX035942 1757 bp linear PAT 15-NOV-2000
DEFINITION Sequence 3 from Patent EP1035207.
ACCESSION AX035942
VERSION AX035942.1 GI:11191484
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Marquardt,A. and Weber,B.H.
TITLE Cdna molecules of the members of gene family encoding human fatty
acid desaturases and their use in diagnosis and therapy
JOURNAL Patent: EP 1035207-A 3 13-SEP-2000;
MULTIGENE BIOTECH GMBH (DE)
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Pred. No.: 438 Length: 1757
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-10-029-756-20 (1-6) x AX035942 (1-1757)
Qy 1 PheGlnIleGluHisHis 6
Db 1277 TTCCAGATCGAGCACCAC 1294

RESULT 92
AF084560
LOCUS AF084560 1757 bp mRNA linear PRI 12-OCT-2000
DEFINITION Homo sapiens fatty acid desaturase 3 (FADS3) mRNA, complete cds.
ACCESSION AF084560
VERSION AF084560.1 GI:10798852
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1757)
AUTHORS Marquardt,A., Soehn,H., White,K. and Weber,B.H.
TITLE cdna cloning, genomic structure, and chromosomal localization of
three members of the human fatty acid desaturase family
JOURNAL Genomics 66 (2), 175-183 (2000)
MEDLINE 20318619
PubMed 10860662
REFERENCE 2 (bases 1 to 1757)
AUTHORS Marquardt,A., Soehn,H., Passmore,L.A., Kraemer,F., Rivera,A. and
Weber,B.H.F.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1998) Institute of Human Genetics, University of
Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany
FEATURES
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            HFQHAKNIPFKHPDVTVAFVLIGSSVSEYKGRRLYPNQOHLVFFLIGPPLLT
            LVNPEVENLAYMLVCMQADLWLAASFYARFELSYLPFYGVGVLLFFVAVRVLESHW
            FVWITOMNHIPKEIGHEKRDWVSQLAATCNVPSLFTNWFSGHLNFQIHHLPFRM
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            /gene="FADS3"
        1738..1743
            /gene="FADS3"
            /note="variant ATTAAA"
ORIGIN
Alignment Scores:
Pred. No.: 438 Length: 1757
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-10-029-756-20 (1-6) x AF084560 (1-1757)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 1277 TTCAGATCGAGCACCAC 1294

## RESULT 93

## BC063726

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

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## PUBMED

## REFERENCE

## AUTHORS

```

VERSION AF309557.1 GI:10954036
KEYWORDS Cyprinus carpio (common carp)
SOURCE Cyprinus carpio
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.

REFERENCE 1 (bases 1 to 1790)
AUTHORS Hastings,N., Agaba,M., Tocher,D.R., Leaver,M.J., Dick,J.R.,
Sargent,J.R. and Teale,A.J.
TITLE A vertebrate fatty acid desaturase with Delta 5 and Delta 6
activities
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)
PUBMED 11724940
REFERENCE 2 (bases 1 to 1790)
AUTHORS Hastings,N., Agaba,M.K., Tocher,D.R., Teale,A.J. and Sargent,J.R.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-2000) Genetics, Institute of Aquaculture,
Stirling FK9 4LA, Scotland
FEATURES
source
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/organism="Cyprinus carpio"
/mol_type="mRNA"
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/cell_type="epitheliona papulosum cyprini cells"
1..1790
/gene="Fads6"
1..1335
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/codon_start=1
/product="putative delta-6 fatty acyl desaturase"
/protein_id="AAG25711.1"
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/translaton="MGCGGQOTDRITGTNGRFGTWTBEVOKHTKFGDQWIEVERKVY
NVSOQVHPGCGVRILGHYAGEDATEATAPDPLRYKYMKPLLIGLEASPSQD
RQKNAALVEDPALRERLEARGCFKQELPLILHSHILLLEALMMWVLGTGWIN
TAIVALLATQAQAEWLQHDPLGUSVPTGRNWHVHKFVVGWIKGASGRWNRHF
VYFQFIHNHIAHGLWDLAWCISYYVRYFLCYTYGVFWAVILFNFVFLKSHWF
VWVVTOMSHI PMQIDYEKHQDRLSMOLVATCNIEQSFNDWFSGLNFOIEHLPTMP
RHYWRAAPHVRELCAKYGIKYQKTLQAGFADVVRSLKSGEITWLDAYNE"

ORIGIN
Alignment Scores:
Pred. No.: 447 Length: 1790
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x AF309557 (1-1790)

Qy 1 PheGlnIleGluHis 6
|||||
Db 1141 TTCAGATCGAGCACAC 1158

RESULT 95
AK058543
LOCUS Oriza sativa (japonica cultivar-group) cDNA clone:001-017-B11, full
insert sequence.
DEFINITION Oriza sativa (japonica cultivar-group) cDNA clone:001-017-B11, full
insert sequence.
ACCESSION AK058543
VERSION AK058543.1 GI:32968561
KEYWORDS FLJ_CDNA; oligo-capping.
SOURCE Oriza sativa (japonica cultivar-group)
ORGANISM Oriza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;

```

```

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kodama,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohneda,E., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
22752273
PUBMED 12869764
2 (bases 1 to 1798)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayaehizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shingawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yanada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602 Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Naniki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,

```

Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

source  
Location/Qualifiers  
1. .1798  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/db\_xref="taxon:39947"  
/clone="001-017-B11"

ORIGIN

Alignment Scores:  
Pred. No.: 449 Length: 1798  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AK058543 (1-1798)

Qy 1 PheGlnIleGluHisHis 6

Db 1275 TTCCAATCGAGCACCAT 1292

RESULT 96

BC004901  
LOCUS Homo sapiens fatty acid desaturase 3, mRNA linear PRI 29-JUN-2004  
DEFINITION IMAGE:3532219, complete cds.

ACCESSION BC004901

VERSION BC004901.2 GI:33870184

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1807)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

JOURNAL  
PUBMED  
12477932  
2 (bases 1 to 1807)  
Strausberg, R.

REFERENCE

Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:13436175.  
Contact: MGC help desk  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amadansystemsbio.org](mailto:amadansystemsbio.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 11 Row: b Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14141181.

FEATURES

source

Location/Qualifiers  
1. .1807  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="MGC:4158 IMAGE:3532219"  
/tissue\_type="Muscle, rhabdomyosarcoma"  
/clone\_lib="NIH\_MGC\_17"  
/lab\_host="DH10B-R"  
/note="Vector: pOTB7"  
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/notes="synonyms: LLCDL3, BC269730\_1, CYB5RP"  
/db\_xref="locusID:3995"  
/db\_xref="MIM:606150"  
154. .1491  
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/product="fatty acid desaturase 3"  
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/db\_xref="locusID:3995"  
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VPSALAAFILAIQAQSCAQHQDLGHASIFKKSWMNHVAOKFVNGQKLGSAHWNFR  
LVHFEAKPNIHFHKDPDVTVAFLGESSVEYGGKKRRYLPYQQHLYFFLIGPLLT  
LNFQVENLAYMLVCQADLLWAASFYARFFLSYLPFYGVPGVLLFFVAVRVLESHT  
FWITQWNHLPKEIGHKRDWSSQALATCNVPSLFTNWFSGHLNFQIEHILFPRM  
PRNYSRVAPLVKSLCAKGLSYEVKPFALTALVDIVRSLSKSGDMLDAYLHQ"

gene

CDS

Alignment Scores:  
Pred. No.: 452 Length: 1807  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x BC004901 (1-1807)

Qy 1 PheGlnIleGluHisHis 6

Db 1297 TTCCAGATCGAGCACCAC 1314

RESULT 97

CQ776468  
LOCUS CQ776468 1816 bp DNA linear PAT 11-MAR-2004  
DEFINITION Sequence 154 from Patent EP1394274.  
ACCESSION CQ776468  
VERSION CQ776468.1 GI:45379858  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuwara, K.

TITLE Methods of testing for bronchial asthma or chronic obstructive pulmonary disease  
JOURNAL Patent: EP 1394274-A 154 03-MAR-2004;  
Genox Research, Inc. (JP)  
FEATURES Location/Qualifiers  
source 1..1816  
/organism="Homo sapiens"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 454 Length: 1816  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CQ776468 (1-1816)  
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Db 1306 TTCAGATCGACCAC 1323

RESULT 98  
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LOCUS CQ777377 1818 bp DNA linear PAT 11-MAR-2004  
DEFINITION Sequence 1063 from Patent EP1394274.  
ACCESSION CQ777377  
VERSION CQ777377.1 GI:45380361  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Sciurognathi; Muridae; Mus.  
REFERENCE 1  
AUTHORS Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuohara, K.  
TITLE Methods of testing for bronchial asthma or chronic obstructive pulmonary disease  
JOURNAL Patent: EP 1394274-A 1063 03-MAR-2004;  
Genox Research, Inc. (JP)  
FEATURES Location/Qualifiers  
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Query Match: 100.00% Indels: 0  
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US-10-029-756-20 (1-6) x CQ777377 (1-1818)  
Qy 1 PheGlnIleGluHis 6  
Db 1282 TTCAGATCGACCAC 1299

RESULT 99  
AB041560  
LOCUS AB041560 1818 bp mRNA linear ROD 30-JUN-2000  
DEFINITION Mus musculus brain cDNA, clone MNCB-0629, similar to Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA.  
ACCESSION AB041560  
VERSION AB041560.1 GI:7670384  
KEYWORDS fis (full insert sequence).  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (sites)  
AUTHORS Osada, N., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Sugano, S. and Hashimoto, K.  
TITLE isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method  
JOURNAL unpublished  
AUTHORS 2 (bases 1 to 1818)  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
COMMENT (E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)  
URL: http://www.nih.go.jp/yoken/genebank/  
Lib Name: Sugano mouse brain mncb  
Lab host: TOP10  
Vector: pME18S-FL3  
1st strand cDNA was primed with an oligo(dT) primer (ATGTCGCTTTTCTTTTCTTTT); double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAGCTGG], 3' end primer [CGACCTGAGCTCGACCA]).  
A part of this sequence is reported in AU035600.  
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Alignment Scores:  
Pred. No.: 455 Length: 1818  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-029-756-20 (1-6) x AB041560 (1-1818)  
Qy 1 PheGlnIleGluHis 6  
Db 1282 TTCAGATCGACCAC 1299  
RESULT 100  
AY458652



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 10:31:05 ; Search time 2403.16 Seconds  
(without alignments)  
95.036 Million cell updates/sec

Title: US-10-029-756-20

Perfect score: 36

Sequence: 1 FQIEHH 6

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Database :

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7: gb\_est6:\*

8: gb\_gse1:\*

9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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BI975702	484181 MA
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AW533321	UI-R-BU0-
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BU012940	QG3F03.Y
CF891989	AO103E09-
BP252288	BP252288
BP252506	BP252506
BP255845	BP255845
BP254298	BP254298
BP255848	BP255848
BM790950	K-EST0070
BP219406	BP219406
BP352319	BP352319
BX513256	BX513256
BU018830	QHL19M16.
CO682308	DG11-14d2
BP242668	BP242668
CB381262	3529 1.45
CA886644	B0147B12-
CD131172	MGI-0024U
CK842824	UI-R-BJ1-
CO683663	DG11-173a
CF892640	AO112E03-
CF894183	AO132D04-
CN299568	170004243
CN283566	170004245
AF084879	AF084879
BG803060	0194-42 M
CK998942	ip37f09.b
CO680131	DG11-111a
CO696232	DG11-95n1
CO703752	DG32-267h
CO687520	DG11-232p
CA343707	673883 NC
CA253461	SCULFLA10
CF750159	UI-M-HJ0-
AV682123	AV682123
CB494661	omykrbbb0
CO687643	DG11-234j
CO685306	DG11-159f
CO685848	DG11-206f
BM322472	PIC1_5_CO
CF725851	UI-M-G50-
CO687019	DG11-225h
AJ723990	AJ723990
CO697676	DG32-116m
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CO680725	DG11-11m1
CO693874	DG11-68n9
CR308748	Medicargo
AW518845	ha44el4.x
CO690386	BP1-274C
BP457290	BP457290



C 229	36	100.0	618	6	CA223458	SCJFPL1C0	302	36	100.0	694	7	CN975137	CN975137	24841_125
230	36	100.0	619	5	BQ515108	EST62523	C 303	36	100.0	698	2	BE613347	BE613347	601452439
231	36	100.0	620	5	BP336712	BP336712	304	36	100.0	699	6	CB549753	CB549753	MMP00010
C 232	36	100.0	621	5	BQ412264	GA_Ed005	305	36	100.0	700	7	CN971323	CN971323	18820_123
C 233	36	100.0	624	6	CB493595	omvKrb1b0	306	36	100.0	700	7	CN977877	CN977877	28550_125
234	36	100.0	624	7	CN987006	62688_125	307	36	100.0	700	7	CV150079	CV150079	Mdfct3074
C 235	36	100.0	624	7	C0685119	CG855119	308	36	100.0	702	5	BU432572	BU432572	603257617
236	36	100.0	625	4	BG163730	602338937	309	36	100.0	703	2	BE265009	BE265009	601193810
C 237	36	100.0	625	7	CF904342	A0421C04-	310	36	100.0	704	4	BI520098	BI520098	603071227
C 238	36	100.0	625	7	C0683285	DG11-167F	C 311	36	100.0	704	4	CF924968	CF924968	M1_MQ1_01
239	36	100.0	626	4	BG764766	602736370	C 312	36	100.0	705	9	AG171809	AG171809	Pan trogl
240	36	100.0	629	4	BG390559	602416330	313	36	100.0	707	4	BG743815	BG743815	602631480
C 241	36	100.0	629	7	C0679910	CG79910	314	36	100.0	708	4	BG743224	BG743224	602834390
242	36	100.0	631	5	BQ266634	NISC fl15	315	36	100.0	709	7	CN979203	CN979203	30404_125
C 243	36	100.0	632	4	BJ580080	BJ580080	316	36	100.0	709	7	CN980205	CN980205	1538_125
244	36	100.0	632	7	CN983167	601780_126	317	36	100.0	710	7	CN991754	CN991754	68839_125
245	36	100.0	633	2	BE313171	611419928	318	36	100.0	712	4	BI220733	BI220733	602938846
246	36	100.0	633	9	CW513287	CW513287	319	36	100.0	712	7	CN283564	CN283564	170005315
247	36	100.0	634	7	CN984291	53246_126	C 320	36	100.0	715	7	CK448975	CK448975	PL1G11.SP
248	36	100.0	635	6	CA889164	BO151B06-	C 321	36	100.0	717	4	BN386441	BN386441	UI-R-CN1
C 249	36	100.0	636	4	BG348983	BG348983	322	36	100.0	719	6	CA316163	CA316163	UI-N-FW0-
C 250	36	100.0	638	7	C0686285	daa35e12.	323	36	100.0	723	2	BF341872	BF341872	602016549
251	36	100.0	639	2	BE394750	601311958	324	36	100.0	723	8	B2393699	B2393699	EINBJ96TF
252	36	100.0	640	9	CR342157	Medicaco	325	36	100.0	724	7	CN283579	CN283579	170004554
C 253	36	100.0	641	2	BE382648	601297091	326	36	100.0	726	4	BG596229	BG596229	602859360
C 254	36	100.0	642	2	AW005365	AW005365	327	36	100.0	727	7	CF662243	CF662243	CCL101801
255	36	100.0	642	2	BE372542	601223991	C 328	36	100.0	727	7	CO681208	CO681208	DG11-126G
256	36	100.0	642	6	CB441017	691336_MA	329	36	100.0	730	5	BU284808	BU284808	603602290
257	36	100.0	642	7	CN283560	CN283560	C 330	36	100.0	730	5	BU626230	BU626230	UI-H-FG1-
258	36	100.0	643	7	CF894273	CF894273	C 331	36	100.0	730	7	CO556817	CO556817	AGENCOURT
259	36	100.0	647	7	CN984455	CN984455	332	36	100.0	732	6	CB984229	CB984229	AGENCOURT
C 260	36	100.0	648	7	CO701254	DG32-199C	C 333	36	100.0	733	5	BQ515109	BQ515109	EST622524
C 261	36	100.0	649	5	BQ830430	BQ830430	334	36	100.0	733	6	CD811236	CD811236	AGENCOURT
C 262	36	100.0	649	7	CO684927	CO684927	C 335	36	100.0	735	7	CO681550	CO681550	DG11-1301
263	36	100.0	650	4	BI220930	602937493	336	36	100.0	737	4	BG696721	BG696721	602659743
264	36	100.0	650	7	CF749409	UI-N-HU0-	337	36	100.0	738	4	BG747608	BG747608	602705067
265	36	100.0	651	4	BG085082	H3108D09-	338	36	100.0	741	5	BX858026	BX858026	EX858026
266	36	100.0	651	7	CV085518	Mdfct3078	C 339	36	100.0	742	9	CL953412	CL953412	OEIRUA000
267	36	100.0	653	6	CA247637	SCCFL506	C 340	36	100.0	744	5	BU617835	BU617835	UI-H-FE1-
268	36	100.0	654	6	CA247656	CA247656	341	36	100.0	744	5	BU772092	BU772092	SJEBM06
269	36	100.0	654	4	BG913139	602811753	342	36	100.0	745	4	BG739802	BG739802	602630537
270	36	100.0	655	4	BI330126	602983730	343	36	100.0	745	9	CNS02231	CNS02231	Tetraodon
C 271	36	100.0	657	4	BI850133	Imagqc_1	344	36	100.0	747	7	CV080482	CV080482	AGENCOURT
C 272	36	100.0	659	7	CO708052	DG32-9665	345	36	100.0	748	7	CN989200	CN989200	65204_125
273	36	100.0	660	2	BE394608	601311841	346	36	100.0	748	9	CC870069	CC870069	NDL_36F21
274	36	100.0	660	6	CA390771	ca114c09.	347	36	100.0	749	6	CD762498	CD762498	GGEZSM102
C 275	36	100.0	663	2	AW476589	fw60d11.y	C 348	36	100.0	749	7	CK129282	CK129282	AGENCOURT
C 276	36	100.0	664	4	BN264661	fw60d11.x	C 349	36	100.0	751	5	BQ174168	BQ174168	UI-N-DJ2-
277	36	100.0	666	6	CA090832	SCUTAM200	350	36	100.0	753	4	BG422898	BG422898	602450074
278	36	100.0	666	6	CD618242	56061114H	351	36	100.0	754	4	BG696675	BG696675	602658982
279	36	100.0	667	4	BI253447	602973776	352	36	100.0	755	5	BU366986	BU366986	603785574
280	36	100.0	667	6	CB502892	ssalplnb5	C 353	36	100.0	755	9	AG413792	AG413792	Mus muscu
281	36	100.0	671	9	CB335063	Medicaco	354	36	100.0	759	7	CN978621	CN978621	29464_125
282	36	100.0	672	7	CN299579	170005399	355	36	100.0	761	7	CK366282	CK366282	AGENCOURT
C 283	36	100.0	672	7	CO700981	DG32-190h	356	36	100.0	764	4	BG741398	BG741398	602631955
C 284	36	100.0	673	6	CD762194	GGEZSM102	357	36	100.0	767	7	CN987671	CN987671	63396_125
C 285	36	100.0	675	4	BM103984	fv41d12.x	358	36	100.0	768	6	CA371783	CA371783	652372_NC
C 286	36	100.0	675	6	CA390905	ca115h10.	C 359	36	100.0	769	5	BU724689	BU724689	SJMBJG09
287	36	100.0	677	4	BI079348	602873712	360	36	100.0	770	7	CN283577	CN283577	170005318
C 288	36	100.0	679	7	CN988761	64620_125	C 361	36	100.0	771	9	CG264591	CG264591	OGWGP72TH
C 289	36	100.0	680	2	BB630084	BB630084	C 362	36	100.0	771	9	CG264591	CG264591	OGWGP72TH
290	36	100.0	683	6	CD353781	UI-M-GM0-	363	36	100.0	772	7	CN324546	CN324546	AGENCOURT
C 291	36	100.0	683	7	CO819352	CSECS153B	364	36	100.0	773	5	BU612805	BU612805	UI-N-EW0-
C 292	36	100.0	685	4	BM156732	fv55b07.x	365	36	100.0	774	4	BG696258	BG696258	602659396
293	36	100.0	685	7	CO058265	Lr_AT1CF	366	36	100.0	778	5	BX860293	BX860293	EX860293
C 294	36	100.0	688	4	BU815215	BJB15215	367	36	100.0	778	5	BX860293	BX860293	EX860293
C 295	36	100.0	688	6	CB171369	JID602700	C 368	36	100.0	779	7	BI697693	BI697693	603348876
296	36	100.0	689	4	BG696921	602658688	369	36	100.0	779	7	CO123633	CO123633	GR_EB050
297	36	100.0	689	4	BG698232	602660143	370	36	100.0	783	4	BG743255	BG743255	603633329
298	36	100.0	689	7	CN988255	60405_125	371	36	100.0	784	4	BM044378	BM044378	603621713
C 299	36	100.0	693	5	BU623713	UI-H-FG1-	372	36	100.0	787	6	CA317271	CA317271	UI-N-FW0-
C 300	36	100.0	693	7	CF543009	S014678w-	373	36	100.0	788	8	CK312256	CK312256	TAM32-20F
301	36	100.0	694	5	BQ967562	QHB30D07.	C 374	36	100.0	790	7	CK025282	CK025282	AGENCOURT

375 36 100.0 794 7 CN991722 68588 125  
376 36 100.0 794 8 B2061358 1kx39h11.  
377 36 100.0 795 4 BG740017 602630980  
378 36 100.0 797 6 CA362547 636727 NC  
379 36 100.0 799 4 BG743597 602633951  
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381 36 100.0 800 7 CN171620 AGNCOURT  
382 36 100.0 801 1 A1317669 uj22b09.Y  
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391 36 100.0 807 4 BG921288 602824131  
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394 36 100.0 810 6 CA416571 UI-H-PB0-  
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398 36 100.0 815 5 BX440551 BX440551  
399 36 100.0 816 5 BU613358 UI-M-EW0-  
400 36 100.0 818 8 A0900998 HS 2079 A  
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403 36 100.0 821 6 CA511352 UI-R-FU0-  
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406 36 100.0 823 5 BU180521 AGNCOURT  
407 36 100.0 824 4 B1246687 602959276  
408 36 100.0 825 8 B2730996 OGEDJ37TM  
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413 36 100.0 832 4 BG753978 602709505  
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424 36 100.0 849 4 BU170559 AGNCOURT  
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426 36 100.0 855 4 B1257178 602973746  
427 36 100.0 857 7 CN324715 AGNCOURT  
428 36 100.0 863 2 BF527707 602404719  
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431 36 100.0 865 6 CD252932 AGNCOURT  
432 36 100.0 866 4 BG676236 602622635  
433 36 100.0 868 4 B1918347 603182855  
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435 36 100.0 871 4 BG697529 602660748  
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439 36 100.0 874 5 BX341258 BX341258  
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36 100.0 894 4 BG743088  
36 100.0 895 6 CA487874 AGNCOURT  
36 100.0 896 6 CB201033 AGNCOURT  
36 100.0 900 4 BG697505 602660710  
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36 100.0 1131 9 AY420234 Homo sapi  
36 100.0 1131 9 AY420236 Homo sapi  
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36 100.0 1270 3 AK079452 Mus muscu  
36 100.0 1318 2 BF384630 602046905  
36 100.0 1335 9 AY418548 Homo sapi  
36 100.0 1335 9 AY418550 Mus muscu  
36 100.0 1521 3 CR611884 full-leng  
36 100.0 1530 3 CR597486 full-leng  
36 100.0 1641 3 CR591980 full-leng  
36 100.0 1689 3 AK080414 Mus muscu

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BU126000 603150058  
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BQ952439 AGNCOURT  
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CR607573 full-leng  
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CG237761 OG9BS48TV  
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BX339327 BX339327  
CC200981 CH261-134  
CL031798 CH216-33G  
CL079671 CH216-156  
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BM462137 AGNCOURT  
AY420234 Homo sapi  
AY420236 Homo sapi  
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BM466315 AGNCOURT  
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AK079452 Mus muscu  
BF384630 602046905  
AY418548 Homo sapi  
AY418550 Mus muscu  
CR611884 full-leng  
CR597486 full-leng  
CR591980 full-leng  
AK080414 Mus muscu

521	36	100.0	1690	3	CR608795	CR508795 full-leng	584	35	97.2	639	8	AZ8085669	AZ8085669 2M0073H13
522	36	100.0	1764	3	AY103762	AY103762 Zea mays	c 595	35	97.2	640	9	BJ230767	BJ230767 BJT230767
523	36	100.0	1943	3	BC068224	BC068224 Danilo rer	c 596	35	97.2	649	9	CC862130	CC862130 NDL_1131U5
524	36	100.0	2272	3	AK076485	AK076485 Mus muscu	c 597	35	97.2	650	4	BJ467082	BJ467082 BJ467082
525	36	100.0	2813	3	AK033308	AK033308 Mus muscu	c 598	35	97.2	655	4	BJ309365	BJ309365 BJ309365
526	36	100.0	2862	3	AK083282	AK083282 Mus muscu	c 599	35	97.2	655	6	CB875305	CB875305 HK07011w
527	36	100.0	3129	3	AK029318	AK029318 Mus muscu	c 600	35	97.2	659	9	CC863158	CC863158 NDL_41C18
528	36	100.0	3318	3	AK083959	AK083959 Mus muscu	c 601	35	97.2	661	5	BQ238879	BQ238879 TaE05040A
529	36	100.0	3697	3	AK090042	AK090042 Mus muscu	c 602	35	97.2	663	4	BJ464983	BJ464983 BJ464983
530	36	100.0	4213	3	HSM802921	AL512760 Homo sapi	603	35	97.2	666	7	CF473213	CF473213 RTW2_1 H
531	35	97.2	158	8	AQ283123	AQ283123 RPCI11-86	604	35	97.2	669	9	CE568430	CE568430 tigr-g88-
532	35	97.2	207	5	BM060876	BM060876 BM060876	605	35	97.2	680	7	CF441824	CF441824 EST678169
533	35	97.2	278	7	CF269399	CF269399 Fcylcoid5	606	35	97.2	682	5	BQ540645	BQ540645 PTM09664
534	35	97.2	278	7	CF269399	CF269399 Fcylcoid5	607	35	97.2	685	5	BQ833409	BQ833409 T047F03 P
535	35	97.2	292	2	BB006919	BB006919 MA55 Fra9	c 608	35	97.2	690	4	BJ468633	BJ468633 BJ468633
536	35	97.2	300	1	AJ484147	AJ484147 AJ484147	c 609	35	97.2	699	4	BJ321063	BJ321063 BJ321063
537	35	97.2	310	7	R04815	R04815 pk32e05.r1	610	35	97.2	702	5	BQ540149	BQ540149 PTM0466
538	35	97.2	325	4	BG605209	BG605209 WHE2330_A	611	35	97.2	710	7	CF473294	CF473294 RTW2_1 H
539	35	97.2	353	8	BZ287498	BZ287498 SALK_0208	612	35	97.2	712	7	CN543497	CN543497 Q0243_1B3
540	35	97.2	362	8	AZ087483	AZ087483 RPCI-23-6	c 613	35	97.2	718	6	CD453035	CD453035 WHE1452_H
541	35	97.2	383	7	CN252847	CN252847 EST018783	c 614	35	97.2	721	9	AG359625	AG359625 Mus muscu
542	35	97.2	395	7	CN243173	CN243173 EST009047	c 615	35	97.2	726	9	AG380501	AG380501 Mus muscu
543	35	97.2	398	9	CG743611	CG743611 ZMBBCC019	c 616	35	97.2	738	9	AG465407	AG465407 Mus muscu
544	35	97.2	404	8	BH602609	BH602609 BOGJD94TF	c 617	35	97.2	745	9	AG359623	AG359623 Mus muscu
545	35	97.2	405	8	B35318	B35318 HS-1028-A2-	c 618	35	97.2	745	9	AG434701	AG434701 Mus muscu
546	35	97.2	417	1	AU292148	AU292148 AU292148	c 619	35	97.2	745	9	AG593243	AG593243 Mus muscu
547	35	97.2	420	2	BE352749	BE352749 EST115 So	c 620	35	97.2	753	9	AG599942	AG599942 Mus muscu
548	35	97.2	442	7	CN968710	CN968710 16207_100	c 621	35	97.2	758	9	AG563870	AG563870 Mus muscu
549	35	97.2	447	7	C0515514	C0515514 s13dSG52E	c 622	35	97.2	774	9	AG552008	AG552008 Mus muscu
550	35	97.2	448	5	BQ040319	BQ040319 gdl4c05.Y	c 623	35	97.2	775	8	BZ564928	BZ564928 pac2-164
551	35	97.2	470	5	BQ697507	BQ697507 NXPV_054	c 624	35	97.2	777	9	CL780616	CL780616 OR_BBA009
552	35	97.2	482	5	BQ297975	BQ297975 ean95h12-	c 625	35	97.2	782	6	CD379795	CD379795 PTM04964
553	35	97.2	488	1	AQ018801	AQ018801 RPCI-23-3	c 626	35	97.2	785	9	CL771096	CL771096 OR_BBA014
554	35	97.2	502	1	A1727921	A1727921 BNLGH1944	c 627	35	97.2	785	9	CL714121	CL714121 OR_BBA003
555	35	97.2	504	4	BM133143	BM133143 TgBSTzyb1	c 628	35	97.2	793	4	BJ574080	BJ574080 BJ574080
556	35	97.2	514	1	A1179320	A1179320 EST223015	c 629	35	97.2	793	7	CV035336	CV035336 RTNACL1_1
557	35	97.2	516	5	BQ236097	BQ236097 TaE05038D	c 630	35	97.2	796	7	CO978640	CO978640 GM89001A2
558	35	97.2	518	5	BH265574	BH265574 UK122TC04	c 631	35	97.2	805	6	CD826502	CD826502 BN25_064A
559	35	97.2	520	4	BI973290	BI973290 sai186d07	c 632	35	97.2	817	2	BE882014	BE882014 B01504694
560	35	97.2	521	4	BJ464683	BJ464683 BJ464683	c 633	35	97.2	828	6	CD815117	CD815117 BN15_025E
561	35	97.2	521	9	CG816778	CG816778 SOYDX94TH	c 634	35	97.2	847	7	CO094655	CO094655 GR_Ea16O
562	35	97.2	525	8	AQ924355	AQ924355 RPCI-23-2	c 635	35	97.2	853	7	CV234475	CV234475 WS01215_B
563	35	97.2	529	5	BQ143599	BQ143599 fmhc-pk0	c 636	35	97.2	872	7	CN248318	CN248318 EST014222
564	35	97.2	531	4	BI289738	BI289738 UI-R-DKO	c 637	35	97.2	873	7	CO071495	CO071495 GR_Ea29L
565	35	97.2	541	2	BB404056	BB404056 WHE0403_B	c 638	35	97.2	879	7	CV130834	CV130834 X9SP05h07
566	35	97.2	543	7	CF114672	CF114672 Shultzomi	c 639	35	97.2	882	7	CO072459	CO072459 GR_Ea31K
567	35	97.2	546	4	BJ218278	BJ218278 BJT218278	c 640	35	97.2	893	7	CV506152	CV506152 72B24_1 M
568	35	97.2	546	8	AJ563010	AJ563010 RPCI-23-2	c 641	35	97.2	897	5	EX698935	EX698935 BX698935
569	35	97.2	551	8	AQ533788	AQ533788 RPCI-11-3	c 642	35	97.2	898	9	CL098602	CL098602 ISB1-3114
570	35	97.2	553	1	A1170075	A1170075 EST215992	c 643	35	97.2	902	7	CV130544	CV130544 B9SP03906
571	35	97.2	553	8	AZ078433	AZ078433 RPCI-23-4	c 644	35	97.2	903	7	CO072315	CO072315 GR_Ea31G
572	35	97.2	554	1	A1233903	A1233903 EST230591	c 645	35	97.2	921	7	CN510503	CN510503 AGENCOURT
573	35	97.2	554	6	CA501548	CA501548 WHE4035_E	c 646	35	97.2	948	6	CN582338	CN582338 EST002013
574	35	97.2	555	1	AL818304	AL818304 AL818304	c 647	35	97.2	963	7	CN805379	CN805379 ILLUMIGEN
575	35	97.2	564	2	BB423694	BB423694 WHE0073_G	c 648	35	97.2	973	9	CNS02M91	AL203806 Tetraodon
576	35	97.2	573	1	AL810658	AL810658 AL810658	649	35	97.2	988	8	CNS0272K	AL814133 Tetraodon
577	35	97.2	585	8	AZ257782	AZ257782 RPCI-23-1	c 650	35	97.2	998	8	CC299589	CC299589 CH261-179
578	35	97.2	587	5	BP034044	BP034044 BP034044	651	35	97.2	1051	8	CC2975163	CC2975163 CH261-121
579	35	97.2	590	8	CL136127	CL136127 NDL_1668	c 652	35	97.2	1215	9	CL050972	CL050972 CH216-73C
580	35	97.2	592	6	CD527844	CD527844 3529_1_12	c 653	35	97.2	1242	6	CD505027	CD505027 CDA71-007
581	35	97.2	593	6	CA498944	CA498944 WHE4001_E	c 654	34	94.4	74	9	CG918264	CG918264 CH240_142
582	35	97.2	600	4	BI989590	BI989590 4043-10 M	c 655	34	94.4	143	9	CC472094	CC472094 CH240_295
583	35	97.2	602	8	B2184221	B2184221 CH230-340	c 656	34	94.4	240	8	BH214192	BH214192 SALK_0103
584	35	97.2	603	7	CF399694	CF399694 RTDS3_25	c 657	34	94.4	262	5	BH898675	BH898675 P024B09_P
585	35	97.2	606	2	AW759993	AW759993 s156f12.Y	c 658	34	94.4	278	8	BZ888347	BZ888347 CH240_219
586	35	97.2	616	4	BJ454984	BJ454984 BJ454984	659	34	94.4	313	2	BF070674	BF070674 s123h04.Y
587	35	97.2	616	8	AZ395503	AZ395503 IM0159D12	c 660	34	94.4	319	9	CC574270	CC574270 NXST_061
588	35	97.2	619	8	AZ707054	AZ707054 RPCI-23-2	c 661	34	94.4	321	5	BQ701283	BQ701283 CH240_451
589	35	97.2	622	1	A1729087	A1729087 BNLGH1125	c 662	34	94.4	325	9	BG666216	BG666216 Na_13_34D
590	35	97.2	628	4	BJ309966	BJ309966 BJ309966	c 663	34	94.4	326	5	AG020236	AG020236 Homo Sapi
591	35	97.2	631	7	CN825448	CN825448 LJPST690	664	34	94.4	330	8	BZ869071	BZ869071 CH240_248
592	35	97.2	632	8	BZ724408	BZ724408 HSC_00482	c 665	34	94.4	340	1	AU111935	AU111935 AU111935
593	35	97.2	632	9	CE370917	CE370917 tigr-g88-	666	34	94.4	342	8	AQ089096	AQ089096 HS_2207_B

667	34	94.4	347	9	CC599867	740	34	94.4	472	7	CV301192	CV301192 EST888535
668	34	94.4	357	4	B1128080	c 741	34	94.4	474	1	AV542586	AV542586 AV542586
c 669	34	94.4	360	1	AV188872	742	34	94.4	474	3	CNS0A42D	BX825701 Arabidops
c 670	34	94.4	360	1	AV196325	743	34	94.4	474	6	CG239303	CG239303 sab67h10.
c 671	34	94.4	360	5	BY000981	c 744	34	94.4	474	8	CG239570	CG239570 Gm_ck1560
c 672	34	94.4	360	6	C101120	745	34	94.4	474	8	B76579	B76579 RBC111-15N1
c 673	34	94.4	360	6	C471129	c 746	34	94.4	476	7	CO487815	T42806 6069 Lambda
c 674	34	94.4	360	7	D763395	747	34	94.4	480	7	T42806	T42806 6069 Lambda
c 675	34	94.4	363	9	CG983463	748	34	94.4	482	5	BQ973207	BQ973207 QH112D08.
c 676	34	94.4	364	5	BF659307	c 749	34	94.4	484	1	AV537777	AV537777 AV537777
c 677	34	94.4	371	1	A1460509	750	34	94.4	484	4	BG651350	BG651350 sad83e08.
c 678	34	94.4	372	4	BW732058	751	34	94.4	487	2	AW133134	AW133134 sei14g05.Y
c 679	34	94.4	372	8	B2912182	752	34	94.4	488	4	BG041585	BG041585 sv36d03.Y
c 680	34	94.4	376	5	B2897113	c 753	34	94.4	489	5	BP614716	BP614716 BP614716
c 681	34	94.4	379	8	B2860290	754	34	94.4	489	9	CC556273	CC556273 CH240_463
c 682	34	94.4	379	8	B2868712	c 755	34	94.4	490	8	BZ906491	BZ906491 CH240_29J
c 683	34	94.4	384	5	BP577440	756	34	94.4	492	1	AA898146	AA898146 NCM2G517
c 684	34	94.4	387	1	AV765585	c 757	34	94.4	493	8	CC114121	CC114121 NDL_68B12
c 685	34	94.4	387	8	AQ081217	c 758	34	94.4	494	4	BJ751861	BJ751861 BJ751861
c 686	34	94.4	395	7	CK089223	c 759	34	94.4	495	1	AV439995	AV439995 AV439995
c 687	34	94.4	400	2	B8474985	760	34	94.4	495	4	BG362965	BG362965 sac14e03.
c 688	34	94.4	403	1	A1988466	761	34	94.4	497	1	AJ497497	AJ497497 AJ497497
c 689	34	94.4	404	1	A1988466	762	34	94.4	497	5	BU964615	BU964615 sa899f07.
c 690	34	94.4	407	5	BP589193	c 763	34	94.4	500	6	CD598424	CD598424 RK113A4f0
c 691	34	94.4	408	7	W43225	764	34	94.4	503	4	BI975023	BI975023 sai176c03.
c 692	34	94.4	410	5	B0134113	c 765	34	94.4	504	5	BP061676	BP061676 BP061676
c 693	34	94.4	411	2	BF071066	c 766	34	94.4	505	1	AV533027	AV533027 AV533027
c 694	34	94.4	418	8	B2935543	767	34	94.4	510	2	AW306317	AW306317 sea49b05.Y
c 695	34	94.4	419	1	AU226921	768	34	94.4	511	4	BM271004	BM271004 sak04b05.
c 696	34	94.4	420	9	CK341625	c 769	34	94.4	514	1	AV547687	AV547687 AV547687
c 697	34	94.4	421	1	AV414665	c 770	34	94.4	517	6	CD013585	CD013585 VWC049D07
c 698	34	94.4	421	1	AV414668	c 771	34	94.4	520	7	CF518091	CF518091 CAP0006.I
c 699	34	94.4	422	7	CK703723	c 772	34	94.4	524	8	AQ059488	AQ059488 HS_5453.A
c 700	34	94.4	425	5	BP621625	c 773	34	94.4	525	2	BP044590	BP044590 BP044590
c 701	34	94.4	425	7	CV003049	774	34	94.4	530	2	BE347138	BE347138 sp55dl0.Y
c 702	34	94.4	427	2	B8801376	775	34	94.4	533	6	CD487836	CD487836 Gm_ckr427
c 703	34	94.4	429	5	B0406442	c 776	34	94.4	535	8	BZ931529	BZ931529 CH240_49I
c 704	34	94.4	429	7	CF420546	777	34	94.4	536	2	AW624957	AW624957 EST313786
c 705	34	94.4	433	1	AV797120	c 778	34	94.4	540	8	AQ699483	AQ699483 HS_5558.B
c 706	34	94.4	433	4	BG239410	c 779	34	94.4	543	5	BQ701814	BQ701814 NX51_170
c 707	34	94.4	436	1	AA059070	c 780	34	94.4	546	9	CD488784	CD488784 CH240_32I
c 708	34	94.4	437	1	AV534177	c 781	34	94.4	547	5	BU548726	BU548726 GmB80015B
c 709	34	94.4	440	5	B0910032	c 782	34	94.4	548	7	CR532803	CR532803 CR532803
c 710	34	94.4	443	5	BQ971716	c 783	34	94.4	548	8	BZ946090	BZ946090 CH240_124
c 711	34	94.4	445	5	BP589563	784	34	94.4	551	2	AW654515	AW654515 104009.MA
c 712	34	94.4	445	5	BQ701728	785	34	94.4	553	7	CK093427	CK093427 G120P22.3
c 713	34	94.4	446	5	BP571977	c 786	34	94.4	554	6	CB401312	CB401312 OSTF193A6
c 714	34	94.4	446	5	BW158579	787	34	94.4	557	8	AZ613050	AZ613050 IM0441B15
c 715	34	94.4	446	8	BZ956393	c 788	34	94.4	558	4	BU765986	BU765986 BU765986
c 716	34	94.4	447	5	BP595522	c 789	34	94.4	560	1	AV535443	AV535443 AV535443
c 717	34	94.4	447	5	BQ973097	790	34	94.4	560	5	BU762385	BU762385 sa889d03.
c 718	34	94.4	448	5	BQ914049	c 791	34	94.4	560	9	CC571046	CC571046 CH240_446
c 719	34	94.4	449	6	CA935212	c 792	34	94.4	562	1	AJ407290	AJ407290 AJ407290
c 720	34	94.4	449	7	CK090134	c 793	34	94.4	564	4	BU124534	BU124534 BJ124534
c 721	34	94.4	452	4	BI787180	c 794	34	94.4	565	7	CV236043	CV236043 WSO1222.B
c 722	34	94.4	452	5	BP611578	795	34	94.4	571	4	BI787611	BI787611 sai147f09.
c 723	34	94.4	452	5	BQ419183	c 796	34	94.4	571	6	CB397650	CB397650 OSTR193A6
c 724	34	94.4	453	5	BU025487	c 797	34	94.4	571	6	CB397667	CB397667 OSTR193A6
c 725	34	94.4	455	5	BP670475	c 798	34	94.4	571	7	CO514509	CO514509 g13SGG43E
c 726	34	94.4	456	5	BU091192	c 799	34	94.4	573	1	AV552225	AV552225 AV552225
c 727	34	94.4	457	5	BP618318	c 800	34	94.4	575	4	BU754543	BU754543 BU754543
c 728	34	94.4	462	5	BP618241	801	34	94.4	575	6	CA938317	CA938317 sav30g08.
c 729	34	94.4	463	1	A1484221	c 802	34	94.4	582	7	CF098735	CF098735 QHNB21.Y
c 730	34	94.4	464	5	BQ913259	c 803	34	94.4	584	9	CR344856	CR344856 Medicago
c 731	34	94.4	465	4	BG550968	804	34	94.4	586	1	AA901995	AA901995 NCC3A173
c 732	34	94.4	466	5	BP053037	c 805	34	94.4	586	6	CD412804	CD412804 Gm_ck4398
c 733	34	94.4	466	5	BP587473	c 806	34	94.4	587	6	CA153679	CA153679 SCUTR2202
c 734	34	94.4	467	5	BQ912248	807	34	94.4	590	5	BU578613	BU578613 sai59c03.
c 735	34	94.4	467	7	CF421312	c 808	34	94.4	595	6	CD012992	CD012992 VVC049D07
c 736	34	94.4	468	6	CA992336	c 809	34	94.4	599	1	AV762683	AV762683 AV762683
c 737	34	94.4	468	6	CA992337	c 810	34	94.4	600	2	BE228082	BE228082 SP5A8.C
c 738	34	94.4	470	5	BQ133972	c 811	34	94.4	602	1	AV439527	AV439527 AV439527
c 739	34	94.4	471	6	CB829321	c 812	34	94.4	602	6	CD399918	CD399918 Gm_ck2165

813	34	94.4	604	9	CC532986	CH240_410	886	34	94.4	702	8	AZ587821	1M0395D18
C 814	34	94.4	605	4	B3080702	B0780702	C 887	34	94.4	706	7	CF587640	USDA-FP_1
C 815	34	94.4	607	7	CK092271	G07621.3	C 888	34	94.4	706	7	CV045539	EST 7246
C 816	34	94.4	608	6	CB387809	OSTF086F1	C 889	34	94.4	706	8	BH969210	odg08g05
C 817	34	94.4	610	5	BU550971	GM880019B	C 890	34	94.4	707	9	CG841796	YnHW2410
C 818	34	94.4	612	8	CB303473	wsa0001_I	C 891	34	94.4	708	4	B3790429	B3790429
C 819	34	94.4	610	8	BZ851346	CH240_242	C 892	34	94.4	708	8	B2939186	CH240_105
C 820	34	94.4	613	6	CB276799	pk91h04.Y	C 893	34	94.4	709	7	CO167565	FLD1_69_E
C 821	34	94.4	614	7	CV098626	FAMU_USDA	C 894	34	94.4	710	6	CA102897	SCEQHR107
C 822	34	94.4	615	2	AW349540	GM210007B	C 895	34	94.4	711	8	BZ911150	CH240_109
C 823	34	94.4	616	6	B3803357	B3803357	C 896	34	94.4	712	9	CC471149	CH240_294
C 824	34	94.4	616	6	CD394782	Gm_CK1456	C 897	34	94.4	715	8	BH927841	odh24e11
C 825	34	94.4	617	8	BZ831616	CH240_257	C 898	34	94.4	717	5	BU028018	QHGSH09.Y
C 826	34	94.4	620	6	CA910169	PCS05532	C 899	34	94.4	719	5	BU001608	QGG28F03
C 827	34	94.4	623	2	BZ245271	601863746	C 900	34	94.4	719	8	AQ415221	RPC1-11-1
C 828	34	94.4	624	8	BZ939652	CH240_106	C 901	34	94.4	721	9	CE267875	tigr-988-
C 829	34	94.4	626	5	BU026694	QHG17L19	C 902	34	94.4	722	5	BU024653	QHF5H12.Y
C 830	34	94.4	627	2	BH657895	GM700003B	C 903	34	94.4	725	5	BU025380	QHF5C20.Y
C 831	34	94.4	629	8	BZ514773	BZ514773	C 904	34	94.4	732	9	CL175711	104_381_1
C 832	34	94.4	631	9	DR28D14S	AL982112	C 905	34	94.4	734	1	AV733382	AV733382
C 833	34	94.4	632	3	CNS0A53D	Danto_rer	C 906	34	94.4	736	5	BU025987	QHG12J15
C 834	34	94.4	634	3	AY389746	AY389746	C 907	34	94.4	737	5	BU025297	QHF6M04.Y
C 835	34	94.4	634	7	CO088960	GR_Ea08D	C 908	34	94.4	737	9	AG605954	Mus muscu
C 836	34	94.4	635	7	CN941799	OL10519AVB	C 909	34	94.4	740	6	CD839082	RFO2_1130
C 837	34	94.4	635	8	AQ423357	CITBI-E1-	C 910	34	94.4	741	4	BU575621	BU575621
C 838	34	94.4	637	7	CV038746	CV038746	C 911	34	94.4	741	5	BU028011	QHG9G05.Y
C 839	34	94.4	642	7	CO879789	BovGen_08	C 912	34	94.4	742	5	BU025031	QHF7E24.Y
C 840	34	94.4	648	5	BU027792	QHG7M11.Y	C 913	34	94.4	745	9	CL175712	104_381_1
C 841	34	94.4	650	6	CD594841	RK09A2D0	C 914	34	94.4	752	1	AV711211	AV711211
C 842	34	94.4	650	6	CD597738	CD597738	C 915	34	94.4	753	8	BH442903	BOGWK55TF
C 843	34	94.4	650	6	CD597844	CD597844	C 916	34	94.4	755	9	CL526507	48m1942.f
C 844	34	94.4	650	9	CC575015	CH240_452	C 917	34	94.4	759	9	CL521213	CH240_368
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C 846	34	94.4	652	9	CC515886	CH240_361	C 919	34	94.4	759	7	CV0504578	71131_1-M
C 847	34	94.4	655	8	AZ378833	1M0133H13	C 920	34	94.4	764	9	BJ778705	BJ778705
C 848	34	94.4	656	4	BJ1310737	EST531248	C 921	34	94.4	766	9	CG926726	CG926726
C 849	34	94.4	657	4	BJ124444	BJ124444	C 922	34	94.4	766	9	CG926726	CG926726
C 850	34	94.4	657	7	BU152844	BU152844	C 923	34	94.4	766	9	CG926726	CG926726
C 851	34	94.4	662	4	BM259784	BM259784	C 924	34	94.4	772	9	BI311411	EST531316
C 852	34	94.4	662	5	BU024108	QHF16F02	C 925	34	94.4	772	9	CC531588	CH240_408
C 853	34	94.4	664	5	BU023904	QHF14L05	C 926	34	94.4	772	9	CC531588	CH240_408
C 854	34	94.4	665	8	BZ922888	BZ922888	C 927	34	94.4	776	2	BE658198	GM700005A
C 855	34	94.4	665	5	BU024529	BU024529	C 928	34	94.4	776	2	CO078421	GR_Ea40L
C 856	34	94.4	666	8	BH716801	BH716801	C 929	34	94.4	776	8	BZ920891	CH240_118
C 857	34	94.4	667	7	CV237698	CV237698	C 930	34	94.4	781	9	CC494563	CH240_329
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C 860	34	94.4	670	5	BU027764	BU027764	C 933	34	94.4	785	5	EX834435	EX834435
C 861	34	94.4	671	9	CC528482	CC528482	C 934	34	94.4	786	7	CNS92104	TTE000106
C 862	34	94.4	674	9	AG157542	AG157542	C 935	34	94.4	786	7	CNS92111	TTE000098
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C 865	34	94.4	678	8	BZ929010	BZ929010	C 938	34	94.4	789	7	CNS92235	TTE000091
C 866	34	94.4	679	7	CF388215	CF388215	C 939	34	94.4	795	9	CC542440	CH240_423
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C 869	34	94.4	686	4	BI753054	BI753054	C 942	34	94.4	801	9	CC166058	FLD1_59_B
C 870	34	94.4	686	7	CV2373432	CV2373432	C 943	34	94.4	801	9	CC524638	CH240_373
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C 874	34	94.4	691	4	BJ348431	BJ348431	C 947	34	94.4	805	7	CNS93013	TTE000088
C 875	34	94.4	691	4	BJ348431	BJ348431	C 948	34	94.4	806	7	CNS93062	TTE000068
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C 878	34	94.4	695	8	BH687953	BH687953	C 951	34	94.4	811	7	CC964469	BOIDS77TR
C 879	34	94.4	695	8	BZ838922	BZ838922	C 952	34	94.4	813	7	CNS93304	TTE000108
C 880	34	94.4	696	5	BQ153475	BQ153475	C 953	34	94.4	814	7	CK091866	FL131P06.3
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C 882	34	94.4	697	8	BZ084396	BZ084396	C 955	34	94.4	820	9	CNS936G2	T7 end of
C 883	34	94.4	700	7	CV246768	CV246768	C 956	34	94.4	826	6	CB972811	CB972811
C 884	34	94.4	701	5	BQ849892	BQ849892	C 957	34	94.4	827	7	CNS94326	ID0000104
C 885	34	94.4	702	5	BU025281	QHF8K24.Y	C 958	34	94.4	827	7	CN763327	ID000016A

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c 959 34 94.4 828 9 CR832588 GROAAA65D
c 960 34 94.4 831 8 A2529126 ENTCL85TR
c 961 34 94.4 833 9 CL612316 OR_BB3000
c 962 34 94.4 840 9 CO366003 RTK1_20_C
c 963 34 94.4 847 9 CN763467 IDOAAA7AF
c 964 34 94.4 847 9 CG824114 SOYAT48TH
c 965 34 94.4 849 7 CN595796 TTR0000067
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c 968 34 94.4 852 7 CN596018 TTR0000136
c 969 34 94.4 854 7 CN596158 TTR0000076
c 970 34 94.4 856 7 CN596270 TTR0000103
c 971 34 94.4 858 7 CN596368 TTR0000075
c 972 34 94.4 858 7 CN596388 TTR0000132
c 973 34 94.4 858 7 CN758082 IDOAAA21B
c 974 34 94.4 858 9 CN506P8C
c 975 34 94.4 863 7 CN596705 TTR0000094
c 976 34 94.4 863 9 CN596705 Anopheles
c 977 34 94.4 864 7 CO369936 RTK1_55_H
c 978 34 94.4 865 7 CV227940 WS0158_B2
c 979 34 94.4 866 2 BF269784 GA_EB000
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c 982 34 94.4 867 8 B2818663 PUFFG62TB
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c 985 34 94.4 868 9 CC515139 CH240_360
c 986 34 94.4 869 7 CO807197 AGENCOURT
c 987 34 94.4 871 9 CL638412 CH243_5A1
c 988 34 94.4 874 9 CC512189 CH240_356
c 989 34 94.4 880 7 CN597795 TTR0000099
c 990 34 94.4 881 7 CN597846 TTR0000105
c 991 34 94.4 881 7 CN597872 TTR0000104
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c 993 34 94.4 883 8 B2671110 PUBDY33TD
c 994 34 94.4 885 7 CN598134 TTR0000092
c 995 34 94.4 889 8 BH147991 ENTP080TF
c 996 34 94.4 890 7 CN598360 TTR0000071
c 997 34 94.4 892 6 CB291093 UTRCS01_0
c 998 34 94.4 892 7 CN598429 TTR0000100
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# ALIGNMENTS

```

RESULT 1
LOCUS HUMGS0003903 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION HUMGS0003903 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
ACCESSION C01909
VERSION C01909.1 GI:1434139
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Okubo,K.
COMMENT BodyMap: human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
sequence 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also

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found there.
FEATURES             source
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /dev_stage="adult"
    /clone_lib="Human adult (K.Okubo)"
    /note="One or more human adult tissue"

ORIGIN
Alignment Scores:      581      Length:      122
Pred. No.:            36.00     Matches:      6
Score:                100.00%   Conservative:  0
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Best Local Similarity: 100.00%   Indels:       0
Query Match:         100.00%   Gaps:         0
DB:                  6

US-10-029-756-20 (1-6) x C01909 (1-122)

Qy 1 PheGlnIlecluhishis 6
Db 100 TTCAGATTGAGCACCAT 117

RESULT 2
LOCUS BF083018/c
DEFINITION QV1-CS0007-180900-376-e08 CS0007 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF083018
VERSION BF083018.1 GI:10876848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 144)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LiCR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV1-CS0007-180
900-376-e08&t3=2000-09-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 7
High quality sequence stop: 143.
FEATURES             source
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    1..144
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /dev_stage="Adult"
    /clone_lib="CS0007"
    /note="Organ: colon_est; Vector: puc18; Site 1: SmaI;
    Site 2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application

```

No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 19 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Alignment Scores:  
Pred. No.: 709 Length: 144  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF083018 (1-144)

Qy 1 PheGlnIleGluHis 6  
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Db 131 TTCAGATTGACCAT 114

RESULT 3  
CO420590  
LOCUS GGEZHC1014H04.g HCl Gallus gallus cDNA clone GGEZHC1014H04, mRNA  
DEFINITION  
sequence.  
ACCESSION CO420590  
VERSION CO420590.1 GI:49636838  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

REFERENCE  
AUTHORS Silva,C.S., Jorge,E.C., Patricio,M., Ledur,M.C. and Coutinho,L.L.  
TITLE Discovery of new genes expressed in the chicken pituitary and hypothalamus

JOURNAL  
COMMENT Unpublished (2004)  
Contact: Clarissa S. Silva  
Laboratory of Animal Biotechnology, Dep. of Animal Production  
ESALQ - University of Sao Paulo  
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
Tel: 55 19 3429 4434  
Fax: 55 19 3429 4285  
Email: cssilva@esalq.usp.br and llcouth@esalq.usp.br  
PCR Primers

## FEATURES

Location/Qualifiers  
1..158  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="GGEZHC1014H04"  
/tissue\_type="pituitary and hypothalamus"  
/dev\_stage="21 days old"  
/lab\_host="DH10B"  
/clone\_lib="HC1"  
/note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI; This cDNA library was constructed with the SuperScript Plasmid System with Gateway technology kit (Invitrogen), following manufacture's protocols. Plasmid DNA was purified using a modified alkaline lysis method. Sequencing reactions were conducted using the kit Big Dye Terminator Cycle Sequencing Ready Reaction (Applied Biosystems) according to the manufacturer's recommendations. Clones were sequenced by the 5' end with T7 primer. Sequencing reactions were analyzed on ABI Prism 3100 Genetic Analyzer (Applied Biosystems). The quality and clustering of the ESTs were analyzed using the softwares Phred/Gap3. Only EST sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."

## ORIGIN

Alignment Scores:

Alignment Scores:  
Pred. No.: 793 Length: 158  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CO420590 (1-158)

Qy 1 PheGlnIleGluHis 6  
|||||

Db 103 TTCAGATTGACCAT 120

RESULT 4

AA841755/c

LOCUS AA841755

DEFINITION MB3D6V6H01T3 Brugia malayi day 6 post-infection third stage larvae

SAW96MLW-BML3d6 Brugia malayi cDNA clone 3D6V6H01 5', mRNA

sequence.

ACCESSION AA841755

VERSION AA841755.1 GI:2923091

KEYWORDS EST.

SOURCE Brugia malayi

ORGANISM Brugia malayi

REFERENCE 1 (bases 1 to 169)

AUTHORS Blaxter,M.L., Waterfall,M., Daub,J., Lizotte-Waniewski,M., Baron,L.

and Jones,S.J.

Genes expressed in day six post-infection, third stage larvae of

Brugia malayi

Unpublished (1997)

Contact: Blaxter ML

Institute of Cell, Animal and Population Biology

University of Edinburgh

Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9

3JT, UK.

Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxter@ed.ac.uk

The ABI trace of this sequence can be viewed at

http://www.sanger.ac.uk/bugia/3D6V6H01T3.html

Seq primer: T3.

FEATURES

Location/Qualifiers

1..169

/organism="Brugia malayi"

/mol\_type="mRNA"

/strain="T3 Labs"

/db\_xref="taxon:6279"

/clone="3D6V6H01"

/sex="mixed"

/dev\_stage="third stage larvae, six days after infection"

/lab\_host="E. coli XLI-Blue"

/clone\_lib="Brugia malayi day 6 post-infection third stage

larvae SAW96MLW-BML3d6"

/note="Vector: lambdaZapII (Unizap XR); Site 1: Eco R I

(5' end); Site 2: Xho I (3' end); Brugia malayi is a

lymphatic filarial nematode parasite of humans. mRNA was

prepared from third stage larvae of Brugia malayi isolated

from the peritoneal cavity of jirds six days after

infection. The mRNA was converted to double stranded cDNA

using reverse transcriptase and oligo(dT) followed by

RNAse H and DNAPol I. The library had 2 x 10E5 independent

recombinants and average insert size was 900 base pairs.

The library was constructed by Michelle Lizotte-Waniewski.

The library is available from The Filarial Genome Project

Resource Center: contact Dr. S.A. Williams, Clark Science

Center, Smith College, Northampton, MA 01063 USA phone +1

413 585 3826 fax +1 413 585 3786 email genome@smith.edu."

ORIGIN

Pred. No.: 859 Length: 169  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA841755 (1-169)

Qy 1 PheGlnIleGluHisHis 6  
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 Db 52 TTTCAAATCGAACCAT 35

# RESULT 5

AI747918 184 bp mRNA linear EST 22-JUN-1999  
 LOCUS u104a01.y1 Sugano mouse kidney mKia Mus musculus cDNA clone  
 DEFINITION IMAGE:2065032 5' similar to TR:060427 BC269730 2. ; mRNA  
 sequence.

AI747918 1 GI:5126182

# ACCESSION

VERSION AI747918.1

# KEYWORDS

SOURCE Mus musculus (house mouse)

# ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 184)  
 AUTHOR Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,  
 Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,  
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
 Waterston,R. and Wilson,R.  
 TITLE The WashU-NCI Mouse EST Project 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:994220

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 69.

Location/Qualifiers

1..184  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CS7BL"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:2065032"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"

/clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII  
 (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA  
 was primed with an oligo(dT) primer  
 [ATCGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was  
 ligated to a DraIII adaptor [TGTTGGCTACTGG], digested  
 and cloned into distinct DraIII sites of the pME18S-FL3  
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
 be used to isolate the cDNA insert. Size selection was  
 performed to exclude fragments <1.5kb. Library  
 constructed by Dr. Sumio Sugano (University of Tokyo  
 Institute of Medical Science). Custom primers for  
 sequencing: 5' end primer CTCTGCTCTAAAGCTCGC and 3' end  
 primer CGACCTGCAGCTCGACCA."

# ORIGIN

Alignment Scores:

Pred. No.: 952 Length: 184  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AI747918 (1-184)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 65 TTCCAGATTGAGCACCAC 82

# RESULT 6

AA369496 196 bp mRNA linear EST 21-APR-1997  
 LOCUS EST80921 Placenta II Homo sapiens cDNA 5' end, mRNA sequence.  
 DEFINITION AA369496  
 ACCESSION AA369496.1 GI:2021816  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

# ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 196)  
 AUTHOR Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.  
 TITLE Rapid cDNA sequencing (expressed sequence tags) from a  
 directionally cloned human infant brain cDNA library  
 Nat. Genet. 4, 373-380 (1993)  
 JOURNAL  
 MEDLINE 94004965  
 PUBMED 8401585

# COMMENT

Other ESTs: THCL52140  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerl@vtigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

# FEATURES

source

1..196  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (inhost):174097"  
 /db\_xref="taxon:9606"  
 /tissue\_type="placenta"  
 /dev\_stage="fetus"  
 /clone\_lib="Placenta II"  
 /note="Organ: placenta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"

# ORIGIN

Alignment Scores:

Pred. No.: 1.03e+03 Length: 196  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA369496 (1-196)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 169 TTCCAGATTGAGCACCAC 186

# RESULT 7

AZ404851/c

# LOCUS

AZ404851 207 bp DNA linear GSS 03-OCT-2000



DEFINITION 1M0173D08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0173D08 F, genomic survey sequence.

ACCESSION AZ404851

VERSION AZ404851.1 GI:10528864

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0173 row: D column: 08  
Seq primer: CGTTGTAAACACGCCGACGT  
Class: plasmid ends  
High quality sequence stop: 207.

## FEATURES

1..207  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0173D08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.1e+03 Length: 207  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AZ404851 (1-207)

Qy 1 PheGlnIleGluHisHis 6  
|||||

99 TTCCAGATCGAGCACCAT 82

RESULT 8  
AW579368/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW579368 240 bp mRNA linear EST 16-MAR-2000  
PM2-DT0062-080100-002-g04 DT0062 Homo sapiens cDNA, mRNA sequence.  
AW579368  
VERSION AW579368.1 GI:7254430  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 240)  
HCGP http://www.ludwig.org.br/ORESTES.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM2&t2=PM2-DT0062-  
080100-002-g04&t3=2000-01-08&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 40  
High quality sequence stop: 240.

FEATURES  
source

1..240  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="DT0062"  
/note="Organ: denis drash; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.31e+03 Length: 240  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW579368 (1-240)

Qy 1 PheGlnIleGluHisHis 6  
|||||

DB 31 TTCCAGATTGAGCACCAT 14

RESULT 9  
BF871924/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BF871924 246 bp mRNA linear EST 17-JAN-2001  
CM4-ET0095-011100-405-h01 ET0095 Homo sapiens cDNA, mRNA sequence.  
BF871924  
VERSION BF871924.1 GI:12262054  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS      1 (bases 1 to 246)
              Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-ET0095-
              01100-405-h01&t3=2000-11-01&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 14
              High quality sequence stop: 246.
              Location/Qualifiers
FEATURES     source
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="ET0095"
                /note="Organ: lung tumor; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from ORSTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.:      1.35e+03      Length:      246
Score:          36.00        Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     100.00%     Indels:        0
DB:              2           Gaps:         0

US-10-029-756-20 (1-6) x BF871924 (1-246)

Qy      1 PheGlnIleGluHisHis 6
        |||||
Db      131 TTCCAGATTGACACCAC 114

RESULT 10
BQ587416/c
LOCUS      BQ587416
DEFINITION S013303-024-010-001-T7 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION  BQ587416
VERSION     BQ587416.1 GI:26116998
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 248)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

```

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and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
PUBMED
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 248 Std Error: 0.00
              Plate: 10 row: 0 column: 01
              Seq primer: T7; GTAATACGACTCATTAGGGC.
              Location/Qualifiers
FEATURES     source
              1..248
                /organism="Beta vulgaris"
                /mol_type="mRNA"
                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"
                /db_xref="GABI:185442"
                /db_xref="taxon:161934"
                /clone="024-010-001"
                /tissue_type="leaf"
                /lab_host="EMDH10B"
                /clone_lib="MPIZ-ADIS-024-leaf"
                /note="vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                orientation:
                SP6-SaII-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN
Alignment Scores:
Pred. No.:      1.36e+03      Length:      248
Score:          36.00        Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     100.00%     Indels:        0
DB:              5           Gaps:         0

US-10-029-756-20 (1-6) x BQ587416 (1-248)

Qy      1 PheGlnIleGluHisHis 6
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Db      195 TTTCNAATTGACATCAT 178

RESULT 11
AL914932
LOCUS      AL914932
DEFINITION AL914932 PJR-Z1+Z2 Danio rerio cDNA clone 147-D03-2, mRNA sequence.
ACCESSION  AL914932
VERSION     AL914932.1 GI:23180229
KEYWORDS   EST.
SOURCE     Danio rerio (zebrafish)
ORGANISM   Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE  1 (bases 1 to 272)
AUTHORS    Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W.,
            Wang,W., Wen,Z. and Peng,J.
            15000 unique zebrafish EST clusters and their future use in
            microarray for profiling gene expression patterns during
            embryogenesis
            Genome Res. 13 (3), 455-466 (2003)
JOURNAL
MEDLINE

```

```

PUBMED
COMMENT
12618376
Contact: Peng J
Lab of Functional Genomics
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore, 117609, Singapore
Email: pengj@imcb.a-star.edu.sg
Clone requests: info@openbiosystems.com
Open Biosystems,
6705 Oodyssey Drive, Huntsville, AL 35806.
Location/Qualifiers
FEATURES
source
1..272
/organism="Danio rerio"
/mol_type="mRNA"
/strain="local wildtype"
/db_xref="taxon:7955"
/clone="147-D03-2"
/tissue_type="whole embryo or fish"
/dev_stage="mixed stages"
/clone_lib="PUR-Z1+Z2"

Alignment Scores:
Pred. No.: 1.52e+03 Length: 272
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AL914932 (1-272)

Qy 1 PheGlnIleGluHisHis 6
Db 23 TTCCAGATCGAGCATCAT 40

RESULT 12
BQ910596/c
LOCUS
DEFINITION BQ910596 291 bp mRNA linear EST 19-AUG-2002
clone QHA14K08, mRNA sequence.
ACCESSION BQ910596
VERSION BQ910596.1 GI:22309375
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE
1 (bases 1 to 291)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig578, see http://cgdb.ucdavis.edu/
for details.
Plate: QHA14 row: K column: 08.
Location/Qualifiers
FEATURES
source
1..291
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA801"
/db_xref="taxon:4232"

/clone="QHA14K08"
/lab_host="E.coli"
/clone_lib="QH ABCDI sunflower RHA801"
/note="Vector: pBRCNASTAB; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=shoots environmental stress
TAG_LIB=QH ABCDI sunflower RHA801
TAG_SEQ=TCGCAACGGG"

ORIGIN
Alignment Scores:
Pred. No.: 1.65e+03 Length: 291
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ910596 (1-291)

Qy 1 PheGlnIleGluHisHis 6
Db 281 TTCCAAATTGAACATCAT 264

RESULT 13
CK855086/c
LOCUS
DEFINITION CK855086 298 bp mRNA linear EST 08-MAR-2004
SWB13CAW35B12SK Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)
Wuchereria bancrofti cDNA clone SWB13CAW35B12 5', mRNA sequence.
ACCESSION CK855086
VERSION CK855086.1 GI:45243709
KEYWORDS EST.
SOURCE Wuchereria bancrofti
ORGANISM Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Wuchereria.
REFERENCE
1 (bases 1 to 298)
Williams,S.A.
Genes Expressed in L3 infective stage larvae of Wuchereria
bancrofti
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
FEATURES
source
1..298
/organism="Wuchereria bancrofti"
/mol_type="mRNA"
/db_xref="taxon:6293"
/clone="SWB13CAW35B12"
/dev_stage="L3 infective stage larvae"
/lab_host="XL1-Blue MRP"
/clone_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from approximately 8,000 L3 isolated
from mosquitoes in Cairo, Egypt and converted to
double-stranded cDNA using reverse transcriptase and
oligo(dT) followed by RNase H and DNA pol I. The library
has 1.0 x 10E6 independent recombinants and the average

```

insert size is ~300 bp. The library was constructed by Michelle. Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.7e+03 Length: 298  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CK855086 (1-298)

Qy 1 PheGlnIleGluHisHis 6  
Db 177 TTTCARATCGAACACCAT 160

## RESULT 14

CG091494 300 bp DNA linear GSS 20-AUG-2003  
LOCUS PUIMK80TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0616N15,  
DEFINITION genomic survey sequence.  
ACCESSION CG091494  
VERSION CG091494.1 GI:33973788  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUIMK80TD  
Contact: Cathy Whitelaw

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: IR  
Class: sheared ends.

## FEATURES

source  
1. .300  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTa0616N15"  
/clone\_lib="ZM 0.6 1.0 KB"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high Cot selected genomic DNA library"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.71e+03 Length: 300  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x CG091494 (1-300)

Qy 1 PheGlnIleGluHisHis 6  
Db 129 TTTCAGATTGACACCAT 112

## RESULT 15

AL914933/c 305 bp mRNA linear EST 06-JUL-2004  
LOCUS AL914933 PJR-Z1+Z2 Danio rerio cDNA clone 127-F03-2, mRNA sequence.  
DEFINITION  
ACCESSION AL914933  
VERSION AL914933.1 GI:23180230  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE  
AUTHORS Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Wang,W., Wen,Z. and Peng,J.

## TITLE

15000 unique zebrafish EST clusters and their future use in

microarray for profiling gene expression patterns during

embryogenesis

Genome Res. 13 (3), 455-466 (2003)

JOURNAL MEDLINE

PUBMED 12618376

## COMMENT

Contact: Peng J  
Lab of Functional Genomics  
Institute of Molecular and Cell Biology  
30 Medical Drive, Singapore, 117609, Singapore  
Email: pengj@imcb.a-star.edu.sg  
Clone requests: info@openbiosystems.com  
Open Biosystems,  
6705 Odyssey Drive, Huntaville, AL 35806.

## FEATURES

source  
1. .305  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="local wildtype"  
/db\_xref="taxon:7955"  
/clone="127-F03-2"  
/tissue\_type="whole embryo or fish"  
/dev\_stage="mixed stages"  
/clone\_lib="PJR-Z1+Z2"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.75e+03 Length: 305  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AL914933 (1-305)

Qy 1 PheGlnIleGluHisHis 6  
Db 141 TTTCAGATCGACCATCAT 124

## RESULT 16

CG091498 307 bp DNA linear GSS 20-AUG-2003  
LOCUS PUIMK80TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0616N15,  
DEFINITION genomic survey sequence.  
ACCESSION CG091498  
VERSION CG091498.1 GI:33973792  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 307)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and

Bennetzen,J.

Maize Genomics Consortium

## TITLE

```

JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUIMK807B
Contact: Cathy Whitelaw
TIGR
7912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..307
/organism="Zea mays"
/mol_type="genomic DNA"
/strains="B73"
/db_xref="taxon:4577"
/clone="ZM8BTA0616N15"
/clone_lib="ZM_0.6-1.0 kb"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+03 Length: 307
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x CG091498 (1-307)

Qy 1 PheGlnlleGluHis 6
Db 165 TTCAGATTGACCAT 182

RESULT 17
CR464551/c 309 bp mRNA linear EST 01-JUL-2004
LOCUS LIONP463C10369 3', mRNA sequence.
DEFINITION
ACCESSION CR464551
VERSION CR464551.1 GI:49596900
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 309)
Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schlueter,T.,
Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Rat ArrayTAG CDNA
Unpublished (2004)
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; LIONP463C10369.
RZPDLIB;
Rat ArrayTAG CDNA
http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=463 Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.
Location/Qualifiers

JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUIMK807B
Contact: Cathy Whitelaw
TIGR
7912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..309
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="LIONP463C10369"
/lab_host="DH10B"
/clone_lib="Rat pBluescript Lion"

ORIGIN
Alignment Scores:
Pred. No.: 1.78e+03 Length: 309
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CR464551 (1-309)

Qy 1 PheGlnlleGluHis 6
Db 306 TTCAGATTGACCCAC 289

RESULT 18
BI432070 316 bp mRNA linear EST 30-APR-2003
LOCUS EST534831 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAL91 5' sequence, mRNA sequence.
ACCESSION BI432070
VERSION BI432070.1 GI:15256760
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 316)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
Bougril,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
Location/Qualifiers
1..316
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="kennebec"
/db_xref="taxon:4113"
/clone="PPCAL91"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
compatible reaction"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University, Fry lab; sequencing:
The Institute for Genomic Research; Whole plants were
challenged with 20,000 sporangia/ml of the compatible p.
infestans isolate US 940480. Leaf tissue was collected at
3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
in liquid nitrogen immediately upon removal. Kennebec
plants showed first symptoms of infection at 48 hours
after inoculation. NOTE: We cannot exclude the
possibility that this sequence is actually derived from
Phytophthora rather than potato."

```

```

ORIGIN
Alignment Scores:
Pred. No.: 1.82e+03 Length: 316
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x B1432070 (1-316)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 196 TTCCAGATTGAGCATCAT 213

RESULT 19
LOCUS B1011761 317 bp mRNA linear EST 13-JUN-2001
DEFINITION CM3-EN0049-050201-714-c08 EN0049 Homo sapiens cDNA, mRNA sequence.
ACCESSION B1011761
VERSION B1011761.1 GI:14415832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 317)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Matzukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&tl2=CM3-EN0049-
050201-714-c08&tl3=2001-02-05&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 317.
FEATURES
source
1. 317
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_libs="EN0049"
/note="Organ: lung normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORFEST PCR (O.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 1.83e+03 Length: 317
Score: 36.00 Matches: 6

ORIGIN
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x B1011761 (1-317)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 195 TTCCAGATTGAGCACCAC 212

RESULT 20
LOCUS CD552411 325 bp mRNA linear EST 11-JUN-2003
DEFINITION B0342D11-5 NIA Mouse E9.5 Whole Embryo cDNA Library (Long) Mus
musculus cDNA clone NIA:B0342D11 IMAGE:30433102 5', mRNA sequence.
ACCESSION CD552411
VERSION CD552411.1 GI:31600142
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 325)
AUTHORS Piao,Y., KO,N.T., Lim,M.K. and Ko,M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Phone: B0342 row: D column: 11
Seq primer: M13 Reverse
High quality sequence stop: 325
POLYA=No.
FEATURES
source
1. 325
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nia:EST:B0342D11-5"
/db_xref="taxon:10090"
/clone_libs="NIA:B0342D11 IMAGE:30433102"
/tissue_type="E9.5 whole embryo"
/dev_stage="whole embryo including extraembryonic tissues
at 9.5-days postcoitum"
/lab_hosts="DH10B"
/clone_libs="NIA Mouse E9.5 Whole Embryo cDNA Library
(Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 16 embryos at 9.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer (Invitrogen:
5'-pGACTAGTTTGTAGATCGAGCGCCGCCCTTTTCTTTT-3')
from 6.1 ug of total RNA, treated with T4 DNA polymerase,
and purified by ethanol-precipitation. The cDNAs were
ligated to Lone-linker LL-Sal4, purified by
phenol/chloroform, and separated from free linkers by
Centricon 100. Then, the cDNAs were amplified by
long-range high fidelity PCR using Ex Taq polymerase
(Takara) with a primer Sal4-S. The products were purified
by phenol/chloroform and Centricon 100. The cDNAs were
digested with SalI and NotI enzymes and cloned into

```



```

library"
/mol_type="mRNA"
/strain="70-15"
/db_xref="taxon:105664"
/clone="mg1005D12f"
/dev_stage="Infection stage, 48hrs, Subtraction with healthy plant"
/clone_lib="Subtracted Rice blast Infection Stage cDNA library"
/notes="Vector: pBluescriptII SK(+) Vector; Rice blast infection stage mRNA population at 48 hrs after inoculation was subtracted with mRNA population of healthy plant."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 1.97e+03 Length: 337
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

```

US-10-029-756-20 (1-6) x AW070147 (1-337)

Qy 1 PheGlnIleGluHis 6

Db 93 TTCCAATCGAGCACCAT 76

## RESULT 23

BQ329017/c

LOCUS BQ329017 341 bp mRNA linear EST 17-MAY-2002

DEFINITION CM3-EN0049-301000-436-c08 EN0049 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ329017

VERSION BQ329017.1 GI:20969093

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 341)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Authors: Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0049-301000-436-c08&t3=2000-10-30&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 40.

## FEATURES

source

```

1..341
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"

```

```

/clone_lib="EN0049"

```

```

/notes="Organ: lung normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 2e+03 Length: 341
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

```

US-10-029-756-20 (1-6) x BQ329017 (1-341)

Qy 1 PheGlnIleGluHis 6

Db 128 TTCAGATTGAGCACCAC 111

## RESULT 24

BF926891/c

LOCUS BF926891 354 bp mRNA linear EST 19-JAN-2001

DEFINITION IL5-NT0228-041200-305-a08 NT0228 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF926891

VERSION BF926891.1 GI:12324619

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 354)

Authors: Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-NT0228-041200-305-a08&t3=2000-12-04&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 353.

## FEATURES

source

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1..354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0228"

```

```

/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

```



tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

ORIGIN
Alignment Scores:
Pred. No.: 2.09e+03 Length: 354
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF926891 (1-354)

QY 1 PheGlnIleGluHis 6
Db 348 TTCCAGATTGACACCAC 331

RESULT 25
W67110
LOCUS me24h09.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:388481 5', mRNA sequence.
ACCESSION W67110
VERSION W67110.1 GI:1375649
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 357)
Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lemon,G., Soares,B., Wilson,R. and
Waterson,K.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marla M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
MGI:240313
Seq primer: ETPRimer
High quality sequence stop: 344.
Location/Qualifiers
1..357
/organism="Mus musculus"
/mol_type="mRNA"
/strain="G57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:388481"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/notes="Vector: pTYT30-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGCGCGCGGAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTYT3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and

```

M.Fatima Bonaldo. "

```

ORIGIN
Alignment Scores:
Pred. No.: 2.11e+03 Length: 357
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x W67110 (1-357)

QY 1 PheGlnIleGluHis 6
Db 322 TTCCAGATTGACACCAC 339

RESULT 26
BH635504
LOCUS 1008005D06.2BL_y1 1008 - RescueMu Grid 1 Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH635504
VERSION BH635504.1 GI:18657741
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 358)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008005 row: 24
Class: transposon-tagged.
Location/Qualifiers
1..358
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid 1"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmldb.iastate.edu and follow the links for
'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Alignment Scores:
Pred. No.: 2.12e+03 Length: 358
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

```

```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x BH635504 (1-358)

Qy 1 PheGlnIleGluHis 6
|||||
Db 273 TTCATATAGACACCAC 290

RESULT 27
AI985774/c
LOCUS
DEFINITION
w20c08.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2508014 3'
similar to TR:060427 O60427 BC269730_2.; mRNA sequence.

ACCESSION
AI985774
VERSION
AI985774.1 GI:5813051
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1662 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 165.
Location/Qualifiers
1. 360
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2508014"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Utl"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

ORIGIN
Alignment Scores:
Pred. No.: 2.13e+03 Length: 360
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AI985774 (1-360)

Qy 1 PheGlnIleGluHis 6
|||||
Db 99 TTCAGATTGACCAT 82

RESULT 28
BY671067
LOCUS
DEFINITION
BY671067 RIKEN full-length enriched, 14.5 days embryo df/df
Rathke's pouches Mus musculus cDNA clone K820015K13 3', mRNA
sequence.
ACCESSION
BY671067.1 GI:27052615
VERSION
BY671067.1 EST.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 368)
Okazaki.Y., Furuno.M., Kasukawa.T., Adachi.J., Bono.H., Kondo.S.,
Nikaido.I., Osato.N., Saito.R., Suzuki.H., Yamanaka.I.,
Kiyosawa.H., Yagi.K., Tomaru.Y., Hasegawa.Y., Nogami.A.,
Schonbach.C., Gojobori.T., Baldarelli.R., Hill.D.P., Bult.C.,
Hume.D.A., Quackenbush.J., Schriml.L.M., Kanapin.A., Matsuda.H.,
Batalov.S., Beisel.K.W., Blake.J.A., Bradt.D., Bruscia.V.,
Chothia.C., Corbani.L.E., Cousins.S., Dalla.E., Dragani.T.A.,
Fletcher.C.F., Forrest.A., Frazer.K.S., Gaasterland.T.,
Gariboldi.M., Gissi.C., Godzik.A., Gough.J., Grimmond.S.,
Gustincich.S., Hirokawa.N., Jackson.I.J., Jarvis.E.D., Kanai.A.,
Kawaji.H., Kawasawa.Y., Kedzierski.R.M., King.B.L., Konagaya.A.,
Kurochkin.I.V., Lee.Y., Lenhard.B., Lyons.P.A., Maglott.D.R.,
Maltais.L., Marchionni.L., McKenzie.L., Miki.H., Nagashima.T.,
Numata.K., Okido.T., Pavan.W.J., Pertea.G., Pesole.G.,
Petrovsky.N., Pillai.R., Pontius.J.U., Qi.D., Ramachandran.S.,
Ravasi.T., Reed.J.C., Reed.D.J., Reid.J., Ring.B.Z., Ringwald.M.,
Sandelin.A., Schneider.C., Sempie.C.A., Setou.M., Shimada.K.,
Sultana.R., Takenaka.Y., Taylor.M.S., Teasdale.R.D., Tomita.M.,
Verardo.R., Wagner.L., Wahlestedt.C., Wang.Y., Watanabe.Y.,
Wells.C., Wilming.L.G., Wynshaw-Boris.A., Yanagisawa.M., Yang.I.,
Yang.L., Yuan.Z., Zavolan.M., Zhu.Y., Zimmer.A., Carninci.P.,
Hayatsu.N., Hirozane-Kishikawa.T., Konno.H., Nakamura.M.,
Sakazume.N., Sato.K., Shiraki.T., Waki.K., Kawai.J., Aizawa.K.,
Arakawa.T., Fukuda.S., Hara.A., Hashizume.W., Imotani.K., Ishii.Y.,
Itoh.M., Kagawa.I., Miyazaki.A., Sakai.K., Sasaki.D., Shibata.K.,
Shingawa.A., Yasunishi.A., Yoshino.M., Waterston.R., Lander.E.S.,
Rogers.J., Birney.E. and Hayashizaki.Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa.K., Akimura.T., Arakawa.T., Carninci.P., Fukuda.S.,
Hirozane.T., Imotani.K., Ishii.Y., Itoh.M., Kawai.J., Konno.H.,
Miyazaki.A., Murata.M., Nakamura.M., Nomura.K., Numazaki.R.,
Ohno.M., Sakai.K., Sakazume.N., Sasaki.D., Sato.K., Shibata.K.,
Shiraki.T., Tagami.M., Waki.K., Watahiki.A., Muramatsu.M. and
Hayashizaki.Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

```

Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
source

Location/Qualifiers  
1..368  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="K820015K13"  
/tissue\_type="Rathke's pouches"  
/dev\_stage="14.5 days embryo df/df"  
/clone\_libs="RIKEN full-length enriched, 14.5 days embryo df/df Rathke's pouches"

ORIGIN

Alignment Scores:  
Pred. No.: 2.19e+03 Length: 368  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BY671067 (1-368)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 56 TTCAGATTGACACCAC 73

RESULT 29

AW045920/c  
LOCUS AW045920 376 bp mRNA linear EST 18-SEP-1999  
DEFINITION UI-M-BH1-aku-d-02-0-UI-s1 NIH\_BMAP\_M\_S2 Mus musculus cDNA clone  
UI-M-BH1-aku-d-02-0-UI 3', mRNA sequence.

ACCESSION AW045920  
VERSION AW045920.1 GI:5906449  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 376)  
Bonaldo M.F., Lennon G. and Soares M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548

COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: m8st@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized amygdala library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.  
Seg primer: M13 Forward  
POLYA=Yes

FEATURES  
source

Location/Qualifiers  
1..376  
/organism="Mus musculus"

/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-BH1-aku-d-02-0-UI"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_libs="NIH\_BMAP\_M\_S2"  
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP\_M\_S2 library is a subtracted library derived from NIH\_BMAP\_M\_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH\_BMAP\_M\_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.  
TAG\_ISSUE=amygdala  
TAG\_LIB=NIH\_BMAP\_M\_S2  
TAG\_SEQ=GTGAG"

Alignment Scores:  
Pred. No.: 2.25e+03 Length: 376  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW045920 (1-376)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 325 TTCAGATTGACACCAC 308

RESULT 30

BP652482  
LOCUS BP652482 383 bp mRNA linear EST 27-JUN-2004  
DEFINITION BP652482 RAF119 Arabidopsis thaliana cDNA clone RAF119-93-E15 3', mRNA sequence.

ACCESSION BP652482  
VERSION BP652482.1 GI:49303952  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 383)  
Seki M., Narusaka M., Kamiya A., Ishida J., Satou M., Sakurai T., Nakajima M., Enju A., Akiyama K., Ono Y., Muramatsu M., Hayashizaki Y., Kawai J., Carninci P., Itoh M., Ishii Y., Arakawa T., Shibata K., Shinagawa A. and Shinozaki K.  
Functional annotation of a full-length Arabidopsis cDNA collection  
Science 296 (5565), 141-145 (2002)

JOURNAL 21932900  
MEDLINE 11910074  
PUBMED

COMMENT Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060

Email: msek@rtc.riken.go.jp  
reversed clone; Please visit our web site  
(<http://pfweb.gsc.riken.go.jp/>) for further details.

FEATURES  
source

Location/Qualifiers  
1..383  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"

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/db xref="taxon:3702"
/clone="RAFL19-93-E15"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL19"
/note="Site 1: BamHI; Site 2: SalI; Subtraction Library"

ORIGIN

Alignment Scores:
Pred. No.:      2.3e+03      Length:      383
Score:          36.00      Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              2          Gaps:      0

US-10-029-756-20 (1-6) x BP652482 (1-383)

Qy      1 PheGlnIleGluHis 6
Db      247 TTCCAGATAGACACCAC 264

RESULT 31
LOCUS   AW437559
DEFINITION 78818 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW437559
VERSION   AW437559.1 GI:6972865
KEYWORDS EST.
SOURCE   Bos taurus (cow)
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 385)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
          Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
          Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
          Chitko-McKown,C.G., Pette,G., Holt,I., Karamycheva,S., Liang,F.,
          Quackenbush,J. and Keefe,J.W.
          Sequence evaluation of four pooled-tissue normalized bovine cDNA
          libraries and construction of a gene index for cattle
JOURNAL   Genome Res. 11 (4), 626-630 (2001)
MEDLINE   21180013
PUBMED    11282378
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 20
          and -minmatch 12 options.
          PCR Primers
          FORWARD: AGGAACAGCTATGACCAT
          BACKWARD: GTTTTCCAGTCACGACG
          Plate: 42 row: H column: 12
          Seq primer: ATTAGGTGACACTATAG.

FEATURES
          source
            1..385
            /organism="Bos taurus"
            /mol_type="mRNA"
            /db_xref="taxon:9913"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /clone_lib="MARC 1BOV"
            /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
            Library made from pooled tissue from lymph node, ovary,
            fat, hypothalamus, and pituitary."

ORIGIN

Alignment Scores:
Pred. No.:      2.31e+03      Length:      385
Score:          36.00      Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              2          Gaps:      0

US-10-029-756-20 (1-6) x AW437559 (1-385)

Qy      1 PheGlnIleGluHis 6
Db      8 TTCCAGATCGAGCACCAT 25

RESULT 32
LOCUS   BM702968
DEFINITION UI-E-CLI-afe-f-03-0-UI.r1 UI-E-CLI Homo sapiens cDNA clone
ACCESSION BM702968
VERSION   BM702968.1 GI:19016226
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 386)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    8889548
COMMENT   Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: bento-soares@uiowa.edu
          Tissue Procurement: Dr. Gregg Hageman
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research
          Genetics (www.resgen.com).
          Seq primer: M13 Reverse.
          Location/Qualifiers
            1..386
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="UI-E-CLI-afe-f-03-0-UI"
            /tissue_type="human retina"
            /dev_stage="adult"
            /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
            /clone_lib="UI-E-CLI"
            /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
            modified polylinker; Site 1: EcoR I; Site 2: Not I;
            UI-E-CLI is a normalized cDNA library containing the
            following tissue(s): retina. The library was constructed
            according to Bonaldo, Lennon and Soares, Genome Research,
            6:791-806, 1996. First strand cDNA synthesis was primed
            with an oligo-dT primer containing a Not I site. Double
            stranded cDNA was ligated to an EcoR I adaptor, digested
            with Not I, and cloned directionally into pT7T3-Pac
            vector. The oligonucleotide used to prime the synthesis of
            first-strand cDNA contains a library tag sequence that is
            located between the Not I site and the (dT)18 tail. The
            sequence tag for this library is CCGCG. This library was
            created for the program, Gene Discovery in the Visual
            System, supported by National Eye Institute (NEI)."
```

ORIGIN

Alignment Scores:

```

Alignment Scores:
Pred. No.: 2.32e+03 Length: 386
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BM702968 (1-386)

QY 1 PheGlnlleGluHis 6
DB 21 TTCACATCGAGCACCAC 38

RESULT 33
LOCUS AA428359 387 bp mRNA linear EST 16-OCT-1997
DEFINITION zw32h10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:771043 5' similar to WP:W08D2.4 C806559 ;, mRNA sequence.
ACCESSION AA428359
VERSION AA428359.1 GI:2112346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 387)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 423
Seq primer: -28mi3 rev2 ET from Amersham
High quality sequence stop: 348.
FEATURES
source
1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980917"
/db_xref="taxon:9606"
/clone="IMAGE:771043"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACCATCGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 2.33e+03 Length: 387
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 0 Gaps: 0

US-10-029-756-20 (1-6) x BM702968 (1-386)

QY 1 PheGlnlleGluHis 6
DB 229 TTTCAGATGAGCACCAC 246

US-10-029-756-20 (1-6) x AA428359 (1-387)

QY 1 PheGlnlleGluHis 6
DB 94 TTCACATCGAGCACCAC 111

RESULT 34
LOCUS BH635847 387 bp DNA linear GSS 14-FEB-2002
DEFINITION 1008007E01.1EL_y1 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.
ACCESSION BH635847
VERSION BH635847.1 GI:18658084
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 387)
AUTHORS Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008007 row: 24
Class: transposon-tagged.
FEATURES
source
1..387
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmldb.iastate.edu and follow the links for
'RescueMu'. Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
ORIGIN
Alignment Scores:
Pred. No.: 2.33e+03 Length: 387
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x BH635847 (1-387)

QY 1 PheGlnlleGluHis 6
DB 229 TTTCAGATGAGCACCAC 246

```

```

RESULT 35
BE097869/c
LOCUS      BE097869      388 bp      mRNA      linear      EST 12-JUN-2000
DEFINITION UI-R-B01-aqc-h-02-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone
ACCESSION BE097869
VERSION   BE097869.1 GI:8488800
KEYWORDS  EST.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
REFERENCE 1 (bases 1 to 388)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    8889548
COMMENT   Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9585
          Email: bento-soares@uiowa.edu
          The sequence contained an oligo-dT track that was present in the
          oligonucleotide that was used to prime the synthesis of first
          strand cDNA and therefore this may represent a bonafide poly A
          tail. The sequence tag present in the cDNA between the NotI site
          and the oligo-dT track served to identify it as a clone from the
          normalized hypothalamus library cDNA Library Preparation: M.B.
          Soares Lab Clonodistribution: clones will be available through
          Research Genetics (www.resgen.com)
          Seq primer: M13 Forward
          POLYA-Yes.

FEATURES             Location/Qualifiers
     source            1..388
     -organism="Rattus norvegicus"
     -mol_type="mRNA"
     -strain="Sprague-Dawley"
     -db_xref="taxon:10116"
     -clones="UI-R-B01-aqc-h-02-0-UI"
     -dev_stage="adult"
     -lab_host="DHI0B (Life Technologies)"
     -clone_lib="UI-R-B01"
     -note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_TISSUE=hypothalamus
TAG_LIB=UI-R-B01
TAG_SEQ=GATGC"

ORIGIN
Alignment Scores:      2.34e+03      Length:      388
Pred. No.:             36.00         Matches:      6
Score:                 100.00%        Conservative: 0
Percent Similarity:    100.00%        Mismatches:  0
Best Local Similarity: 100.00%        Indels:       0
Query Match:           100.00%        Gaps:         2
DB:

US-10-029-756-20 (1-6) x BE097869 (1-388)

```

```

Qy      1 PheGlnIleGluHisHis 6
Db      337 TTCAGATTGACACCAC 320

RESULT 36
CB774012
LOCUS      CB774012      393 bp      mRNA      linear      EST 16-MAY-2003
DEFINITION AMNNUC-MRP84-00130-F3-A mrpe4 (10380) Rattus norvegicus cDNA clone
ACCESSION CB774012
VERSION   CB774012.1 GI:29862403
KEYWORDS  EST.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
REFERENCE 1 (bases 1 to 393)
AUTHORS   Angen EST Program.
TITLE     Angen Rat EST Program
JOURNAL   Unpublished (2003)
COMMENT   Contact: Dan Fitzpatrick
          Angen, Inc
          One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
          Tel: 805 447-4881
          Plate: 00130 row: f column: 3.

FEATURES             Location/Qualifiers
     source            1..393
     -organism="Rattus norvegicus"
     -mol_type="mRNA"
     -db_xref="taxon:10116"
     -clone="mrpe4-00130-f3"
     -tissue_type="placenta embryo"
     -clone_lib="mrpe4 (10380)"
     -notes="vector: pSPORT1; Site_1: SalI; Site_2: NotI;
placenta embryo day 17"

ORIGIN
Alignment Scores:      2.37e+03      Length:      393
Pred. No.:             36.00         Matches:      6
Score:                 100.00%        Conservative: 0
Percent Similarity:    100.00%        Mismatches:  0
Best Local Similarity: 100.00%        Indels:       0
Query Match:           100.00%        Gaps:         0
DB:

US-10-029-756-20 (1-6) x CB774012 (1-393)

```

```

Qy      1 PheGlnIleGluHisHis 6
Db      361 TTCAGATTGACACCAC 378

```

```

RESULT 37
AA279631
LOCUS      AA279631      398 bp      mRNA      linear      EST 15-AUG-1997
DEFINITION z86R09.r1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:704417 5'
ACCESSION AA279631
VERSION   AA279631.1 GI:1921149
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 398)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL   Tumor Gene Index
COMMENT   Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          This clone is available royalty-free through LLNL ; contact the

```

IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 790 Std Error: 0.00  
 Seq primer: -28mi3 rev2 ET from Amersham  
 High quality sequence stop: 369.

# FEATURES

source  
 1..398  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:704417"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_GCB1"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, Igp-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATGTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3', 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.41e+03 Length: 398  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA279631 (1-398)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 153 TTCAGATCGAGCACCAC 170

## RESULT 38

BM716358  
 LOCUS BM716358 402 bp mRNA linear EST 28-FEB-2002  
 DEFINITION UI-E-C11-age-i-20-0-UI-r2 UI-E-C11 Homo sapiens cDNA clone  
 UI-E-C11-age-i-20-0-UI 5', mRNA sequence.

ACCESSION BM716358.1 GI:19029616

VERSION BM716358.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 402)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477

MEDLINE 8889548

PUBMED

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

# FEATURES

source

1..402  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-C11-age-i-20-0-UI"  
 /tissue\_type="RPE and Choroid"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-C11"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-C11 is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.44e+03 Length: 402  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BM716358 (1-402)

Qy 1 PheGlnIleGluHisHis 6

|||||

Db 358 TTCAGATTGAGCACCAT 375

## RESULT 39

BM7079544  
 LOCUS BM7079544 408 bp mRNA linear EST 18-OCT-2000  
 DEFINITION 230188 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.  
 ACCESSION BM7079544  
 VERSION BM7079544.1 GI:10873383

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Bases 1 to 408)

Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,

Vallet,J.,Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,

Quackenbush,J. and Keeler,J.W.

Porcine gene discovery by normalized cDNA-library sequencing and

EST cluster assembly

Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL 22213789

MEDLINE 12226715

PUBMED

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -minmatch 12 options.

PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTACGACG  
 Plate: 46 row: G column: 17  
 Seq primer: ATTTAGGTGACACTATAG.  
 Location/Qualifiers  
 1..408  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="WARC 2PIC"

## FEATURES

source

/note=vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from testis, ovary,  
 endometrium, hypothalamus, pituitary, and placenta."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.48e+03 Length: 408  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF079544 (1-408)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 135 TTTCAGATTGACCAT 152

## RESULT 40

CB338121/c

## LOCUS

DEFINITION kb62g09.y1 Brugia malayi L3 pAMP1 v2 Brugia malayi cDNA 5' similar to TR:O61388 O61388 DELTA6-FATTY-ACID-DESATURASE. [2] TR:Q23221 ;, mRNA sequence.

## ACCESSION

CB338121

## VERSION

CB338121.1

## KEYWORDS

EST.

## SOURCE

Brugia malayi

## ORGANISM

Brugia malayi

## REFERENCE

1 (bases 1 to 408)

## AUTHORS

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,

Tsagariehvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R., and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Nematodes were provided by Dr. Ben-Wen Li and Dr. Gary Weil of

Washington University, St. Louis, MO (weillab@imgate.wustl.edu).

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gibco.

Location/Qualifiers

1..408

/organism="Brugia malayi"

/mol\_type="mRNA"

/db\_xref="taxon:6279"

/dev\_stage="L3"

/clone\_lib="Brugia malayi L3 pAMP1 v2"

/note=vector: pAMP1 (Invitrogen); Site 1: NotI; Site 2: SalI; The library was constructed by Amy Rush, Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Ben-Wen Li and Dr. Gary Weil of Washington University, St. Louis, MO (weillab@imgate.wustl.edu)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.48e+03 Length: 408  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB338121 (1-408)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 184 TTTCAGATTGACCAT 167

## RESULT 41

BP664452

## LOCUS

DEFINITION BP664452 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-12-G01 3', mRNA sequence.

## ACCESSION

BP664452

## VERSION

BP664452.1

## KEYWORDS

EST.

## SOURCE

Arabidopsis thaliana

## ORGANISM

Arabidopsis thaliana

## REFERENCE

1 (bases 1 to 410)

## AUTHORS

Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,

Nakajima, M., Enju, A., Akiyama, K., Ono, Y., Muramatsu, M.,

Hayaishizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,

Arakawa, T., Shibata, K., Shinagawa, A., and Shinozaki, K.

Functional annotation of a full-length Arabidopsis cDNA collection

Science 296 (5565), 141-145 (2002)

21932900

## JOURNAL

11910074

## MEDLINE

## PUBMED

## COMMENT

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msek@tc.riken.go.jp

reversed clone; please visit our web site

(http://pfgweb.gsc.riken.go.jp/) for further details.

## FEATURES

source

1..410

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="RAFL21-12-G01"

/lab\_host="DH10B"

/clone\_lib="RAFL21"

/note="Site 1: BamHI; Site 2: SalI; Subtraction Library. The sequence was obtained from samples subjected to various stress and plant hormones-treated"

## ORIGIN

Alignment Scores:

Pred. No.: 2.5e+03

Length: 410



Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BP664452 (1-410)

Qy 1 PheGlnIleGluHis 6

Db 331 TTTCAATCGAACACAC 348

RESULT 42

CB803565

LOCUS CB803565 410 bp mRNA linear EST 16-MAY-2003

DEFINITION AMGNNUC:MRPE4-00118-B12-A mrpe4 (10380) Rattus norvegicus cDNA

clone mrpe4-00118-b12 5', mRNA sequence.

ACCESSION CB803565

VERSION CB803565.1 GI:29918875

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 410)

AUTHORS Angen EST Program.

TITLE Angen Rat EST Program

JOURNAL Unpublished (2003)

COMMENT Contact: Dan Fitzpatrick

Amgen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00118 row: b column: 12.

Location/Qualifiers

1..410

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clone="mrpe4-00118-b12"

/tissue\_type="placenta embryo"

/note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI;

placenta embryo day 17"

ORIGIN

Alignment Scores:

Pred. No.: 2.5e+03 Length: 410

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB803565 (1-410)

Qy 1 PheGlnIleGluHis 6

Db 328 TTCAGATTGACACAC 345

RESULT 43

BE019170

LOCUS BE019170 411 bp mRNA linear EST 06-JUN-2000

DEFINITION bb49d08.y1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3009999 5'

similar to TR:060427 060427 BC269730 2.; mRNA sequence.

ACCESSION BE019170

VERSION BE019170.1 GI:8279231

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 411)

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: bb49d08.x1

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

Seq primer: -40RP from Gibco

High quality sequence stop: 282.

FEATURES

source

1..411

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3009999"

/tissue\_type="rhabdomyosarcoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_17"

/note="Organ: muscle; Vector: pOTB7; Site\_1: EcoRI;

Site\_2: XhoI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.: 2.5e+03 Length: 411

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE019170 (1-411)

Qy 1 PheGlnIleGluHis 6

Db 229 TTCAGATTGACACCAT 246

RESULT 44

BQ491147/c

LOCUS BQ491147 413 bp mRNA linear EST 31-OCT-2002

DEFINITION BQ491147

ACCESSION BQ491147

VERSION BQ491147.1 GI:24434615

KEYWORDS EST.

SOURCE

Paracoccidioides brasiliensis

Paracoccidioides brasiliensis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Paracoccidioides.

REFERENCE 1 (bases 1 to 413)

AUTHORS

Goldman,G.H., dos Reis Marques,E., Duarte Ribeiro,D.C., de Souza

Bernardes,L.A., Outapin,A.C., Vitorelli,P.M., Savoldi,M.,

Senighini,C.P., de Oliveira,R.C., Nunes,L.R., Travassos,L.R.,

Puccia,R., Batista,W.L., Ferreira,L.E., Moreira,J.C., and

Bogosian,A.P., Tekala,F., Nobrega,M.P., Nobrega,F.G. and

Goldman,M.H.

Expressed sequence tag analysis of the human pathogen

Paracoccidioides brasiliensis yeast phase: identification of

putative homologues of Candida albicans virulence and pathogenicity

genes

Eukaryot. Cell 2 (1), 34-48 (2003)

Contact: Gustavo Henrique Goldman

Laboratory of Molecular Biology

Universidade de Sao Paulo - USP - FCFRP  
Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil  
Email: ggoldman@usp.br.

#### FEATURES

source  
Location/Qualifiers  
1. .413  
/organism="Paracoccidioides brasiliensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:121759"  
/clone\_lib="PB0001"

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.52e+03 Length: 413  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ491147 (1-413)

Qy 1 PheGlnIleGluHis 6

Db 170 TTCCAGATTGACATCAT 153

#### RESULT 45

BB783485  
LOCUS BB783485 RIKEN full-length enriched, brain CRL-1443 BC3H1 cDNA Mus  
DEFINITION musculus cDNA clone G43008K22 3', mRNA sequence.  
ACCESSION BB783485  
VERSION BB783485.1 GI:16951981

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

1 (bases 1 to 414)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,  
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,  
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,  
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,  
Okazaki,Y., Okido,T., Saito,K., Sakai,C., Sakai,K., Sakazume,N.,  
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.  
2001)

Unpublished (2001)

#### JOURNAL

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,  
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.  
and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,  
Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

e mouse tissues.

#### FEATURES

source  
Location/Qualifiers  
1. .414  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C3H"  
/db\_xref="taxon:10090"  
/clone="G43008K22"  
/tissue\_type="brain"  
/cell\_line="CRL-1443 BC3H1"  
/clone\_lib="RIKEN full-length enriched, brain CRL-1443  
BC3H1 cDNA"

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.52e+03 Length: 414  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BB783485 (1-414)

Qy 1 PheGlnIleGluHis 6

Db 29 TTCCAGATTGACACCAC 46

#### RESULT 46

LOCUS AU283982/c

DEFINITION AU283982 Molgula tectiformis library Molgula tectiformis cDNA clone  
MT08B2G01R 5', mRNA sequence.  
ACCESSION AU283982  
VERSION AU283982.1 GI:26023516

KEYWORDS EST.

SOURCE Molgula tectiformis

ORGANISM Molgula tectiformis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
Stolidobranchia; Molgulidae; Molgula.  
1 (bases 1 to 416)

AUTHORS Takada,N., Murakami,S.D., Swalla,B.J. and Satoh,N.

TITLE EST analysis of tailless ascidian M. tectiformis

JOURNAL Unpublished (2002)

COMMENT Contact: Seiko D. Murakami

Graduate School of Science, Department of Zoology

Kyoto University

Sakyo-ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4095

Fax: 81-75-705-1113

Email: seiko@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

source

1. .416  
/organism="Molgula tectiformis"  
/mol\_type="mRNA"  
/db\_xref="taxon:30286"  
/clone="MT08B2G01R"  
/clone\_lib="Molgula tectiformis library"

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.54e+03 Length: 416  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AU283982 (1-416)

QY 1 PheGlnlleGluHis 6  
 DB 410 TTCCAAATCGAACCAT 393

RESULT 47  
 AA430733  
 LOCUS  
 DEFINITION zw20g08.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone  
 IMAGE:769886 5' similar to WP:W08D2.4 CE06559 ;, mRNA sequence.

ACCESSION  
 AA430733  
 VERSION  
 AA430733.1 GI:2111272  
 KEYWORDS  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES  
 Location/Qualifiers  
 1..418  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5973761"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:769886"  
 /sex="Female"  
 /tissue\_type="ovarian tumor"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares ovary tumor NbHOT"  
 /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGAGCGCGCGGTTTTTTTTTTTTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.55e+03 Length: 418  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA430733 (1-418)

QY 1 PheGlnlleGluHis 6  
 DB 95 TTCCAGATTGACCAT 112

RESULT 48  
 AA488546  
 LOCUS  
 DEFINITION ab37g09.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone

IMAGE:843040 5' similar to WP:W08D2.4 CE06559 ;, mRNA sequence.  
 AA488546  
 VERSION  
 AA488546.1 GI:2215977  
 KEYWORDS  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-NCI human EST Project  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 656 Std Error: 0.00  
 Seq primer: -28ml3 rev1 ET from Amersham  
 High quality sequence stop: 359.  
 Location/Qualifiers  
 1..418  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:843040"  
 /sex="female"  
 /dev\_stage="HeLa S3 cell line"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene HeLa cell s3 937216"  
 /note="Vector: pBluescript SK-; Site 1: SmaRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3 epitheloid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR Vector. -5' adaptor sequence: 5' GAATTCGCGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.55e+03 Length: 418  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA488546 (1-418)

QY 1 PheGlnlleGluHis 6  
 DB 246 TTCCAGATTGACCAT 263

RESULT 49  
 CB764557  
 LOCUS  
 DEFINITION AMGNNUC:MRPE4-00118-B11-A mrpe4 (10380) Rattus norvegicus cDNA clone mrpe4-00118-b11 5', mRNA sequence.

ACCESSION  
 CB764557  
 VERSION  
 CB764557.1 GI:29852948  
 KEYWORDS  
 EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus

REFERENCE  
 AUTHORS Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 419)  
 Amgen EST Program.

TITLE Angen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Angen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00118 row: b column: 11.

#### FEATURES

Location/Qualifiers  
1. .419  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="mrpe4-00118-b11"  
/tissue\_type="placenta embryo"  
/clone\_lib="mrpe4 (10380)"  
/note="vector: pSPOR1; Site\_1: SalI; Site\_2: NotI;  
placenta embryo day 17"

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.56e+03 Length: 419  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB764557 (1-419)

Qy 1 PheGlnIleGluHisHis 6

Db 317 TTCCAGATTGAACACCAC 334

#### RESULT 50

AW297013/c

#### LOCUS

DEFINITION UI-H-BW0-ajf-d-04-0-UI-s1 NCI CGAP\_Sub6 Homo sapiens cDNA clone  
IMAGE:2731447 3', mRNA sequence.

#### ACCESSION

AW297013

#### VERSION

AW297013.1 GI:6703649

#### KEYWORDS

#### SOURCE

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dt track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
POLYA=Yes.

#### FEATURES

Location/Qualifiers  
1. .420  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2731447"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI-CGAP\_Sub6"

/note="vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; NCI CGAP Sub6  
is a subtracted library derived from BW, which consists of  
a mixture of four normalized libraries: NCI\_CGAP\_Brn50,

NCI CGAP Lul3, NCI CGAP Ov18, GBC1. The NCI CGAP Sub6  
library had 7 million recombinants. A single-stranded DNA  
preparation of BW was used as a tracer in a subtractive  
hybridization with a driver comprising: the IMAGE pool  
(NCI-CGAP\_Kid3 pool 1 LLAM 3334-3337, 3682-3683,  
3798-3803 (IMAGE Clones 132376-132391,  
145608-145675, 150052-150285); NCI CGAP Kid5 pool 1  
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones  
1323912-1325831, 1471368-1472903, 1492104-1493255);  
NCI-CGAP\_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE  
Clones 1414920-1417991, 1520904-1522439); NCI-CGAP\_C4  
pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE  
Clones 1257096-1258631, 1469064-1470983,  
1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459,  
2758-2759, 3062-3068 (IMAGE Clones 985608-986759,  
1101192-1101959, 1217928-1220615); NCI-CGAP\_Col10 pool 1  
LLAM 2644-2653, 2871-2872 (IMAGE Clones  
1057416-1061255, 1144584-1145351). (50% of the driver  
population), plus a pool of 3,840 arrayed clones from  
NCI CGAP Sub1 (IMAGE Clones 2708616-2710535) and  
NCI-CGAP\_Sub2 (IMAGE Clones 2710536-2712455) (20% of  
the driver population), plus a pool of 11,136 clones from  
NCI-CGAP\_Sub3 (IMAGE Clones 2712456-2723591) (30% of  
the driver population). Subtraction was performed as  
previously described [Bonaldo, Lennon & Soares (1996):  
Normalization and Subtraction: Two Approaches To  
Facilitate Gene Discovery. Genome Research 6, 791-806.  
TAG\_TISSUE=lung  
TAG\_LIB=NCI CGAP-Lul3  
TAG\_SEQ=GCCGG"

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.57e+03 Length: 420  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW297013 (1-420)

Qy 1 PheGlnIleGluHisHis 6

Db 414 TTCCAGATTGAACACCAC 397

#### RESULT 51

CF140245

#### LOCUS

DEFINITION UI-HF-CB0-abg-b-09-0-UI-r1 NIH\_MGC\_210 Homo sapiens cDNA clone  
IMAGE:3097937 5', mRNA sequence.

#### ACCESSION

CF140245

#### VERSION

CF140245.1 GI:33255689

#### KEYWORDS

#### SOURCE

#### ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 421)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

#### JOURNAL

97044477

#### MEDLINE

8889548

#### COMMENT

Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Tim Ratliff

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/humanfl.html>  
 Seq primer: pYX-5.

# FEATURES

Location/Qualifiers  
 1..421

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3097937"

/tissue\_type="CNCAP(3)T-225 cell line"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH MGC 210"

/note="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I;  
 Site 2: Not I; The library was constructed according  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with Not I and then cloned  
 directionally into pT7T3 Pac vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is CCCAC. Tissue was provided by Tim Ratliff."

# ORIGIN

Alignment Scores:  
 Pred. No.: 2.58e+03 Length: 421  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CF140245 (1-421)

Qy 1 PheGlnIleGluHis 6

Db 198 TTCCAGATTGAGCACCAC 215

# RESULT 52

CO707465/c

LOCUS

DEFINITION DG32-82122 DG32-liver Canis familiaris cDNA 3', mRNA linear EST 26-JUL-2004

ACCESSION CO707465

VERSION CO707465.1 GI:50656167

KEYWORDS EST.

SOURCE

ORGANISM

Canis familiaris (dog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,

Henrich,J. and Loebeert,R.

Dog arrayTAG cDNA clone collection

Unpublished (2004)

Contact: Thomas Schlueter

LION Bioscience AG

Walhoferstrasse 98, D-69123 Heidelberg, Germany

Tel: +49 6221 4038 150

Fax: +49 6221 4038 290

Email: Thomas.Schlueter@lionbioscience.com.

Location/Qualifiers

1..421

/organism="Canis familiaris"

/mol\_type="mRNA"

/strain="Beagle"

/db\_xref="taxon:9615"

/tissue\_type="liver"

/dev\_stage="adult"

/lab\_host="DH10B"

# ORIGIN

Alignment Scores:

Pred. No.: 2.58e+03 Length: 421  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CO707465 (1-421)

Qy 1 PheGlnIleGluHis 6

Db 294 TTCCAGATTGAGCACCAC 277

# RESULT 53

CB762663

LOCUS

DEFINITION AMGNNUC:NRHW1-00304-E12-A W rat hypo+pit (10478) Rattus norvegicus

ACCESSION CB762663

VERSION CB762663.1 GI:29851054

KEYWORDS EST.

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 423)

Angen EST Program.

Angen Rat EST Program

Unpublished (2003)

JOURNAL

COMMENT

Contact: Dan Fitzpatrick

Angen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00304 row: e column: 12.

Location/Qualifiers

1..423

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clone="nrhw1-00304-e12"

/tissue\_type="hypo+pit"

/clone\_lib="W rat hypo+pit (10478)"

/note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; W rat

hypo+pit Wistar rat"

# ORIGIN

Alignment Scores:

Pred. No.: 2.59e+03 Length: 423  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB762663 (1-423)

Qy 1 PheGlnIleGluHis 6

Db 279 TTCCAGATTGAGCACCAC 296

# RESULT 54

AV615350/c

LOCUS

DEFINITION AV615350 Bos taurus adipocyte cell line Bos taurus cDNA clone

ACCESSION AV615350

VERSION AV615350.1 GI:9751020

KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 429)  
AUTHORS Takasuga A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.  
and Sugimoto, Y.  
TITLE Establishment of a high throughput EST sequencing system using  
poly(A) tail-removed cDNA libraries and determination of 36,000  
bovine ESTs  
JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)  
MEDLINE 21570554  
PUBMED 11713328  
COMMENT Contact: Yoshikazu Sugimoto  
Animal Genetics Division  
Shirakawa Institute of Animal Genetics  
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan  
Tel: 81-248-25-5641  
Fax: 81-248-25-5725  
Email: kazusugi@ocn.ocn.ne.jp  
Single pass sequencing.  
This clone was obtained from a polyA-deleted cDNA library.  
FEATURES  
source  
1..429  
Location/Qualifiers  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clones="E1AD011C10"  
/cell\_type="an adipocyte cell line"  
/lab\_host="DH10B"  
/clone\_lib="Bos taurus adipocyte cell line"  
/note="Vector: pZn1; Site\_1: SalI; Site\_2: NotI; Poly A  
was deleted from a NotI site"  
ORIGIN  
Alignment Scores:  
Pred. No.: 2.64e+03 Length: 429  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-10-029-756-20 (1-6) x AV615350 (1-429)  
Qy 1 PheGlnIleGluHisHis 6  
Db 204 TTCCAGATTGAGCACCAT 197  
RESULT 55  
W53753  
LOCUS Mus musculus 429 bp mRNA linear EST 03-JUN-1996  
DEFINITION md12f10.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA  
clone IMAGE:368203 5' similar to PIR:S54809 S54809 delta 6  
deaturase - Spirulina platensis ; mRNA sequence.  
ACCESSION W53753  
VERSION W53753.1 GI:1357588  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 429)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
TITLE The WashU-HHMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:229635  
Possible reversed clone: similarity on wrong strand  
Seq primer: ETPRimer  
High quality sequence stop: 346.  
FEATURES  
source  
1..429  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:368203"  
/sex="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse embryo NbME13.5 14.5"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT  
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2  
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne  
State Univ., from 2 ]; double-stranded cDNA was ligated to  
Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pT7T3 vector. Library went through one round of  
normalization, and was constructed by Bento Soares and  
M.Patima Bonaldo. "  
ORIGIN  
Alignment Scores:  
Pred. No.: 2.64e+03 Length: 429  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0  
US-10-029-756-20 (1-6) x W53753 (1-429)  
Qy 1 PheGlnIleGluHisHis 6  
Db 322 TTCCAGATTGAGCACCAC 339  
RESULT 56  
BE763399/c  
LOCUS Mus musculus 430 bp mRNA linear EST 19-SEP-2000  
DEFINITION RCO-NT0036-010600-031-d05 NT0036 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE763399  
VERSION BE763399.1 GI:10193323  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 430)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE  
20202663  
10737800  
PUBMED  
COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ci=82-RC0-NT0036-010  
600-031-d05&t3=2000-06-01&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 10  
High quality sequence stop: 430.

#### FEATURES

Location/Qualifiers  
1..430  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NT0036"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.64e+03 Length: 430  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE763399 (1-430)

Qy 1 PheGlnIleGluHisHis 6

Db 39 TTCAGATCGAGCACAC 22

#### RESULT 57

BG302890/c

LOCUS

DEFINITION BG302890 430 bp mRNA linear EST 23-FEB-2001  
IMAGE:3816388 3' similar to TR:095864 095864 DELTA-6 FATTY ACID  
DESATURASE. ; mRNA sequence.

ACCESSION BG302890

VERSION BG302890.1 GI:13100417

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 430)

AUTHORS Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S.,  
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,  
Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B.,  
Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.

WASHU Zebrafish EST Project 1999

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: S.L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA  
Sequencing by: Washington University Genome Sequencing Center Clone  
distribution information can be found through the I.M.A.G.E.

Consortium/LLNL, send email to: info@image.llnl.gov

Trace considered overall poor quality

Seq primer: 17 from Gibco

High quality sequence stop: 1.

Location/Qualifiers

#### FEATURES

source

1..430

/organism="Danio rerio"

/mol\_type="mRNA"

/strain="AB"

/db\_xref="taxon:7955"

/clones="IMAGE:3816388"

/sex="mixed (one male and one female, including

unfertilized eggs)"

/dev\_stage="adult"

/lab\_hosts="DH10B (phage resistant)"

/clone\_lib="Sugano Kawakami zebrafish DR"

/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);

Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCTTTTITTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTGGCTTACTGG], digested and cloned into distinct DraIII

sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site

CACCATGTG). XhoI should be used to isolate the cDNA

insert. Size selection was performed to exclude fragments

<1.5kb. Library constructed by Dr. Sumio Sugano

(University of Tokyo Institute of Medical Science) and

kindly donated by Dr. Koichi Kawakami. Custom primers for

sequencing: 5' end primer CTTCTGCTCTAAAGCTGG and 3' end

primer CGACCTGCAGCTCGACACA."

ORIGIN

Alignment Scores:

Pred. No.: 2.64e+03 Length: 430

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BG302890 (1-430)

Qy 1 PheGlnIleGluHisHis 6

Db 190 TTCAGATCGAGCATCAT 173

#### RESULT 58

AA003204

LOCUS

DEFINITION

AA003204

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 431)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:261385

Seq primer: BTPRimer  
 High quality sequence stop: 358.  
 Location/Qualifiers  
 1. .431

#### FEATURES

source

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:426833"  
 /sex="unknown"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5-14.5dpc total fetus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mouse embryo NbME13.5 14.5"  
 /note="Vector: pTT3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TGTTCACATCTGAAGTCGGAGCGCGCGGAATTTTTTTTTTTTTTTT  
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2  
 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne  
 State Univ., from 2 ); double-stranded cDNA was ligated to  
 Eco RI adaptors (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of the modified  
 pTT73 vector. Library went through one round of  
 normalization, and was constructed by Bento Soares and  
 M.Patima Bonaldo."

#### ORIGIN

Alignment Scores:  
 Pred. No.: 2.65e+03 Length: 431  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA003204 (1-431)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 288 TTCAGATTGAACACCAC 305

#### RESULT 59

BE763432/c

LOCUS BE763432 435 bp mRNA linear EST 19-SEP-2000  
 DEFINITION RCO-NT0036-100700-032-e08 NT0036 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE763432

VERSION BE763432.1 GI:10193356

KEYWORDS EST.

SOURCE Homo sapiens (human)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

#### REFERENCE

1 (bases 1 to 435)

AUTHORS Nagai M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

PUBMED 10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RCO-NT0036-100  
 700-032-e08&t3=2000-07-10&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 14

High quality sequence stop: 435.

#### FEATURES

source

1. .435  
 /location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="NT0036"  
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

#### ORIGIN

Alignment Scores:  
 Pred. No.: 2.68e+03 Length: 435  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE763432 (1-435)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 42 TTCAGATCGACACCAC 25

#### RESULT 60

AA049958

LOCUS AA049958 436 bp mRNA linear EST 09-SEP-1996

DEFINITION mJ3809.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA

Clone IMAGE:478432 5', mRNA sequence.

ACCESSION AA049958

VERSION AA049958.1 GI:1529629

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

1 (bases 1 to 436)

AUTHORS Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:289176



```

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 430.
Location/Qualifiers
1..436
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:478432"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NMB13.5 14.5"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAGTGGGAGCGCGGGAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Patima Bonaldo."

ORIGIN
Alignment Scores:
Pred. No.: 2.69e+03 Length: 436
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA049958 (1-436)

Qy 1 PheGlnIleGluHis 6
|||||
Db 289 TTCCAGATTGACACCAC 306

RESULT 61
AL047548 440 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp586D0421.r1 586 (synonym: hutel) Homo sapiens cDNA clone
DEFINITION DKFZp586D0421, mRNA sequence.
ACCESSION AL047548.1 GI:4728544
VERSION AL047548.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
This clone (DKFZp586D0421) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..440

FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 2.69e+03 Length: 436
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA049958 (1-436)

Qy 1 PheGlnIleGluHis 6
|||||
Db 289 TTCCAGATTGACACCAC 306

RESULT 61
AL047548 440 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp586D0421.r1 586 (synonym: hutel) Homo sapiens cDNA clone
DEFINITION DKFZp586D0421, mRNA sequence.
ACCESSION AL047548.1 GI:4728544
VERSION AL047548.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
This clone (DKFZp586D0421) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..440

FEATURES
source

```

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp586D0421"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="586 (synonym: hutel)"
/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

ORIGIN
Alignment Scores:
Pred. No.: 2.72e+03 Length: 440
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AL047548 (1-440)

Qy 1 PheGlnIleGluHis 6
|||||
Db 29 TTCCAGATTGACACCAC 46

RESULT 62
CD618243/c
LOCUS CD618243 441 bp mRNA linear EST 12-JAN-2004
DEFINITION 56061114J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD618243
VERSION CD618243.1 GI:40266508
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/notes="Vector: pDrive Cloning Vector"

ORIGIN
Alignment Scores:
Pred. No.: 2.72e+03 Length: 441
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CD618243 (1-441)

Qy 1 PheGlnIleGluHis 6
|||||
Db 432 TTCCAGATTGACACCAC 415

RESULT 63
CN959568
LOCUS CN959568 442 bp mRNA linear EST 08-JUN-2004
DEFINITION 7068_100133_85 Fundulus Heteroclitus Liver Fundulus heteroclitus

```

```

cDNA, mRNA sequence.
CN959568
CN959568.1 GI:48441157
EST.
Fundulus heteroclitus (killifish)
ORGANISM
Fundulus heteroclitus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Fundulidae; Fundulus.
REFERENCE
1 (bases 1 to 442)
Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
Roach,J.L. and Whitehead,J.A.
TITLE
Fundulus Functional Genomics: EST Database for Teleost Fish
JOURNAL
Unpublished (2004)
COMMENT
Contact: Crawford, Douglas L.
Marine Genomics - Crawford Lab
Rosenstiel School of Marine and Atmospheric Science - University of
Miami
4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA
Tel: 305 361 4121
Email: dcrawford@rsmas.miami.edu
Database Web Interface
http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 100133 row: D column: 11.
FEATURES
source
Location/Qualifiers
1..442
/organism="Fundulus heteroclitus"
/mol_type="mRNA"
/db_xref="taxon:8078"
/tissue_type="Liver"
/clone_lib="Fundulus Heteroclitus Liver"
/notes="Organ: Liver"
ORIGIN
Alignment Scores:
Pred. No.: 2.73e+03 Length: 442
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-029-756-20 (1-6) x CN959568 (1-442)
Qy 1 PheGlnIleGluHis 6
Db 255 TTCCAATCGAGCATCAT 272
RESULT 64
CN962628 442 bp mRNA linear EST 08-JUN-2004
LOCUS
DEFINITION
10125_100235 27 Fundulus Heteroclitus Liver Fundulus heteroclitus
cDNA similar to Delta-5/delta-6 fatty acid desaturase (BC 1.14.19,
mRNA sequence.
CN962628
CN962628.1 GI:48444217
EST.
Fundulus heteroclitus (killifish)
ORGANISM
Fundulus heteroclitus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Fundulidae; Fundulus.
REFERENCE
1 (bases 1 to 442)
Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
Roach,J.L. and Whitehead,J.A.
TITLE
Fundulus Functional Genomics: EST Database for Teleost Fish
JOURNAL
Unpublished (2004)
COMMENT
Contact: Crawford, Douglas L.
Marine Genomics - Crawford Lab
Rosenstiel School of Marine and Atmospheric Science - University of
Miami

```

```

4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA
Tel: 305 361 4121
Email: dcrawford@rsmas.miami.edu
Database Web Interface
http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 100235 row: F column: 4.
FEATURES
source
Location/Qualifiers
1..442
/organism="Fundulus heteroclitus"
/mol_type="mRNA"
/db_xref="taxon:8078"
/tissue_type="Liver"
/clone_lib="Fundulus Heteroclitus Liver"
/notes="Organ: Liver"
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Alignment Scores:
Pred. No.: 2.73e+03 Length: 442
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-029-756-20 (1-6) x CN962628 (1-442)
Qy 1 PheGlnIleGluHis 6
Db 195 TTCCAATCGACCATCAT 212
RESULT 65
CN966615 442 bp mRNA linear EST 08-JUN-2004
LOCUS
DEFINITION
14112_100293 58 Fundulus Heteroclitus Liver Fundulus heteroclitus
cDNA similar to Delta-5/delta-6 fatty acid desaturase (BC 1.14.19,
mRNA sequence.
CN966615
CN966615.1 GI:48448204
EST.
Fundulus heteroclitus (killifish)
ORGANISM
Fundulus heteroclitus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Fundulidae; Fundulus.
REFERENCE
1 (bases 1 to 442)
Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
Roach,J.L. and Whitehead,J.A.
TITLE
Fundulus Functional Genomics: EST Database for Teleost Fish
JOURNAL
Unpublished (2004)
COMMENT
Contact: Crawford, Douglas L.
Marine Genomics - Crawford Lab
Rosenstiel School of Marine and Atmospheric Science - University of
Miami
4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA
Tel: 305 361 4121
Email: dcrawford@rsmas.miami.edu
Database Web Interface
http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 100235 row: G column: 8.
FEATURES
source
Location/Qualifiers
1..442
/organism="Fundulus heteroclitus"
/mol_type="mRNA"
/db_xref="taxon:8078"
/tissue_type="Liver"
/clone_lib="Fundulus Heteroclitus Liver"
/notes="Organ: Liver"
ORIGIN
Alignment Scores:
Pred. No.: 2.73e+03 Length: 442
Score: 36.00 Matches: 6

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CN966615 (1-442)

Qy 1 PheGlnIleGluHisHis 6
Db 217 TTTCARATCGAACACCAT 234

RESULT 66
AA310580
LOCUS AA310580 443 bp mRNA linear EST 19-APR-1997
DEFINITION EST181401 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA310580
VERSION AA310580.1 GI:1962927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Pritchman,J.L., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.-Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Other ESTs: THCI52140
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES
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Location/Qualifiers
1..443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):156619"
/db_xref="taxon:9606"
/call_type="T-lymphocyte"
/clone_lib="Jurkat T-cells V"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
ORIGIN
Alignment Scores: 2.74e+03 Length: 443
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x CN966615 (1-442)

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x AA310580 (1-443)

Qy 1 PheGlnIleGluHisHis 6
Db 149 TTCCAGATTGAGCACCAT 166

RESULT 67
BF750956
LOCUS BF750956 444 bp mRNA linear EST 10-JAN-2001
DEFINITION RCI-BN0414-021100-021-h03 BN0414 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF750956
VERSION BF750956.1 GI:12077632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0414-021100-021-h03&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 443.
FEATURES
source
Location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0414"
/notes="Organ: breast normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Alignment Scores: 2.75e+03 Length: 444
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF750956 (1-444)

```

```

QY      1 PheGlnIleGluHisHis 6
Db      379 TTCAGATTGACGACCAC 362

RESULT 68
BF890295
LOCUS   BF890295          444 bp    mRNA    linear    EST 25-APR-2001
DEFINITION 21915 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF890295
VERSION   BF890295.1   GI:12281825
KEYWORDS EST.
SOURCE    Bos taurus (cow)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 444)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL   Genome Res. 11 (4), 626-630 (2001)
MEDLINE   21180013
PUBMED    11282978
COMMENT   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 57 row: G column: 16
Seq primer: ATTTAGGTGACACTATAG.
FEATURES             source
    source
    1..444
        /organism="Bos taurus"
        /mol_type="mRNA"
        /db_xref="taxon:9913"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /clone_lib="MARC 3BOV"
        /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
ORIGIN
Alignment Scores:
Pred. No.:          2.75e+03          Length:          444
Score:              36.00             Matches:          6
Percent Similarity: 100.00%           Conservative:     0
Best Local Similarity: 100.00%         Mismatches:      0
Query Match:        100.00%           Indels:          0
DB:                 2                  Gaps:            0

US-10-029-756-20 (1-6) x BF890295 (1-444)

QY      1 PheGlnIleGluHisHis 6
Db      101 TTCAGATTGACGACCAC 118

RESULT 69
BQ101252
LOCUS   BQ101252          444 bp    mRNA    linear    EST 29-APR-2002
DEFINITION 21915 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BQ101252
VERSION   BQ101252.1   GI:20134236
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisshvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE     Endocrine Pancreas Consortium
JOURNAL   Unpublished (2000)
PUBMED    Other ESTs: ij25h11.xl
COMMENT   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Putative full length read
vector to vector length is 547
Seq primer: -40RP from Gibco.
FEATURES             source
    source
    1..444
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:6135813"
        /sex="Both"
        /tissue_type="Islets of Langerhans"
        /dev_stage="Adult"
        /lab_host="DH10B"
        /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
        /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library made from BQ101252, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
ORIGIN
Alignment Scores:
Pred. No.:          2.75e+03          Length:          444
Score:              36.00             Matches:          6
Percent Similarity: 100.00%           Conservative:     0
Best Local Similarity: 100.00%         Mismatches:      0
Query Match:        100.00%           Indels:          0
DB:                 5                  Gaps:            0

US-10-029-756-20 (1-6) x BQ101252 (1-444)

QY      1 PheGlnIleGluHisHis 6
Db      101 TTCAGATTGACGACCAC 118

RESULT 69
BQ101252
LOCUS   BQ101252          444 bp    mRNA    linear    EST 29-APR-2002
DEFINITION 21915 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BQ101252
VERSION   BQ101252.1   GI:20134236
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisshvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE     Endocrine Pancreas Consortium
JOURNAL   Unpublished (2000)
PUBMED    Other ESTs: ij25h11.xl
COMMENT   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Putative full length read
vector to vector length is 547
Seq primer: -40RP from Gibco.
FEATURES             source
    source
    1..444
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:6135813"
        /sex="Both"
        /tissue_type="Islets of Langerhans"
        /dev_stage="Adult"
        /lab_host="DH10B"
        /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
        /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library made from BQ101252, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
ORIGIN
Alignment Scores:
Pred. No.:          2.75e+03          Length:          444
Score:              36.00             Matches:          6
Percent Similarity: 100.00%           Conservative:     0
Best Local Similarity: 100.00%         Mismatches:      0
Query Match:        100.00%           Indels:          0
DB:                 5                  Gaps:            0

US-10-029-756-20 (1-6) x BQ101252 (1-444)

```

```

Db      45 TTCCAGATGAGCACCAC 62
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RESULT 70
LOCUS   BG412193
DEFINITION OV2_39_A06.b1_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BG412193
VERSION   BG412193
KEYWORDS  EST.
SOURCE    Sorghum bicolor (sorghum)
ORGANISM  Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 445)
AUTHORS  Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
TITLE     An EST database from Sorghum: ovaries of varying immature stages
JOURNAL   Unpublished (2000)
COMMENT   Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 444
POLYA=No.

FEATURES
source
1..445
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Ovary 2 (OV2)"
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made
from Poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

ORIGIN
Alignment Scores:
Pred. No.: 2.75e+03 Length: 445
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BG412193 (1-445)

Qy      1 PheGlnIleGluHisHis 6
|||||
Db      187 TTCCAGATTGAGCACCAC 204
|||||

RESULT 71
LOCUS   AA488410/c
DEFINITION ab37909.g1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
IMAGE:843040 3' similar to WP.W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION AA488410
VERSION   AA488410
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 446)
AUTHORS  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

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Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 656 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 440.

FEATURES
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1..446
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:843040"
/sex="female"
/dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene HeLa cell s3 937216"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. HeLa S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-ZAP XR
Vector. -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 2.76e+03 Length: 446
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA488410 (1-446)

Qy      1 PheGlnIleGluHisHis 6
|||||
Db      328 TTCCAGATTGAGCACCAC 311
|||||

RESULT 72
LOCUS   CB841818
DEFINITION M15E-2428 MOUSE EMBRYONIC DAY 15.5 EYE Mus musculus cDNA 5', mRNA
sequence.
ACCESSION CB841818
VERSION   CB841818.1 GI:34373088
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 446)
AUTHORS  Yu,J., Farjo,R., MacNee,S.P., Baehr,W., Stambolian,D.E. and
Swaroop,A.
TITLE     Annotation and analysis of 10,000 expressed sequence tags from
developing mouse eye and adult retina
JOURNAL   Genome Biol. 4 (10), R65 (2003)
MEDLINE   22881944
PUBMED    14519200
Contact: Swaroop, A.
Department of Ophthalmology and Visual Sciences
Kellogg Eye Center, University of Michigan
540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
Tel: 734 615 2246
Fax: 734 647 0228

```

Email: swaroop@umich.edu.

# FEATURES source

1. .446  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="eye"  
/clone\_lib="MOUSE EMBRYONIC DAY 15.5 EYE"  
/note="vector: pSPORT1"

## ORIGIN

Alignment Scores:  
Pred. No.: 2.76e+03 Length: 446  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB841818 (1-446)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 160 TTCAGATTGACACCAC 177

## RESULT 73

CK345055/c  
LOCUS 447 bp mRNA linear EST 22-DEC-2003  
DEFINITION L0034F07-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA  
Library Mus musculus cDNA clone L0034F07 3', mRNA sequence.

ACCESSION CK345055  
VERSION CK345055.1 GI:40300668  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 447)

REFERENCE Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
AUTHORS Construction of long-transcript enriched cDNA libraries from  
TITLE submicrogram amounts of total RNAs by a universal PCR amplification  
method

Genome Res. 11 (9), 1553-1558 (2001)

21429098

11544199

CONTACT: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@igsun.grc.nia.nih.gov

Plate: L0034 row: F column: 07

Seq primer: -21M13 Forward

High quality sequence stop: 447

POLYA=Yes.

# FEATURES source

Location/Qualifiers  
1. .447  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="niaEST:L0034F07-3"  
/db\_xref="taxon:10090"  
/clone="L0034F07"  
/sex="female"  
/dev stage="12.5dpc"  
/lab host="DH10B"  
/clone\_lib="NIA Mouse E12.5 Female Mesonephros and Gonads  
cDNA Library"  
/note="vector: pSPORT1 (Gibco/BRL Life Technology);  
Site 1: SalI; Site 2: NotI; Total RNAs were extracted from  
2 Mesonephros. The double-stranded cDNA was synthesized  
by Gibco's kit with an Oligo(dT) primer (NotI  
primer-adaptor from Gibco/BRL)  
[5'-PGACTAGTCTTAGATCGGCGCGCCCTTTTTTTTTTTT-3'] from

3.42ug of total RNA . The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal3 (include SalI sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.77e+03 Length: 447  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CK345055 (1-447)

Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 266 TTCAGATTGACACCAC 249

## RESULT 74

BF890281

LOCUS

DEFINITION

BF890281

ACCESSION

BF890281.1

VERSION

BF890281.1

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 449)

REFERENCE

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,  
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,  
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,  
Quackenbush, J. and Keefe, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

21180013

11282978

CONTACT: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

Plate: 57 row: D column: 16

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1. .449

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3BOV"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.78e+03 Length: 449  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF002756 (1-449)

Qy 1 PheGlnIleGluHisHis 6

Db 92 TTCCAGATCGAGCACCAT 109

## RESULT 75

BF002756/c

LOCUS

DEFINITION BF002756 449 bp mRNA linear EST 06-OCT-2000  
similar to TR:O60427 O60427 BC269730.2.; mRNA sequence.

ACCESSION BF002756

VERSION BF002756.1

KEYWORDS EST.

SOURCE

ORGANISM

Homosapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco.

## FEATURES

source

1..449 Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3310877"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; Plasmid DNA from the  
normalized library NCI CGAP Pr22 was prepared, and ss  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
985608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaudo."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.78e+03 Length: 449  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF002756 (1-449)

Qy 1 PheGlnIleGluHisHis 6

Db 348 TTCCAGATTGAGCACCAT 331

## RESULT 76

AA531459

LOCUS

DEFINITION

AA531459

VERSION

KEYWORDS

SOURCE

ORGANISM

Homosapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuvaqui,

M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 977 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 395.

Location/Qualifiers

1..452

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:997172"

/sex="male"

/tissue\_type="invasive prostate tumor"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Pr10"

/note="Organ: prostate; Vector: pAMP10; mRNA made from

invasive prostate tumor, cDNA made by oligo-dt priming.

Non-directionally cloned. Size-selected on agarose gel,

average insert size 600 bp. Library made by D. Krizman,

NIH."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.81e+03 Length: 452  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA531459 (1-452)

Qy 1 PheGlnIleGluHisHis 6

Db 359 TTCCAGATCGAGACCAC 376

RESULT 77  
BY260760  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BY260760 455 bp mRNA linear EST 10-DEC-2002  
BY260760 RIKEN full-length enriched, visual cortex Mus musculus  
cDNA clone K330303J05 5', mRNA sequence.  
BY260760  
BY260760.1 GI:26442272  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 455)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, K.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,  
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,  
Ciothlav, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,  
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,  
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, R., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S.,  
Ravasi, T., Reed, J. C., Reid, D. J., Reid, J., Ring, B. Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Sample, C. A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,  
Verardo, R., Wagner, L. G., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9216  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, K.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Tissues were provided by Michela Fagiolini and Takao K. Hensch (   
Laboratory for Neuronal Circuit Development Brain Science Institute  
RIKEN 2-1 Hiroasawa, Wako-shi, Saitama 351-0198 Japan ) whose  
assistance we gratefully acknowledge. Please visit our web site  
(http://genome.gsc.riken.go.jp) for further details.

FEATURES  
Location/Qualifiers  
source  
1. .455  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="K330303J05"  
/tissue\_type="visual cortex"  
/clone\_lib="RIKEN full-length enriched, visual cortex"

ORIGIN  
Alignment Scores:  
Pred. No.: 2.83e+03 Length: 455  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0  
US-10-029-756-20 (1-6) x BY260760 (1-455)  
Qy 1 PheGlnIleGluHisHis 6  
|||||  
Db 17 TTCCAGATTCGACACCAC 34  
RESULT 78  
BF917591  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

BF917591 458 bp mRNA linear EST 18-JAN-2001  
IL3-UT01114-211200-360-E07 UT0114 Homo sapiens cDNA, mRNA sequence.  
BF917591  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 458)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,  
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,  
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,  
Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V.,  
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and  
Simpson, A. J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-  
211200-360-E07&t3=2000-12-21&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 457.  
Location/Qualifiers  
source  
1. .458



/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="UT0114"

/note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.85e+03 Length: 458  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF917591 (1-458)

Qy 1 PheGlnIleGluHis 6  
Db 87 TTTCAAATAGAACACCAC 104

## RESULT 79

BF917881  
LOCUS BF917881 458 bp mRNA linear EST 18-JAN-2001  
DEFINITION IL3-UT0114-221200-360-E07 UT0114 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF917881  
VERSION BF917881.1 GI:12309339  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 458)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Mateukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-UT0114-  
221200-360-E07&t3=2000-12-22&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 457.

Location/Qualifiers  
1. 458

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="UT0114"  
/note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI;

## ORIGIN

Alignment Scores:  
Pred. No.: 2.85e+03 Length: 458  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF917881 (1-458)

Qy 1 PheGlnIleGluHis 6  
Db 87 TTTCAAATAGAACACCAC 104

## RESULT 80

BF059742  
LOCUS BF059742 458 bp mRNA linear EST 15-JUN-2001  
DEFINITION IL3-UT0114-080101-360-E07 UT0114 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF059742  
VERSION BF059742.1 GI:14467269  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 458)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Mateukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-UT0114-  
080101-360-E07&t3=2001-01-08&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 457.

Location/Qualifiers  
1. 458

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="UT0114"

/note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Alignment Scores: 2.85e+03 458  
 Pred. No.: 36.00 Matches: 6  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 4

US-10-029-756-20 (1-6) x BI059742 (1-458)

Oy 1 PheGlnlleGluHisHis 6

|||||

87 TTTCATAGACACAC 104

## RESULT 81

CN006019

LOCUS

DEFINITION ip37f09.g1 Brain - Cerebellum Library (DOGE8T8) Canis familiaris

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 458)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 Balijs, V., Nascimento, L.U. and McCombie, W.R.  
 ESTs from Canis familiaris cerebellum (dog)  
 Unpublished (2004)  
 Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org  
 Plate: ip37 row: f column: 09  
 High quality sequence stop: 458.

## FEATURES

source

1..458  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9615"  
 /clone="ip37f09"  
 /sex="Unknown"  
 /tissue\_type="Cerebellum"  
 /dev\_stage="3 month old normal canine"  
 /lab\_host="XLI0 Gold"  
 /clone\_lib="Brain - Cerebellum Library (DOGE8T8)"  
 /note="Organ: Brain; Vector: pBluescript II SK; Site 1:  
 EcoRI; Site 2: XhoI; Library constructed using pBluescript  
 XR kit from Stratagene. Cloned cDNA was size selected  
 between 1-3 kb. Mark Haskins VMD, PhD, Pathology and  
 Medical Genetics, School of Veterinary Medicine,  
 University of Pennsylvania, 3800 Spruce Street,  
 Philadelphia, PA 19104-6051"

## ORIGIN

Alignment Scores: 2.85e+03 458  
 Pred. No.: 36.00 Matches: 6  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 7

US-10-029-756-20 (1-6) x CN006019 (1-458)

Oy 1 PheGlnlleGluHisHis 6

|||||

Db

## RESULT 82

BM721986/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

MEDLINE

PUBMED

COMMENT

1 (bases 1 to 461)

Bonaldi, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA

sequence: 85-159, >MIR#SINE/MIR

Seq primer: M13 Reverse.

Location/Qualifiers

1..461

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-E00-ahw-e-22-0-UI"

/tissue\_type="fetal eye"

/dev\_stage="fetal"

/lab\_host="UI-E-E00"

/clone\_lib="UI-E-E00"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-E-E00 is a cDNA library containing the following

tissue(s): fetal eye. The library was constructed

according to Bonaldi, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is GCGGTATACC. This library

was created for the program, Gene Discovery in the Visual

System, supported by National Eye Institute (NEI)."

83 TTCCAGATCGACACAC 100

BM721986

UI-E-E00-ahw-e-22-0-UI.r1

UI-E-E00-ahw-e-22-0-UI 5', mRNA sequence.

BM721986

BM721986.1

GI:19042251

EST.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 461)

Bonaldi, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA

sequence: 85-159, >MIR#SINE/MIR

Seq primer: M13 Reverse.

Location/Qualifiers

1..461

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-E00-ahw-e-22-0-UI"

/tissue\_type="fetal eye"

/dev\_stage="fetal"

/lab\_host="UI-E-E00"

/clone\_lib="UI-E-E00"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-E-E00 is a cDNA library containing the following

tissue(s): fetal eye. The library was constructed

according to Bonaldi, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is GCGGTATACC. This library

was created for the program, Gene Discovery in the Visual

System, supported by National Eye Institute (NEI)."

## ORIGIN

Alignment Scores: 2.87e+03 461  
 Pred. No.: 36.00 Matches: 6  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 4

US-10-029-756-20 (1-6) x BM721986 (1-461)

```

QY      1 PheGlnIleGluHis 6
DB      248 TTTCAGATAGACATCAT 231

RESULT 83
LOCUS   CA902069/c
DEFINITION Phaeolus coccineus
ACCESSION CA902069
VERSION   1
KEYWORDS  EST.
SOURCE    Phaeolus coccineus
ORGANISM  Phaeolus coccineus
REFERENCE 1 (bases 1 to 463)
AUTHORS   Bui, A.O., Le, B.H., Weterings, K., Bi, Y.-P., Choi, J.-S.,
           McElroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and
           Goldberg, R.B.
TITLE     Gene Activity in Different Regions of a Post-Fertilization Plant
JOURNAL  Unpublished (2002)
COMMENT   Department of Molecular, Cell, & Developmental Biology
           University of California, Los Angeles
           621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
           Tel: 310 825 3270
           Fax: 310 825 8201
           Email: bobg@ucla.edu
           Seg primer: 5' Triplex
POLYA=No.

FEATURES             Location/Qualifiers
     source           1..463
                     /organism="Phaeolus coccineus"
                     /mol_type="mRNA"
                     /cultiivar="Hammond's Dwarf Scarlet"
                     /db_xref="taxon:3986"
                     /dev_stage="6-days post-pollination"
                     /clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
                     /note="Organ: Suspensor Region of Globular-Stage Embryos;
                     Vector: Triplex2; Site 1: SfiIA; Site 2: SfiIB; Suspensor
                     regions were micro-dissected from globular-stage embryos
                     six days after pollination from greenhouse-grown plants
                     [Weterings et al., Plant Cell 13, 2409-2425 (2001)].
                     Double-stranded cDNA was synthesized from suspensor mRNA
                     using the SMART cDNA Library Construction Kit according to
                     the manufacturer (Clontech). The suspensor cDNA fragments
                     were directionally ligated into the SfiI restriction site
                     of the lambda Triplex2 vector (Clontech), and the
                     recombinant cDNAs were transformed into E. coli XL1-Blue
                     cells (Clontech). Suspensor cDNA plasmids used for
                     directional sequencing were obtained by in vivo excision
                     from the lambda Triplex2 recombinants in E. coli BM25.8
                     cells (Clontech)."

ORIGIN
Alignment Scores:  2.89e+03  Length: 463
Pred. No.:        36.00    Matches: 6
Score:            100.00%   Conservative: 0
Best Similarity:  100.00%   Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:      6        Gaps: 0
DB:

US-10-029-756-20 (1-6) x CA902069 (1-463)

QY      1 PheGlnIleGluHis 6
DB      248 TTTCAGATAGACATCAT 231

RESULT 84
LOCUS   CD430143
DEFINITION Phaeolus bicolor
ACCESSION CD430143
VERSION   1
KEYWORDS  EST.
SOURCE    Sorghum bicolor (sorghum)
ORGANISM  Sorghum bicolor
REFERENCE 1 (bases 1 to 465)
AUTHORS   Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R.,
           Chua fan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P.,
           Olaseinde, O., Eastman, A. and Pratt, L.H.
TITLE     An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
           (ACC)-treated seedlings
JOURNAL  Unpublished (2003)
COMMENT   Other ESTs: ETH1_17_D05.g1.A002
           Contact: Cordnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
           the Human Genome Center, University of Tokyo Institute of Medical
           Science; plant material and RNA prepared at Texas A & M University;
           sequencing done in the Laboratory for Genomics and Bioinformatics,
           University of Georgia. Sequence ends have been trimmed to exclude
           vector and regions below Phred quality 16. Three-prime sequences
           are presented as their reverse complement and have been trimmed to
           exclude polyA.
           Seg primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..465
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /cultiivar="BTx623"
                     /db_xref="taxon:4558"
                     /clone_lib="ETH1_17_D05_A002"
                     /lab_hosts="DH10B-T1 phage-resistant E. coli"
                     /note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
                     library was prepared from polyA+ RNA from seedlings grown
                     in hydroponic culture. At 8 days of age, medium was
                     supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
                     acid (ACC) to induce endogenous ethylene (ETH) production.
                     Roots and shoots were harvested after 27 and 72 hr and
                     material from both time points was combined prior to RNA
                     isolation. Double-stranded cDNA was cloned
                     unidirectionally into different DraIII sites of the
                     pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
                     3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
                     insert."

ORIGIN
Alignment Scores:  2.9e+03  Length: 465
Pred. No.:        36.00    Matches: 6
Score:            100.00%   Conservative: 0
Best Similarity:  100.00%   Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:      6        Gaps: 0
DB:

US-10-029-756-20 (1-6) x CD430143 (1-465)

```

```

Qy 1 PheGlnIleGluHisHis 6
Db 66 TTCAGATTGAGCACCAT 83

RESULT 85
CV520815/c 465 bp mRNA linear EST 06-OCT-2004
LOCUS 089P0050Z.xl D11 Mimulus guttatus library 2 Mimulus guttatus cDNA
DEFINITION clone 089P0050Z.xl D11, mRNA sequence.
ACCESSION CV520815
VERSION CV520815.1 GI:53847347
KEYWORDS EST.
SOURCE Mimulus guttatus (spotted monkey flower)
ORGANISM Mimulus guttatus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Lamiales; Lamiales; Lamiales incertae sedis; Mimuleae;
Mimulus.
REFERENCE 1 (bases 1 to 465)
AUTHORS Willis, J., Vision, T., Dietrich, P.S. and Allen, A.
TITLE Mimulus guttatus cDNA sequence
JOURNAL Unpublished (2004)
COMMENT Contact: Willis J
Department of Biology
Duke University
072-A Biological Sciences Science Drive, Durham, NC 27708, USA
Tel: 919 660 7340
Fax: 919 660 7293
Email: jwillis@duke.edu
Plate: 089P0050 row: 11 column: D
Seq primer: T7
High quality sequence start: 15
High quality sequence stop: 692.
FEATURES
source
1..465
/organism="Mimulus guttatus"
/mol_type="mRNA"
/db_xref="taxon:4155"
/clone="089P0050Z.xl D11"
/clone_lib="Mimulus guttatus library 2"
/notes="Vector: pGEM-T Easy; a Mimulus guttatus cDNA library"
ORIGIN
Alignment Scores:
Pred. No.: 2.9e+03 Length: 465
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CV520815 (1-465)

Qy 1 PheGlnIleGluHisHis 6
Db 417 TTCAGATCGAGCACCAT 400

RESULT 86
AA478552/c 469 bp mRNA linear EST 08-AUG-1997
LOCUS zw95h12.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone
DEFINITION IMAGE:784775 3', mRNA sequence.
ACCESSION AA478552
VERSION AA478552.1 GI:2207186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

```

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-Merck EST Project 1997  
Unpublished (1997)

#### TITLE JOURNAL COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 459.

#### FEATURES source

1..469  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:5982393"  
/db\_xref="taxon:9606"  
/clone="IMAGE:784775"  
/dev\_stage="8-9 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares total\_fetus Nb2HF8\_9w"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTACCAATCTGAGTGGAGCGCGCTTAATTTTTTTTTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.93e+03 Length: 469  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA478552 (1-469)

Qy 1 PheGlnIleGluHisHis 6  
Db 409 TTCAGATTGAGCACCAC 392

#### RESULT 87

AA490669

LOCUS

DEFINITION

UI-M-BH3-ast-g-05-0-UI.s1 NIH BMAP M.S4 Mus musculus cDNA clone

UI-M-BH3-ast-g-05-0-UI 3', mRNA sequence.

ACCESSION AA490669

VERSION AA490669.1

KEYWORDS EST.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 470)

AUTHORS

TITLE

Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL

MEDLINE

PUBMED

COMMENT

Genome Res. 6 (9), 791-806 (1996)

97044477

889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements  
Seq primer: M13 Forward  
POLYA-Yes.

#### FEATURES

Location/Qualifiers  
1..470  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UI-M-BH3-ast-g-05-0-UI"  
/dev\_stages="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_libs="NIH BMAP M S4"  
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP M S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH BMAP M S4, NIH BMAP M S3.3, NIH BMAP M S3.2, NIH BMAP M S3.1, NIH BMAP M S2, NIH BMAP M S1. The subtracted library (NIH BMAP M S4) was constructed as follows: PCR amplified cDNA inserts from NIH BMAP M S3.3, NIH BMAP M S3.2, and NIH BMAP M S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH BMAP M S3.3, NIH BMAP M S3.2, and NIH BMAP M S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH BMAP M S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_TISSUE=brain-stems  
TAG\_LIB=NIH BMAP M\_S4  
TAG\_SEQ=TCATG"

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.94e+03 Length: 470  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW490669 (1-470)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 300 TTCAGATTGAACACCAC 317

RESULT 88

#### BF706865

LOCUS 281517 MARC 3BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001  
DEFINITION BF706865  
ACCESSION BF706865  
VERSION BF706865.1 GI:11998526  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

#### REFERENCE

1 (bases 1 to 473)  
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.  
Bovinae; Bos.

#### TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

#### JOURNAL

#### MEDLINE

#### PUBMED

#### COMMENT

Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

#### PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCAGCAGC

Plate: 79 row: 0 column: 2

Seq primer: ATTAGTGACATAG.

#### FEATURES

##### source

1..473  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3BOV"  
/note="Vector: pQMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinous muscle, and fetal longissimus muscle."

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.96e+03 Length: 473  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF706865 (1-473)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 199 TTCAGATCGAGCCAT 216

#### RESULT 89

##### BF756742

LOCUS BE756742 210977 MARC 2BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001  
DEFINITION BE756742  
ACCESSION BE756742  
VERSION BE756742.1 GI:10170734  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

**REFERENCE**  
**AUTHORS**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 474)

**TITLE**  
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

**JOURNAL**  
**MEDLINE**  
**PUBMED**  
 Genome Res. 11 (4), 626-630 (2001)  
 11282978

**COMMENT**  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTTCCAGTCACGACG  
 Plate: 59 row: C column: 24  
 Seq primer: ATTAGGTGACACTATAG.  
 Location/Qualifiers  
 1. 474  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 2BOV"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

**FEATURES**  
 source  
 1. 474  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 2BOV"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2.97e+03 Length: 474  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-029-756-20 (1-6) x BE756742 (1-474)

**Qy**  
 1 PheGlnIleGluHisHis 6  
 |||||  
 122 TTCCAGATCGAGCACCAT 139

**Db**  
 1 PheGlnIleGluHisHis 6  
 |||||  
 122 TTCCAGATCGAGCACCAT 139

**RESULT 90**  
 BF890300  
 LOCUS  
 DEFINITION  
 291921 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
 477 bp mRNA linear EST 25-APR-2001  
 ACCSSION  
 BF890300  
 VERSION  
 BF890300.1 GI:12281830  
 EST.  
 KEYWORDS  
 SOURCE  
 Bos taurus (cow)  
 ORGANISM  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 477)

**REFERENCE**  
**AUTHORS**  
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,

**TITLE**  
 Quackenbush, J. and Keele, J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

**JOURNAL**  
**MEDLINE**  
**PUBMED**  
 Genome Res. 11 (4), 626-630 (2001)  
 11282978

**COMMENT**  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTTCCAGTCACGACG  
 Plate: 57 row: H column: 16  
 Seq primer: ATTAGGTGACACTATAG.  
 Location/Qualifiers  
 1. 477  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3BOV"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

**FEATURES**  
 source  
 1. 477  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3BOV"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2.99e+03 Length: 477  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-029-756-20 (1-6) x BF890300 (1-477)

**Qy**  
 1 PheGlnIleGluHisHis 6  
 |||||  
 119 TTCCAGATCGAGCACCAT 136

**Db**  
 1 PheGlnIleGluHisHis 6  
 |||||  
 119 TTCCAGATCGAGCACCAT 136

**RESULT 91**  
 BG158520  
 LOCUS  
 DEFINITION  
 RHIZ2\_41\_D11.g1\_A003 Rhizome2 (RHIZ2) Sorghum propinquum cDNA, mRNA sequence.  
 477 bp mRNA linear EST 06-FEB-2001  
 ACCSSION  
 BG158520  
 VERSION  
 BG158520.1 GI:12692184  
 EST.  
 KEYWORDS  
 SOURCE  
 Sorghum propinquum  
 ORGANISM  
 Sorghum propinquum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 477)  
 Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.  
 An EST database from Sorghum: Sorghum propinquum rhizomes Unpublished (2000)  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu

Seq primer: PolyTwix  
High quality sequence start: 115  
High quality sequence stop: 476  
POLYA=No.

#### FEATURES

Location/Qualifiers  
1..477  
/organism="Sorghum propinquum"  
/mol\_type="mRNA"  
/db\_xref="taxon:132711"  
/clone\_lib="Rhizome2 (RHIZ2)"  
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.99e+03 Length: 477  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BG158520 (1-477)

QY 1 PheGlnIleGluHis 6  
|||||  
DB 58 TTCCAGATTGAGCACCAT 75

#### RESULT 92

BM689101  
LOCUS BM689101 477 bp mRNA linear EST 28-FEB-2002  
DEFINITION UI-E-CQ1-act-b-04-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone  
ACCESSION BM689101  
VERSION BM689101.1 GI:19002359  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery  
Genome Res. 6 (9), 791-806 (1996)

9704477

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1..477

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-CQ1-act-b-04-0-UI"

/tissue\_type="optic nerve"

/dev\_stages="adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-CQ1"

#### FEATURES

source

Location/Qualifiers

1..480

/organism="Eimeria tenella"

/mol\_type="mRNA"

/db\_xref="taxon:5802"

/dev\_stages="LS18"

/lab\_host="E.coli DH10B (GeneHog, Invitrogen, Inc)"

/clone\_lib="Eimeria tenella MS-6 Excised cDNA"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CQ1 is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAACTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

#### ORIGIN

Alignment Scores:  
Pred. No.: 2.99e+03 Length: 477  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BM689101 (1-477)

QY 1 PheGlnIleGluHis 6  
|||||  
DB 126 TTCCAGATCGAGCACCAC 143

#### RESULT 93

CD343234  
LOCUS CD343234 480 bp mRNA linear EST 29-MAY-2003  
DEFINITION EctSte66f08.y1 Eimeria tenella MS-6 Excised cDNA Eimeria tenella  
cDNA 5' similar to TR:O15902 O15902 ACTIN DEPOLYMERIZING FACTOR. ; mRNA sequence.

CD343234

CD343234.1 GI:31134855

EST.

Eimeria tenella

Eimeria tenella

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;

Eimeria.

1 (bases 1 to 480)

Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,

Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B.,

Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D.,

Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T.,

Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and

Sibley, D.

WashU-Merck Eimeria tenella project

Unpublished (1999)

Contact: David Sibley, Ph.D.

WashU-Merck Eimeria tenella project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Contact David Sibley (toxoeat@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High quality sequence stop: 304.

Location/Qualifiers

1..480

/organism="Eimeria tenella"

/mol\_type="mRNA"

/db\_xref="taxon:5802"

/dev\_stages="LS18"

/lab\_host="E.coli DH10B (GeneHog, Invitrogen, Inc)"

/clone\_lib="Eimeria tenella MS-6 Excised cDNA"

/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Sporozoites were obtained from in vitro sporulated and excysted oocysts of E.tenella grown in chickens. cDNA containing a xhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on sephacryl S500. The cDNA were ligated to EcoRI/XhoI prepared lambda ZapII (Stratagene). The primary library was mass excised using ExAssist helper phage (Stratagene). The phagemids were precipitated with PEG 8000, extracted with phenol/chloroform and electroporated into DH10B cells. The library may contain a small percentage of host or bacterial contaminants. Library materials provided by: Paul Liberator, Merck Research Labs Library constructed by: Paul Liberator, Merck Research Labs."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.02e+03 Length: 480  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CD343234 (1-480)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 316 TTCAGATTGAGCACCAT 333

## RESULT 94

BF654535  
 LOCUS 278752 MARC 3BOV Bos taurus cDNA 5' mRNA linear EST 25-APR-2001  
 DEFINITION  
 ACCESSION BF654535  
 VERSION BF654535.1 GI:11919667  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS Smith,T.P.L., Grossee,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.  
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
 JOURNAL Genome Res. 11 (4), 626-630 (2001)  
 MEDLINE 21180013  
 PUBMED 11282978

COMMENT  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 71 row: G column: 19  
 Seq primer: ATTTAGGTGACACTATAG.

## FEATURES

source  
 1. .487  
 /organism="Bos taurus"  
 /mol\_type="mRNA"

/db xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3BOV"  
 /notes="vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
 Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.07e+03 Length: 487  
 Score: 36.00 Matches: 6  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF654535 (1-487)

Qy 1 PheGlnIleGluHisHis 6  
 |||||  
 Db 215 TTCAGATCGAGCACCAT 232

## RESULT 95

AW231075  
 LOCUS u070e04.y1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:2647902 5'  
 DEFINITION similar to TR:095864 O95864 DELTA-6 FATTY ACID DESATURASE. ;, mRNA  
 ACCESSION AW231075  
 VERSION AW231075.1 GI:6560307  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS 1 (bases 1 to 489)  
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 COMMENT Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-x@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

MG1:1028354

Seq primer: -40RP from Gibco  
 High quality sequence stop: 434.

FEATURES  
 source

1. .489  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db xref="taxon:10090"  
 /clones="IMAGE:2647902"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, virgin"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Mam1"  
 /notes="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"

## ORIGIN

Alignment Scores:



Pred. No.:	3.08e+03	Length:	489
Score:	36.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0
US-10-029-756-20 (1-6) x AW231075 (1-489)			
QY	1 PheGlnIleGluHis 6		
Db	260 TTCCAGATTGAGCACCAC 277		
RESULT 96	BQ499479/c		
LOCUS	BQ499479		
DEFINITION	EST08704 PB0001 Paracoccidioides brasiliensis cDNA, mRNA sequence.		
ACCESSION	BQ499479		
VERSION	BQ499479.1 GI:24452790		
KEYWORDS	EST.		
SOURCE	Paracoccidioides brasiliensis		
ORGANISM	Paracoccidioides brasiliensis		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Paracoccidioides.		
AUTHORS	1 (bases 1 to 489)		
Goldman, G.H., dos Reis Marques, E., Duarte Ribeiro, D.C., de Souza			
Bernardes, L.A., Quispin, A.C., Vitorelli, P.M., Savoldi, M.,			
Semighini, C.P., de Oliveira, R.C., Nunes, L.R., Travassos, L.R.,			
Puccia, R., Batista, W.L., Ferreira, L.E., Moreira, J.C.,			
Bogossian, A.P., Tekalia, F., Nobrega, M.P., Nobrega, F.G. and			
Goldman, M.H.			
TITLE	Expressed sequence tag analysis of the human pathogen Paracoccidioides brasiliensis yeast phase: identification of putative homologues of Candida albicans virulence and pathogenicity genes		
JOURNAL	Eukaryot. Cell 2 (1), 34-48 (2003)		
COMMENT	Contact: Gustavo Henrique Goldman Laboratory of Molecular Biology Universidade de Sao Paulo - USP - FCFRP Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil Email: ggoldman@usp.br		
FEATURES	Location/Qualifiers		
source	1..489		
/organism="Paracoccidioides brasiliensis"			
/mol_type="mRNA"			
/db_xref="taxon:121759"			
/clone_lib="PB0001"			
ORIGIN	Alignment Scores:		
Pred. No.:	3.08e+03	Length:	489
Score:	36.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0
US-10-029-756-20 (1-6) x BQ499479 (1-489)			
QY	1 PheGlnIleGluHis 6		
Db	157 TTCCAGATTGAGCACCAC 140		
RESULT 97	BF774199		
LOCUS	BF774199		
DEFINITION	283791 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.		
ACCESSION	BF774199		
VERSION	BF774199.1 GI:12122099		
KEYWORDS	EST.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```

MEDLINE 97044477
PUBMED 889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized hypothalamus library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
    source
        1..492
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /strain="Sprague-Dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-B01-afx-f-12-0-UI"
        /dev_stage="adult"
        /lab_host="DHI08 (Life Technologies)"
        /clone_lib="UI-R-B01"
        /note="Vector: p7T3D-Pac (Pharmacia) with a modified
        polylinker; Site 1: Not I; Site 2: Eco RI; The library
        (UI-R-B01) is a subcloned library derived from a mixture
        of the following tissues: thalamus, cerebellum,
        hypothalamus, medulla, pons, midbrain, cerebral cortex,
        corpus striatum and hippocampus. For a detailed
        description of the library from which this clone was
        derived, please visit our web site at
        ratseq.eng.uiowa.edu. The subtraction has been previously
        described in (Bonaldo, Lennon and Soares, Genome Research
        6:791-806, 1996)
        TAG_TISSUE=hypothalamus
        TAG_LIB=UI-R-B01
        TAG_SEQ=GATGC"

ORIGIN
Alignment Scores:
Pred. No.: 3.11e+03 Length: 492
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US-10-029-756-20 (1-6) x BE097454 (1-492)

Qy 1 PheGlnIleGluHisHis 6
Db 337 TTCCAGATTGACACCAC 320

RESULT 99
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LOCUS Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
DEFINITION truncatula, genomic survey sequence.
ACCESSION CR305637
VERSION CR305637.1 GI:44851781
KEYWORDS GSS.
SOURCE Medicago truncatula (barral medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 496)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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US-10-029-756-20 (1-6) x CR305637 (1-496)

Qy 1 PheGlnIleGluHisHis 6
Db 16 TTTCAAATTGAGCATCAT 33

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DEFINITION
ACCESSION CO696980
VERSION CO696980.1 GI:50645534
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 501)
AUTHORS Schlueter, T., Hermanns, J., Weindel, M., Schuetter, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
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Query Match: 100.00% Indels: 0

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DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CO696980 (1-501)

Qy 1 PheGlnIleGluHis 6

Db 292 TTCCAGATTGAGCACCAT 275

Search completed: June 8, 2005, 15:13:56  
Job time : 2534.16 secs

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GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 8, 2005, 11:36:25 ; Search time 91.5789 Seconds  
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107.204 Million cell updates/sec

Title: US-10-029-756-20

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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	3	36	100.0	347	4	US-09-702-705-355	Sequence 355, App
	4	36	100.0	347	4	US-09-736-457-355	Sequence 355, App
	5	36	100.0	347	4	US-09-614-124B-355	Sequence 355, App
	6	36	100.0	347	4	US-09-671-325-355	Sequence 355, App
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## ALIGNMENTS

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RESULT 1
US-09-313-294A-3256
; Sequence 3256, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
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; NAME/KEY: unsure
; LOCATION: 262
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3256
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Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

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; Sequence 1966, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1966
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
; NAME/KEY: unsure
; LOCATION: 256
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-1966
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Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-10-029-756-20 (1-6) x US-09-313-294A-1966 (1-291)
Qy 1 PheGlnIleGluHis 6
Db 228 TTCAGATTGAGCACCAT 245

RESULT 3
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; Sequence 355, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-355

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Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-702-705-355 (1-347)

Qy 1 PheGlnIleGluHis 6
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; Sequence 355, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
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US-09-736-457-355

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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-736-457-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 5
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; Sequence 355, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-614-124B-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 6
US-09-671-325-355/c
; Sequence 355, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-671-325-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 7
US-09-589-184-355/c
; Sequence 355, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
```

```

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-589-184-355 (1-347)

Qy 1 PheGlnIleGluHisHis 6
Db 284 TTCCAGATCGAGCACCAC 267

RESULT 8
US-09-658-824-355/c
; Sequence 355, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-658-824-355 (1-347)

Qy 1 PheGlnIleGluHisHis 6
```

```

Db 284 TTCCAGATCGAGCACCAC 267

RESULT 9
US-09-710-279-1855/c
; Sequence 1855, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1855
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1855

Alignment Scores:
Pred. No.: 50.4 Length: 372
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-1855 (1-372)

Qy 1 PheGlnIleGluHisHis 6
Db 154 TTTCANATCGAGCACCAT 137

RESULT 10
US-09-134-001C-1672/c
; Sequence 1672, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1672
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1672

Alignment Scores:
Pred. No.: 55.5 Length: 405
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-134-001C-1672 (1-405)

Qy 1 PheGlnIleGluHisHis 6
```

```
Db 187 TTTCAATCGAGCACCAT 170
|||||
RESULT 11
US-09-439-261-38
; Sequence 38, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: k = g or t/u at position 5
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: m = a or c at position 6
US-09-439-261-38

Alignment Scores:
Pred. No.: 62.4 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-38 (1-449)
Qy 1 PheGlnIleGluHis 6
|||||
Db 248 TTCCAGATTGAGCACCAT 265
|||||

RESULT 12
US-09-227-613-37
; Sequence 37, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-37
```

```
Alignment Scores:
Pred. No.: 62.4 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-37 (1-449)
Qy 1 PheGlnIleGluHis 6
|||||
Db 248 TTCCAGATTGAGCACCAT 265
|||||

RESULT 13
US-09-439-261-37
; Sequence 37, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-37

Alignment Scores:
Pred. No.: 66.2 Length: 473
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-37 (1-473)
Qy 1 PheGlnIleGluHis 6
|||||
Db 279 TTCCAGATTGAGCACCAT 296
|||||

RESULT 14
US-09-227-613-36
; Sequence 36, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 473
```

```
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-36

Alignment Scores:
Pred. No.: 66.2 Length: 473
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-36 (1-473)

Qy 1 PheGlnIleGluHisHis 6
Db 279 TTCCAGATTGAGCACCAC 296

RESULT 15
US-09-439-261-3
; Sequence 3, Application US/09439261
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-3

Alignment Scores:
Pred. No.: 95.7 Length: 655
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-3 (1-655)

Qy 1 PheGlnIleGluHisHis 6
Db 242 TTCCAGATTGAGCACCAC 259

RESULT 16
US-09-227-613-3
; Sequence 3, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; FILE REFERENCE: 1997-04-11
```

```
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-3

Alignment Scores:
Pred. No.: 95.7 Length: 655
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-3 (1-655)

Qy 1 PheGlnIleGluHisHis 6
Db 242 TTCCAGATTGAGCACCAC 259

RESULT 17
US-09-439-261-12
; Sequence 12, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-12

Alignment Scores:
Pred. No.: 131 Length: 864
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-12 (1-864)

Qy 1 PheGlnIleGluHisHis 6
Db 670 TTCCAGATTGAGCACCAC 687

RESULT 18
US-09-227-613-13
; Sequence 13, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
```



; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 864  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-13

Alignment Scores:  
Pred. No.: 131 Length: 864  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-13 (1-864)

Qy 1 PheGlnIleGluHisHis 6  
Db 670 TTCCAGATTGAGCACCAC 687

## RESULT 19

US-09-248-796A-2259/c  
; Sequence 2259, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 2259  
; LENGTH: 876  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-2259

Alignment Scores:  
Pred. No.: 133 Length: 876  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-248-796A-2259 (1-876)

Qy 1 PheGlnIleGluHisHis 6  
Db 478 TTCCAAATTGACACCAC 461

## RESULT 20

US-09-710-279-4425  
; Sequence 4425, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3490US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4425  
; LENGTH: 1132  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-4425

Alignment Scores:  
Pred. No.: 178 Length: 1132  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-4425 (1-1132)

Qy 1 PheGlnIleGluHisHis 6  
Db 359 TTTCAAATCGAGCACCAC 376

## RESULT 21

US-09-769-863-28  
; Sequence 28, Application US/09769863  
; Patent No. 6635451  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Das, Tapas  
; APPLICANT: Thurmond, Jennifer  
; APPLICANT: Pereira, Suzette L.  
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
; FILE REFERENCE: 6763 US.O1  
; CURRENT APPLICATION NUMBER: US/09/769,863  
; CURRENT FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 1320  
; TYPE: DNA  
; ORGANISM: Thraustochytrium aureum  
US-09-769-863-28

Alignment Scores:  
Pred. No.: 212 Length: 1320  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-769-863-28 (1-1320)

Qy 1 PheGlnIleGluHisHis 6  
Db 1123 TTTCAGATCGAGCACCAC 1140

## RESULT 22

US-09-439-261-1  
; Sequence 1, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

```
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-1

Alignment Scores:
Pred. No.: 214 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-1 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
Db 1141 TTCCAGATTGACCCAT 1158

RESULT 23
US-09-227-613-1
; Sequence 1, Application US/09227613A
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-1

Alignment Scores:
Pred. No.: 214 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-1 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
Db 1141 TTCCAGATTGACCCAT 1158

RESULT 24
US-09-148-545-63
; Sequence 63, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

[illegible]

```

, EARLIER APPLICATION NUMBER: 60/047,585
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/047,586
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/047,590
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/047,594
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/047,589
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/047,593
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/047,614
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/043,578
, EARLIER FILING DATE: 1997-04-11
, EARLIER APPLICATION NUMBER: 60/043,576
, EARLIER FILING DATE: 1997-04-11
, EARLIER APPLICATION NUMBER: 60/047,501
, EARLIER FILING DATE: 1997-05-23
, EARLIER APPLICATION NUMBER: 60/043,670
, EARLIER FILING DATE: 1997-04-11
, EARLIER APPLICATION NUMBER: 60/056,632
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,664
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,876
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,881
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,909
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,875
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,862
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,887
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,908
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/048,964
, EARLIER FILING DATE: 1997-06-06
, EARLIER APPLICATION NUMBER: 60/057,650
, EARLIER FILING DATE: 1997-09-05
, EARLIER APPLICATION NUMBER: 60/056,884
, EARLIER FILING DATE: 1997-08-22
, NUMBER OF SEQ ID NOS: 280
, SEQ ID NO 63
, SEQUENCE: Patentin ver. 2.0
, LENGTH: 1478

Alignment Scores:
Pred. No.: 241 Length:
Score: 36.00 Matches:
Percent Similarity: 100.00% Conservatively
Best Local Similarity: 100.00% Mismatches:
Query Match: 100.00% Indels:
DB: 4 Gaps:

US-10-029-756-20 (1-6) x US-09-148-545-63 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCGATGATGAGACCCAC 964

RESULT 25
US-08-831-570-1
, Sequence 1, Application US/08831570
, Patent No. 5959175
, GENERAL INFORMATION:
, APPLICANT: Thomas, Terry L.
, APPLICANT: Nunberg, Andrew N.
, APPLICANT: Beremand, Philip D.

```



TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1685 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-366-779-4

Alignment Scores:  
Pred. No.: 279 Length: 1685  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x US-08-366-779-4 (1-1685)

Qy 1 PheGlnIleGluHisHis 6  
Db 1157 TTCCAATTGAGCATCAT 1174

RESULT 28

US-08-789-936-4  
; Sequence 4, Application US/08789936  
; Patent No. 5789220  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; APPLICANT: Reddy, Avutu S.  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Preyasinet, Georges L.  
; APPLICANT: Nunberg, Andrew N.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; TITLE OF INVENTION: DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 28-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; FILING DATE: 30-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 83832YXW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-08-789-936-4  
Alignment Scores:  
Pred. No.: 279 Length: 1685  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-10-029-756-20 (1-6) x US-08-789-936-4 (1-1685)  
Qy 1 PheGlnIleGluHisHis 6  
Db 1157 TTCCAATTGAGCATCAT 1174  
RESULT 29  
US-08-934-254-4  
; Sequence 4, Application US/08934254  
; Patent No. 6355861  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; TITLE OF INVENTION: DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/934,254  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 83832YXWVU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-934-254-4  
Alignment Scores:  
Pred. No.: 279 Length: 1685  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-20 (1-6) x US-08-934-254-4 (1-1685)  
Qy 1 PheGlnIleGluHisHis 6  
Db 1157 TTCCAATTGAGCATCAT 1174  
RESULT 30

US-09-685-775-4  
; Sequence 4, Application US/09685775  
; Patent No. 6683232  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING APPLICATION NUMBER: US/09/685,775  
; FILING DATE: 10-Oct-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,254  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; -- LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-685-775-4  
Alignment Scores:  
Pred. No.: 279 Length: 1685  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-685-775-4 (1-1685)  
Qy 1 PheGlnIleGluHis 6  
Db 1157 TTCACAAATTGAGCATCAT 1174  
RESULT 31  
US-09-439-261-6  
; Sequence 6, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295-US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610

; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1686  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-439-261-6  
Alignment Scores:  
Pred. No.: 279 Length: 1686  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-439-261-6 (1-1686)  
Qy 1 PheGlnIleGluHis 6  
Db 534 TTCACAGATTGAGCACCAC 551  
RESULT 32  
US-09-227-613-6  
; Sequence 6, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295-US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 1686  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-6  
Alignment Scores:  
Pred. No.: 279 Length: 1686  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-227-613-6 (1-1686)  
Qy 1 PheGlnIleGluHis 6  
Db 534 TTCACAGATTGAGCACCAC 551  
RESULT 33  
US-09-048-888-2  
; Sequence 2, Application US/09048888  
; Patent No. 6492108  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/048,888  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Certone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0494 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: ENDANOT01  
CLONE: 2451043  
US-09-048-888-2

Alignment Scores:  
Pred. No.: 285 Length: 1717  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-048-888-2 (1-1717)

Qy 1 PheGlnIleGluHisHis 6  
Db 1218 TTCCAGATCGAGCACCAC 1235

RESULT 34  
US-09-949-016-4904  
Sequence 4904, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4904  
LENGTH: 1758

TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4904

Alignment Scores:  
Pred. No.: 293 Length: 1758  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-4904 (1-1758)

Qy 1 PheGlnIleGluHisHis 6  
Db 1277 TTCCAGATCGAGCACCAC 1294

RESULT 35  
US-09-439-261-7  
Sequence 7, Application US/09439261  
Patent No. 6428990  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pradip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295 US.P2  
CURRENT APPLICATION NUMBER: US/09/439,261  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 1843  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-439-261-7

Alignment Scores:  
Pred. No.: 309 Length: 1843  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-7 (1-1843)

Qy 1 PheGlnIleGluHisHis 6  
Db 691 TTCCAGATCGAGCACCAC 708

RESULT 36  
US-09-227-613-7  
Sequence 7, Application US/09227613A  
Patent No. 6432684  
GENERAL INFORMATION:  
APPLICANT: Mukerji, Pradip  
APPLICANT: LEONARD, Amanda E.  
APPLICANT: HUANG, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295 US.P1  
CURRENT APPLICATION NUMBER: US/09/227,613A  
CURRENT FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 08/833,610  
PRIOR FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 1843  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-7

Alignment Scores: 309 Length: 1843  
Pred. No.: 36.00 Matches: 6  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 3

US-10-029-756-20 (1-6) x US-09-227-613-7 (1-1843)

Qy 1 PheGlnIleGluHis 6  
Db 691 TTCAGATTGAGCACCAC 708

RESULT 37

US-09-048-888-4

; Sequence 4, Application US/09048888

; Patent No. 6492108

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Guegler, Karl J.

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/048,888

; FILING DATE: Filed Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C.

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0494 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1928 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: BEPINOT01

; CLONE: 2056310

US-09-048-888-4

Alignment Scores:

Pred. No.: 325 Length: 1928

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-048-888-4 (1-1928)

Qy 1 PheGlnIleGluHis 6

Db 1224 TTCAGATTGAGCACCAC 1241

RESULT 38

US-09-148-545-119

; Sequence 119, Application US/09148545

; Patent No. 6590075

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 70 Human Secreted Proteins

; FILE REFERENCE: PZ001P1

; CURRENT APPLICATION NUMBER: US/09/148,545

; CURRENT FILING DATE: 1998-09-04

; EARLIER APPLICATION NUMBER: PCT/US98/04482

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,161

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,618

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,503

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,592

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,581

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,584

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,500

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,587

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,492

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,598

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,613

; EARLIER FILING DATE: 1997-05-23



; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910

; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 05-Sep-1997  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 280  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 2016

Alignment Scores:  
Pred. No.: 342 Length: 2016  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-148-545-119 (1-2016)  
Qy 1 PheGlnIleGluHisHis 6  
Db 1498 TTCCAGATCGAGCACCAC 1515  
RESULT 39  
US-09-439-261-8  
; Sequence 8, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2257  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-439-261-8  
Alignment Scores:  
Pred. No.: 389 Length: 2257  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-439-261-8 (1-2257)  
Qy 1 PheGlnIleGluHisHis 6  
Db 1105 TTCCAGATTGAGCACCAC 1122  
RESULT 40  
US-09-227-613-8  
; Sequence 8, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pardeep  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 2257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-8  
Alignment Scores:  
Pred. No.: 444 Length: 2254  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-023-655-295 (1-2540)  
Qy 1 PheGlnIleGluHisHis 6

Pred. No.: 389 Length: 2257  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-227-613-8 (1-2257)  
Qy 1 PheGlnIleGluHisHis 6  
Db 1105 TTCCAGATTGAGCACCAC 1122  
RESULT 41  
US-09-023-655-295  
; Sequence 295, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 295:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2540 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT11  
; CLONE: 1346478  
US-09-023-655-295  
Alignment Scores:  
Pred. No.: 444 Length: 2540  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-023-655-295 (1-2540)  
Qy 1 PheGlnIleGluHisHis 6

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Db      674  TTTCCAGATTGAGCACCAC 691
RESULT 42
US-09-949-016-4613
; Sequence 4613, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4613
; LENGTH: 3158
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4613
Alignment Scores:
Pred. No.:      569      Length:      3158
Score:          36.00    Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     4      Indels:      0
DB:              Gaps:      0
US-10-029-756-20 (1-6) x US-09-949-016-4613 (1-3158)
Qy      1  PheGlnIleGluHis 6
Db      1305  TTTCCAGATTGAGCACCAC 1322
RESULT 43
US-09-710-279-4180
; Sequence 4180, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4180
; LENGTH: 4103
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-4180
Alignment Scores:
Pred. No.:      765      Length:      4103
Score:          36.00    Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     4      Indels:      0
DB:              Gaps:      0
US-10-029-756-20 (1-6) x US-09-949-016-16077 (1-15595)
Qy      1  PheGlnIleGluHis 6
Db      14170  TTTCCAGATAGACATCAC 14187
RESULT 45
US-09-949-016-15109
; Sequence 15109, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15109
; LENGTH: 26684
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(26684)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15109
US-10-029-756-20 (1-6) x US-09-949-016-16077 (1-15595)
Qy      1  PheGlnIleGluHis 6
Db      14170  TTTCCAGATAGACATCAC 14187
RESULT 45
US-09-949-016-15109
; Sequence 15109, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15109
; LENGTH: 26684
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(26684)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15109
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; Sequence 16089, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16089  
; LENGTH: 175265  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(175265)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16089

Alignment Scores:  
Pred. No.: 5.31e+04 Length: 175265  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-16089 (1-175265)

Qy 1 PheGlnIleGluHisHis 6  
|||||:|||||  
Db 161293 TTTCATTTGAGCATCAT 161310

RESULT 50  
US-09-672-265-7/c  
; Sequence 7, Application US/09672265  
; Patent No. 6812019  
; GENERAL INFORMATION:  
; APPLICANT: Roche Diagnostics GmbH  
; TITLE OF INVENTION: Process for the recombinant production of holo-citrate lyase  
; FILE REFERENCE: BMID 9975 US  
; CURRENT APPLICATION NUMBER: US/09/672,265  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: DE 99119404.4  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 5593  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-672-265-7

Alignment Scores:  
Pred. No.: 1.74e+03 Length: 5593  
Score: 35.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 97.22% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-672-265-7 (1-5593)

Qy 1 PheGlnIleGluHisHis 6  
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Db 1576 TTCCAGGTCGACATCATC 1559

RESULT 51

US-09-415-522-5/c  
; Sequence 5, Application US/09415522A  
; Patent No. 6291660  
; GENERAL INFORMATION:  
; APPLICANT: Gaffney, Thomas  
; APPLICANT: Wendland, Juergen  
; APPLICANT: Philippsen, Peter  
; TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And  
; TITLE OF INVENTION: Development  
; FILE REFERENCE: CGC2046  
; CURRENT APPLICATION NUMBER: US/09/415,522A  
; CURRENT FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 6216  
; TYPE: DNA  
; ORGANISM: Ashbya gossypii  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(6216)  
US-09-415-522-5

Alignment Scores:  
Pred. No.: 1.97e+03 Length: 6216  
Score: 35.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 97.22% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-415-522-5 (1-6216)

Qy 1 PheGlnIleGluHisHis 6  
|||||:|||||

Db 3547 TTTCAGGTCGACATCAT 3530

RESULT 52

US-08-834-655-14/c  
; Sequence 14, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERT, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,655  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RAE-VENTER, BARBARA  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CGNE.124.00US

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-14

Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x US-08-834-655-14 (1-33)

Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13

RESULT 53
US-08-834-033A-22/c
; Sequence 22, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300, USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-8716
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-033A-22

Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x US-08-834-655-14 (1-33)

Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13

RESULT 54
US-09-363-574-14/c
; Sequence 14, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,574
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-363-574-14

Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-363-574-14 (1-33)

Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13
```

RESULT 55  
US-09-363-526-14/c  
; Sequence 14, Application US/09363526  
; Patent No. 6410288  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/363,526  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WARD, MICHAEL R.  
; REGISTRATION NUMBER: 38,651  
; REFERENCE/DOCKET NUMBER: CGAB-201 USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 433-4150  
; TELEFAX: (415) 433-8716  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-09-363-526-14  
Alignment Scores:  
Pred. No.: 8.37 Length: 33  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 3 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-363-526-14 (1-33)  
Oy 1 PheGlnIleGluHis 6  
Db 30 TTTCAGCTTGAGCATCAT 13  
RESULT 56  
US-09-489-039A-5096/c  
; Sequence 5096, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 5096  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-5096  
Alignment Scores:  
Pred. No.: 108 Length: 315  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-489-039A-5096 (1-315)  
Oy 1 PheGlnIleGluHis 6  
Db 31 TTTCAGCTTGAGCATCAC 14  
RESULT 57  
US-08-836-075A-3  
; Sequence 3, Application US/08836075A  
; Patent No. 6180768  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: STUYVER, LIEVEN  
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
; TITLE OF INVENTION: AGENTS  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE  
; STREET: P.O. BOX 4433  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Microsoft Word 6.0 / ASCII text output  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,075A  
; FILING DATE: 21 Apr 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/04155  
; FILING DATE: 23 Oct 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870166.9  
; FILING DATE: 21 Oct 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870076.7  
; FILING DATE: 28 Jun 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAMMERER, PATRICIA A.  
; REGISTRATION NUMBER: 29,775  
; REFERENCE/DOCKET NUMBER: INNS:004  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 447 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-08-836-075A-3  
Alignment Scores:

Pred. No.: 160 Length: 447  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 83.33%  
 Query Match: 94.44%  
 DB: 3 Indels: 0  
 Gaps: 0

US-10-029-756-20 (1-6) x US-08-836-075A-3 (1-447)

Qy 1 PheGlnIleGluHis 6  
 Db 144 TTCCAACTCGAGCATCAT 161

RESULT 58

US-08-836-075A-7  
 ; Sequence 7, Application US/08836075A  
 ; Patent No. 6180768  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAERTENS, GEERT  
 ; APPLICANT: STUTVER, LIEVEN  
 ; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
 ; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
 ; FILE REFERENCE: CL001307  
 ; NUMBER OF SEQUENCES: 207  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE  
 ; STREET: P.O. BOX 4433  
 ; CITY: HOUSTON  
 ; STATE: TEXAS  
 ; COUNTRY: USA  
 ; ZIP: 77210-4433  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Microsoft Word 6.0 / ASCII text output  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/836.075A  
 ; FILING DATE: 21 Apr 1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP95/04155  
 ; FILING DATE: 23 Oct 1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 94870166.9  
 ; FILING DATE: 21 Oct 1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95870076.7  
 ; FILING DATE: 28 Jun 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KAMMERER, PATRICIA A.  
 ; REGISTRATION NUMBER: 29,775  
 ; REFERENCE/DOCKET NUMBER: INNS:004  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 447 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-08-836-075A-7

Alignment Scores:  
 Pred. No.: 160 Length: 447  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 83.33%  
 Query Match: 94.44%  
 DB: 3 Indels: 0  
 Gaps: 0

US-10-029-756-20 (1-6) x US-08-836-075A-7 (1-447)

Qy 1 PheGlnIleGluHis 6  
 Db 144 TTCCAACTCGAGCATCAT 161

RESULT 59

US-09-949-016-202174/c  
 ; Sequence 202174, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 202174  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-202174

Alignment Scores:  
 Pred. No.: 224 Length: 601  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 83.33%  
 Query Match: 94.44%  
 DB: 4 Indels: 0  
 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-202174 (1-601)

Qy 1 PheGlnIleGluHis 6  
 Db 369 TTCCAACTCGAGCATCAT 352

RESULT 60

US-09-949-016-202175/c  
 ; Sequence 202175, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 202175  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-202175

Alignment Scores:  
 Pred. No.: 224 Length: 601  
 Score: 34.00 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 83.33%  
 Query Match: 94.44%  
 DB: 4 Indels: 0  
 Gaps: 0



Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-949-016-202175 (1-601)  
Qy 1 PheGlnIleGluHis 6  
Db 430 TTCCAACTTGAACATCAT 413

RESULT 61  
US-09-949-016-202176/c  
; Sequence 202176, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 202176  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-202176

Alignment Scores:  
Pred. No.: 224 Length: 601  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-202176 (1-601)

Qy 1 PheGlnIleGluHis 6  
Db 585 TTCCAACTTGAACATCAT 568

RESULT 62  
US-09-578-063-34/c  
; Sequence 34, Application US/09578063  
; Patent No. 6764677  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Barnes, Thomas M  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,  
; PREVENTIVE, THERAPEUTIC, AND OTHER USES  
; FILE REFERENCE: 210147.0023/6U1  
; CURRENT APPLICATION NUMBER: US/09/578,063  
; CURRENT FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-578-063-34

Alignment Scores:

Pred. No.: 567 Length: 1365  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0  
US-10-029-756-20 (1-6) x US-09-578-063-34 (1-1365)  
Qy 1 PheGlnIleGluHis 6  
Db 139 TTCACGCTTGAACCAT 122

RESULT 63  
US-08-934-254-26  
; Sequence 26, Application US/08934254  
; Patent No. 6355861  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; TITLE OF INVENTION: DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/934,254  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 83832YXWVU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1702 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 48..1406  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 48..1406  
US-08-934-254-26

Alignment Scores:  
Pred. No.: 728 Length: 1702  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-934-254-26 (1-1702)

Qy 1 PheGlnIleGluHis 6  
Db 1 PheGlnIleGluHis 6

Db 1164 TTCAGTTGGAGCACCAC 1181

RESULT 64

US-09-685-775-26

; Sequence 26, Application US/09685775

; Patent No. 6683232

; GENERAL INFORMATION:

; APPLICANT: Thomas, Terry L.

; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

; DELTA 6-DESATURASE

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: United States

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/685,775

; FILING DATE: 10-Oct-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,254

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Presser, Leopold

; REGISTRATION NUMBER: 19,827

; REFERENCE/DOCKET NUMBER: 8383ZYXWU

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1702 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 48..1406

FEATURE:

NAME/KEY: CDS

LOCATION: 48..1406

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-685-775-26

Alignment Scores:

Pred. No.: 728 Length: 1702

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-685-775-26 (1-1702)

Qy 1 PheGlnIleGluHisHis 6

Db 1164 TTCAGTTGGAGCACCAC 1181

RESULT 65

US-09-578-063-33/c

; Sequence 33, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 33

; LENGTH: 1980

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-578-063-33

Alignment Scores:

Pred. No.: 864 Length: 1980

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-578-063-33 (1-1980)

Qy 1 PheGlnIleGluHisHis 6

Db 271 TTCAGCTTGACACCAT 254

RESULT 66

US-09-489-039A-5328/c

; Sequence 5328, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 5328

; LENGTH: 2688

; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-5328

Alignment Scores:

Pred. No.: 1,22e+03 Length: 2688

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-489-039A-5328 (1-2688)

Qy 1 PheGlnIleGluHisHis 6

Db 1455 TTCAGCTTGACATCAC 1438

RESULT 67

US-08-956-171E-186

; Sequence 186, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

;;  
;; Gil H. Choi  
;; Patrick S. Dillion  
;; Craig A. Rosen  
;; Steven C. Barash  
;; Michael R. Fannon  
;;  
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
;; NUMBER OF SEQUENCES: 5256  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Key West Avenue  
;; CITY: Rockville  
;; STATE: Maryland  
;; COUNTRY: USA  
;; ZIP: 20850  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/956,171E  
;; FILING DATE: 20-Oct-1997  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/009,861  
;; FILING DATE: January 5, 1996  
;; APPLICATION NUMBER: 08/781,986  
;; FILING DATE: January 3, 1997  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mark J. Hyman  
;; REGISTRATION NUMBER: 46,789  
;; REFERENCE/DOCKET NUMBER: PB248P1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (240) 314-1224  
;; TELEFAX: (301) 309-8439  
;;  
;; INFORMATION FOR SEQ ID NO: 186:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6876 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 186:  
US-08-956-171E-186  
  
Alignment Scores:  
Pred. No.: 3.54e+03 Length: 6876  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-029-756-20 (1-6) x US-08-956-171E-186 (1-6876)  
  
Qy 1 PheGlnIleGluHisHis 6  
|||||:|||||  
Db 1425 TTCCAACTCGAACACCAT 1442  
  
RESULT 68  
US-08-781-986A-186  
; Sequence 186, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
  
Alignment Scores:  
Pred. No.: 7.2e+04 Length: 99580  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0

;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/781,986A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Benson, Bob  
;; REGISTRATION NUMBER: 30,446  
;; REFERENCE/DOCKET NUMBER: PB248PP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (301) 309-8504  
;; TELEFAX: (301) 309-8512  
;;  
;; INFORMATION FOR SEQ ID NO: 186:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6876 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;;  
;; US-08-781-986A-186  
  
Alignment Scores:  
Pred. No.: 3.54e+03 Length: 6876  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-029-756-20 (1-6) x US-08-781-986A-186 (1-6876)  
  
Qy 1 PheGlnIleGluHisHis 6  
|||||:|||||  
Db 1425 TTCCAACTCGAACACCAT 1442  
  
RESULT 69  
US-09-949-016-17411  
; Sequence 17411, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17411  
; LENGTH: 99580  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-17411  
  
Alignment Scores:  
Pred. No.: 7.2e+04 Length: 99580  
Score: 34.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 94.44% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-17411 (1-99580)

Qy 1 PheGlnIleGluHis 6

Db 92428 TTCCAACCTGGAACATCAT 92445

RESULT 70

US-09-949-016-12805/c

; Sequence 12805, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12805

; LENGTH: 421491

; TYPE: DNA

; ORGANISM: Human

; NAME/KEY: misc feature

; LOCATION: (1)...(421491)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12805

Alignment Scores:

Pred. No.: 3.47e+05 Length: 421491

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-12805 (1-421491)

Qy 1 PheGlnIleGluHis 6

Db 192589 TTCCAACCTGGAACATCAT 192572

RESULT 71

US-09-949-016-14060/c

; Sequence 14060, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14060

; LENGTH: 421494

; TYPE: DNA

; ORGANISM: Human

; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(421494)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14060

Alignment Scores:

Pred. No.: 3.47e+05 Length: 421494

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-14060 (1-421494)

Qy 1 PheGlnIleGluHis 6

Db 192589 TTCCAACCTGGAACATCAT 192572

RESULT 72

US-09-134-001C-2030/c

; Sequence 2030, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 2030

; LENGTH: 249

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2030

Alignment Scores:

Pred. No.: 133 Length: 249

Score: 33.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 91.67% Indels: 0

DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-134-001C-2030 (1-249)

Qy 1 PheGlnIleGluHis 6

Db 67 TTTCATAATACACATCATC 50

RESULT 73

US-09-248-796A-9501/c

; Sequence 9501, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 9501



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; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Euglena gracilis
US-09-857-583B-3

Alignment Scores:
Pred. No.:      848      Length:      1281
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:      91.67% Indels:      0
DB:               4      Gaps:      0

US-10-029-756-20 (1-6) x US-09-857-583B-3 (1-1281)

Qy      1 PheGlnIleGluHis 6
      ::::::::::::::::::::
Db      1079 TACCAGATCGACCAT 1096

RESULT 78
US-09-857-583B-1
; Sequence 1, Application US/09857583B
; Patent No. 6825017
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browse, John A
; APPLICANT: Wallis, James G
; APPLICANT: Watts, Jennifer L.
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 4630-58963
; CURRENT APPLICATION NUMBER: US/09/857,583B
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-857-583B-1

Alignment Scores:
Pred. No.:      984      Length:      1461
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:      91.67% Indels:      0
DB:               4      Gaps:      0

US-10-029-756-20 (1-6) x US-09-857-583B-1 (1-1461)

Qy      1 PheGlnIleGluHis 6
      ::::::::::::::::::::
Db      1189 TACCAGATTGACCAT 1206

RESULT 79
US-08-834-655-1
; Sequence 1, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
```

```
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Alignment Scores:
Pred. No.:      11e+03    Length:      1617
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:      91.67% Indels:      0
DB:               2      Gaps:      0

US-10-029-756-20 (1-6) x US-08-834-655-1 (1-1617)

Qy      1 PheGlnIleGluHis 6
      ::::::::::::::::::::
Db      1250 TATCAGATCGACCAT 1267

RESULT 80
US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
```

ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,033A  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-300.USA  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-834-033A-1

Alignment Scores:  
Pred. No.: 1,1e+03 Length: 1617  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-834-033A-1 (1-1617)

QY 1 PheGlnIleGluHis 6  
:::|||||

Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 81  
US-09-363-574-1  
Sequence 1, Application US/09363574  
Patent No. 6136574  
GENERAL INFORMATION:  
APPLICANT: KNUTZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,574  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-202 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-09-363-574-1

Alignment Scores:  
Pred. No.: 1,1e+03 Length: 1617  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-363-574-1 (1-1617)

QY 1 PheGlnIleGluHis 6  
:::|||||

Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 82  
US-09-363-526-1  
Sequence 1, Application US/09363526  
Patent No. 6410288  
GENERAL INFORMATION:  
APPLICANT: KNUTZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-09-363-526-1

Alignment Scores:  
Pred. No.: 1.1e+03 Length: 1617  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-363-526-1 (1-1617)

Qy 1 PheGlnIleGluHis 6  
:::|||||  
Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 83  
US-09-330-235-17  
; Sequence 17, Application US/09330235  
; Patent No. 6459018  
; GENERAL INFORMATION:  
; APPLICANT: Knutson, Debbie  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
; FILE REFERENCE: MOCO.156.00US  
; CURRENT APPLICATION NUMBER: US/09/330,235  
; CURRENT FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: 60/089,043  
; PRIOR FILING DATE: 1998-06-12  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Mortierella alpina  
US-09-330-235-17

Alignment Scores:  
Pred. No.: 1.1e+03 Length: 1617  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-330-235-17 (1-1617)

Qy 1 PheGlnIleGluHis 6  
:::|||||  
Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 84  
US-09-710-279-1595/c  
; Sequence 1595, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1595  
; LENGTH: 1980  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-1595

Alignment Scores:

Pred. No.: 1.39e+03 Length: 1980  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-1595 (1-1980)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 622 TTTCAAATTGATCACCAT 605

RESULT 85  
US-09-134-001C-2101/c  
; Sequence 2101, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 2101  
; LENGTH: 2073  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-2101

Alignment Scores:  
Pred. No.: 1.46e+03 Length: 2073  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-134-001C-2101 (1-2073)

Qy 1 PheGlnIleGluHis 6  
|||||  
Db 715 TTTCAAATTGATCACCAT 698

RESULT 86  
US-09-710-279-4299  
; Sequence 4299, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4299  
; LENGTH: 3004  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-4299

Alignment Scores:



Pred. No.: 2.23e+03 Length: 3004  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-4299 (1-3004)

Qy 1 PheGlnIleGluHis 6  
Db 183 TTTCATATGATCACCAT 200

## RESULT 87

US-09-710-279-3717/c  
; Sequence 3717, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3717  
; LENGTH: 3177  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-3717

Alignment Scores:  
Pred. No.: 2.37e+03 Length: 3177  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-3717 (1-3177)

Qy 1 PheGlnIleGluHis 6  
Db 864 TTTCATATGATCACCAT 847

## RESULT 88

US-09-710-279-3649/c  
; Sequence 3649, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3649  
; LENGTH: 3320  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-3649

Alignment Scores:  
Pred. No.: 2.49e+03 Length: 3320  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-3649 (1-3320)

Qy 1 PheGlnIleGluHis 6  
Db 2542 TTTCATATGATCACCAT 2525

## RESULT 89

US-09-016-434-1363  
; Sequence 1363, Application US/09016434  
; Patent No. 8500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1363:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9425220  
; US-09-016-434-1363

Alignment Scores:  
Pred. No.: 2.61e+03 Length: 3459  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-016-434-1363 (1-3459)

Qy 1 PheGlnIleGluHis 6



;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
;; NUMBER OF SEQUENCES: 5255  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Key West Avenue  
;; CITY: Rockville  
;; STATE: Maryland  
;; COUNTRY: USA  
;; ZIP: 20850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/781,986A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Benson, Bob  
;; REGISTRATION NUMBER: 30,446  
;; REFERENCE/DOCKET NUMBER: PB248PP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (301) 309-8504  
;; TELEFAX: (301) 309-8512  
;; INFORMATION FOR SEQ ID NO: 102:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15249 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
US-08-781-986A-102

Alignment Scores:  
Pred. No.: 1.4e+04 Length: 15249  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-08-781-986A-102 (1-15249)

Qy 1 PheGlnIleGluHis 6  
Db 10238 TATCAATAGACCAACCAC 10255

RESULT 94  
US-09-949-016-16231  
; Sequence 16231, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16231  
; LENGTH: 30053  
; TYPE: DNA  
; ORGANISM: Human

US-09-949-016-16231

Alignment Scores:  
Pred. No.: 3e+04 Length: 30053  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-16231 (1-30053)

Qy 1 PheGlnIleGluHis 6  
Db 12299 TTTCAGATTGACCACCAC 12316

RESULT 95  
US-08-920-422-17  
; Sequence 17, Application US/08920422A  
; Patent No. 6255473  
; GENERAL INFORMATION:  
; APPLICANT: Vitek, Michael P.  
; APPLICANT: Mitsuda, No. 6255473iaki  
; APPLICANT: Roses, Allen D.  
; TITLE OF INVENTION: Presenilin-1 Gene Promoter  
; FILE REFERENCE: VITEKPRESENTLIN  
; CURRENT APPLICATION NUMBER: US/08/920,422A  
; CURRENT FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 48974  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-08-920-422-17

Alignment Scores:  
Pred. No.: 5.2e+04 Length: 48974  
Score: 33.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 91.67% Indels: 0  
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-920-422-17 (1-48974)

Qy 1 PheGlnIleGluHis 6  
Db 1500 TTTCAGATACCAACCACAT 1517

RESULT 96  
US-09-949-016-14094  
; Sequence 14094, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14094  
; LENGTH: 69752  
; TYPE: DNA  
; ORGANISM: Human

```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(69752)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14094

Alignment Scores:
Pred. No.: 7.71e+04 Length: 69752
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-14094 (1-69752)
Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 68492 TTTCAGATTGATCATCAT 68509

RESULT 97
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Alignment Scores:
Pred. No.: 9.36e+05 Length: 767677
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-12147 (1-767677)
Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 22102 TTTCAGATTGATCATCAT 22085

RESULT 98
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Alignment Scores:
Pred. No.: 9.36e+05 Length: 767677
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-17361 (1-767677)
Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 22102 TTTCAGATTGATCATCAT 22085

RESULT 99
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Alignment Scores:
Pred. No.: 9.55e+05 Length: 786431
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-751-389-3 (1-786431)
Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 665664 TTTCAGATTGATCATCAT 665681

RESULT 100
US-08-916-421B-1/c
```

```
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 1664976
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
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; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
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; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
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; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
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; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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Alignment Scores:
Pred. No.: 1.67e+06 Length: 1664976
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0
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US-10-029-756-20 (1-6) x US-08-916-421B-1 (1-1664976)

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Oy 1 PheGlnIleGluHisHis 6
Db 1586301 TTCCARATACACACCAT 1586284
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Search completed: June 8, 2005, 15:36:06  
Job time : 493.579 secs